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A; Molecule type: mRNA
A; Residues: 27-81,'L',83-103 <RYA2>
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A; Accession: S04892
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C; Species: Homo sapiens (man)
C; Date: 28-May-1986 #sequence_revision 01-Sep-1995 #text_change 08-Dec-2000
C; Accession: A38513; S06715; S24270; A24828; S06496; A35428; A30147; A33116; S64674; S63
7250; I37251; I37252; I37253; I37254; I55338; I59535; I61910
R; Ryan, M.C.; Sieraski, M.; Sandell, L.J.
Genomics 8, 41-48, 1990
A; Title: The human type II procollagen gene: identification of an additional protein-cod A; Reference number: A38513; MUID:91184811; PMID:2081599
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R;Su, M.W.; Lee, B.; Ramirez, F.; Machado, M.; Horton, W.
Nucleic Acids Res. 17, 9473, 1989
A;Title: Nucleotide sequence of the full length cDNA encoding for human type II procolla
A;Reference number: S06715; MUID:90067946; PMID:2587267
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A; Residues: 1-28, fk', 99-1487 <502>
A; Cross-references: EMBL:X16468; NID:929515; PIDN:CAA34488.1; PID:929516
A; Note: alternative splice form 1
R; Vikkula, M.; Metsaeranta, M.; Syvaenen, A.C.; Ala-Kokko, L.; Vuorio, E.; Peltonen, L.
Biochem. J. 285, 287-284, 1992
A; Title: Structural analysis of the regulatory elements of the type-II procollagen gene.
A; Reference number: S24270; MUID:92344585; PMID:1637314
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A;Residues: 7-28, 'R',99-157,'P',159-440,'G',442-456,'E',458-640,'A',642-831,'PA',834,'F'
A;Cross-references: EMBL:X16711; NID:930040; PIDN:CAA34683.1; PID:930041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collagen alpha 1(II) chain precursor [validated] - human
N'Alternate names: procollagen alpha 1(II) chain
N'Contains: chondrocalcin; collagen alpha 1(II) chain precursor splice form 1; collagen
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A;Note: this translation is not annotated in GenBank entry HSPROCOE1, release 111.0
R;Nunez, A.M.; Kohno, K.; Martin, G.R.; Yamada, Y.
A;Nunez, A.M.; Kohno, K.; Martin, G.R.; Yamada, Y.
A;Title: Promoter region of the human pro-alpha-1-(II)-collagen gene.
A;Reference number: A24828; MUID:87031574; PMID:3021582
                                                                                                                                                                                                                                                                                    ---As 1195
                                                                                                                                                       --GlyLeuArgProHisAspGl 1184
                                                                                                                                                                                                                                                                                                                                                                                                              1195 nGlnIleGluSerIleArgSer-ProGluGlySerArgLysAsnPro---AlaArgThrC 1214
                             -- 1177
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                                                                                                                                                                                                                      ------GTTCTCAGCCCATGCTCAACACCTGCTGTGGGGGCACCTCAGTGGGG
                                                                                        176 GCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCA
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pProLeuGlnTyrMetArgAlaAspGluAlaAlaGly
                                                                                                                                                                                                                                                                                 1184 uGluValGluAlaThrLeuLysSerLeuAsn----
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A; Residues: 1-28 <VIK>
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A;Title: Organization of the exons coding for Pro alpha-1(II) collagen N-propeptide c A;Reference number: A30147; MUID:89233138; PMID:2714801
A;Accession: A30147
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A; Residues: 171-172, CC, ,174-175 <ALA>
A; Note: mutant sequence from a family with family with primary generalized osteoarthr
R; Diab, M.; Wu, J.J.; Eyre, D.R.
Biochem J. 314, 327-332, 1996
A; Title: Collagen type IX from human cartilage: a structural profile of intermolecula
A; Reference number: $64673; MUID:96195147; PMID:8660302
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A, Residues: 243-261;575-590;756-763, 'X', 765-779 <FRA>
R;Tiller, G.E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; By Am. J. Hum. Genet. 56, 388-395, 1995
A;Title: An RNA-splicing mutation (G+51VS20) in the type II collagen gene (COL2A1) in A; Reference number: 138867; MUID:95150028; PMID:7847372
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A; Residues: 630-640, A', 642-785 < VIK2>

A; Cross-references: EMBL:X16158; NID:929951; PIDN:CAA34278.1; PID:91335018; PIDN:CAA3

A; Cross-references: EMBL:X16158; NID:929951; PIDN:CAA34284.1; PID:91335024

B; Bogaert, R.; Tiller G.E.; Wels, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre

B; Bogaert, R.; Tiller G.E.; Wels, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre

A; Fitle: An amino acid substitution (Gly855-->Glu) in the collagen alpha 1(II) chain

A; Reference number: A44309; MuID:93054548; PMID:1429602

A; Accession: A44309
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A;Residues: 188-189, 'X', 191-195,1224-1230, 'X', 1232-1236 <DIA>
R;Rismoc, S.; Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbag
Eur. J. Blochem. 234, 125-131, 1995
A;Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil
A;Reference number: S63514; MUID:96096730; PMID:8529631
                                                              cysteine-rich domain in the amino-terminal prop
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                                                                                                                                                                                                                                                                                                                                                                                                be under developmental regulat
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A, Residues: 104-157, Pr. 159-236 <SUM>
A, Cross-references: GB:J03065; GB:M23660; GB:M25655; GB:M25656; GB:M25730; GB:M32168; R, Ala-Kokko, L.; Baldwin, C.T.; Moskowitz, R.W.; Prockop, D.J.
Proc. Natl. Acad. Sci. U.S.A. 87, 6565-6568, 1990

A, 71tle: Single base mutation in the type II procollagen gene (COL2A1) as a cause of A, Reference number: A94227; MUID:90370826; PMID:1975693
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A;Molecule type: DNA
A;Residues: 440,'G',442-456,'E',458-480,'P',482-509 <TILl>
A;Cross-references: EMBL:U15195; NID:9557053; PIDN:AAB60370.1; PID:9557054
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A; Residues: 501-676, A', 678-783, A', 785-831, 'PA', 834, 'F', 836-1214 <RAM>
A; Cross-references: EMBL: X13783; NID:930037; PIDN: CAA32030.1; PID:9930050
R; Vikkula, M.; Peltonen, L.
FEBS Lett. 250, 171-174, 1989
J. Biol. Chem. 265, 10334-10339, 1990
A;Title: Differential expression of a cysteine-rich dome
A;Reference number: A35428; MUID:90285153; PMID:2355003
A;Accession: A35428
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R;Su, M.W.; Benson-Chanda, V.; Vissing, H.; Ramirez, F.
Genomics 4, 438-441, 1989
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 541-560 <SAN3>
A;Cross-references: EMBL:X02378; GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
A;Accession: I37251
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Mismatches:
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A; Note: this translation is not annotated and this publication is not cited in GenBank e Note: untant sequence associated with perinatal lethal hypochondrogenesis R; Tiller, G.E.; Rimoin, D.L.; Murray, L.W.; Cohn, D.H.
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A; Title: Tandem duplication within a type II collagen gene (COLZAI) exon in an individua A; Reference number: $16502; MUID: 90251662; PMID: 2339128
                                                                                                                                                                                                                                                                         A.Cross-references: EMBL:M37126; NID:9180808; PIDN:AAA52037.1; PID:9180809
A.Note: mutant sequence from a patient with spondyloepiphyseal dysplasia
R.Cheah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveld, F.G.; Solomon, E.
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A.Title: Identification and characterization of the human type II collagen gene (COLZAI)
A.Reference number: A02858; MUID:85190534; PMID:3857598
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A; Residues: 1296-1358 <NUN2>
A; Residues: 1296-1358 <NUN2>
A; Cross: references: 68 MI2048; NID:9180017

A; Cross: references: 68 MI2048; NID:9180017

A; Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0

A; Note: the codons given for 1333-Lys (AGG) and 1350-Gly (GCA) are inconsistent with the R; Sangiorgi, F.O.; Benson-Chanda, V.; de Wet, W.J.; Sobel, M.E.; Tsipouras, P.; Ramirez, Mucleic Acids Res. 13, 2207-2225, 1985

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R,Strom, C.M.; Upholt, W.B.
Nucleic Acids Res. 12, 1025-1038, 1984
A;Title: Isolation and characterization of genomic clones corresponding to the human typ
A;Reference number: A21733; MUID:84118798; PMID:6320112
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A;Residues: 1245-1295 <STR1>
A;Cross-references: EMBL:X00339; EMBL:X00298; NID:g394699; PIDN:CAA25092.1; PID:g4378975
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A;Residues: 7-28;'R',99-114;541-578;786-802;1055-1056,'N',1058-1068,'T',1070-1109;1200-1
A;Accession: 184453
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A; Residues: 1032-1056, N', 1058-1068, T', 1070-1487 <CHE>
A; Cross-references: GB: J00116; NID: 9180395; PIDN: AAA51997.1; PID: 9180396
A; Elima, K.; Vuorio, T.; Vuorio, E.; Vuorio, E.; Vuorio, E.; Vuorio, E.; Vuorio, E.; Vuorio, E.; A199-2564, 1987
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A; Reference number: A27280; MUID: 88067771; PMID: 2825137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 'XE', 1244-1246,'N', 1248,'X', 1250-1265;1295-1305;1395-1408 <VAN>
A; Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: fetal epiphyseal cartilage
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A; Title: Chondrocalcin is identical with the C-propeptide of type II procollagen.
A; Reference number: A57033; MUID:87099927; PMID:3800925
A; Accession: A57033
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A;Note: the GenBank PID is based on an incorrect reading frame
A;Accession: 137250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:X06268; NID:g30096; PIDN:CAA29604.1; PID:g30097
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A;Residues: 1164-1184,'GPSGKDGANGIPGPI',1185-1199 <TIL2>
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A; Molecule type: DNA
A; Residues: 894-909, 'PE' <STR2>
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:Molecule type: DNA; mRNA
:Residues: 1175-1487 <ELI>
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A: Residues: 7-28 <SAN2>
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186

521 829 541 775 561 715 580 665	Qy 619 CAGCCCTGCTAGCCGGCCGGCCC Db 617 laGly Qy 563AGGACAGTGCCCAGATGAGG Qy 503 euArgGlyLeubro Qy 505 GGCTGAGCCTAGGAGCGGACAC Qy 505 GGCTGAGCCTAGGAGCGGACAC Db 635 spGlyGluThrGlyAlaGluGly Qy 466 TGGACCAATGCCCAGCACCATGG Qy 466 TGGACCAATGCCCAGCACCATGG Qy 406 AGGCGGCCACATAGCTGIYPro Qy 406 AGGCGGCCACATAGGTGATGCCTG Qy 670	Qy 175 CCTAGGAATCAGCCAGGCGCCCCP 11 ::: 111 10 ::: 111 11 ::: 111 0y 133GCCGGTCCAGCTTCTCAGC 0y 10 10 1111 11 11 10 772 G1uLysG1yProG1uG1yAlaPa 10 792 G1y-ProProG1yProG1aG1yAlaPa 0y 48CGAGGCGCGCGC 0y 48CGAGGCGCGCGCGCG 0y 48CGAGGCGCGCGCGCG 0y 48CGAGGCGCGCGCGCG 0y 48
214 ProbladlyalaProGlyPheGlnGlyAsnProGlyGluProGlyGlu 232 1742 CCCGGCCCGGAACCACCTGGTGGGGGCTCACCCACCACCACCGTACG 1690 1743 CCCGGCCCGGAACCACCTGGTGGGGGCTCACCACCACCACACGTACG 1690 233 ProGlyValSerGlyProMetGlyProArgGlyProProGlyProProGlyLysProGly 252 1689 GAGACATCACAGGCAGAGCCCCCGCAGAGCGCGGGGGGGG	ACCCTCCTCCCCGTGGTAGAGGGAGGCCAGTGTGTAGGGCCAGGATCTGC	CGACA
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TCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTG 176
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rgGlyAlaAlaGlyIleAlaGlyProLySGlyAspArgGlyAspValGly 771
                                                                                                                                         620
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|GlyalaGluGlyProProGlyProAlaGlyProAlaGlyGluArgGlyG 655
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                                                                                                                                                                                                                                                                                                             PheProGly------ProLysGlyAlaAsnGlyGluProGlyLysA 617
                                                                                                                                                                                                                                                                                                                                                                                  ------GluLysGlyLeuProGlyAlaProGlyL 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAGGGGACACAGACCAGGCCCAGCA-------C 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCCAGCACCATGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'AGGTGATGCCTGCGGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTT 347
GlyProLysGlyAlaProGlyGluArgGlyProSerGlyLeuAlaGlyP 541
                                    GCAGGA-----GGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGC 776
                                                               SCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACTCAGATCCTGGC-- 49
                                                                                                                                                                                                                                                                          ---CCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAG
                                                                                                                                                                                                                                                                                                                                                    GCCAGCCGGCCCTTGGGATGAGAAGGGCTCAGCAGGATGCCCA----
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955 CCCCACCGAGCAGAGGCTGTCGCCCCCTTGTCGCCCCATGCTGCTGCTGTG 1014 :::	308 arrpproepropheteuLeuPneAspThrAspTrpMetGlyLysGluValTyrGlyTh 1195 GCCAGAGCTGAGCCGGGCACCGAGACACTATGATGAAGGCGTTCGGATGGG :::	342 1315 362	1369 382 1429	Db 395 aGlu	Qy 1549 CAGTGAGGACAGCCTGATGACCAGGCCCTAAGCCTGGAGCTCCTTCCC 1608 Db 405		1753 GES 1753 GGA 1754 LSE 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Qy 1796	RESULT 22 843142 sucrose transport protein - castor bean N.Alternate names: sucrose carrier
N'Alternate names: sucrose carrier protein; sucrose permease C;Species: Spinacia oleracea (spinach) C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jul-2000 C;Accession: S28052 R;Resmeier, J.W.; Willmitzer, L.; Frommer, W.B. EMBO J. 11, 4705-4713, 1992 A;Title: Isolation and characterization of a sucrose carrier cDNA from spinach by functinaterence number: S28052; MUID:93099843; PMID:1464305 A;Reference number: S28052 A;Residues: 1-525 ARIE> A;Residues: 1-525 ARIE> A;Cross-references: EMBL:X67125; NID:921318; PIDN:CAA47604.1; PID:921319 C;Superfamily: common tobacco sucrose transport protein C;Reywords: transmembrane protein	Alignment Scores: 3.32e-12	US-09-759-143-110 (1-3410) x S28052 (1-525) QY 310 CCTGCGGGACGGGAAAGCCCAGCTCTTGCTGGTCAACCTTTGGCCTGGA 369	370 GGTGTGTTTGGCCGCAGCCATCACCTAT	61 oTyrvalGlnLeuGlylleProHisThrTrpAlaAlaTyrIleTrpLeuCysGlyPr 81 466 AGTGCTGGTCTGTCTCCCGCTCCACCACACACACACACAC	GCCGCCGCCCTTCATCTGGCACTGTCTTGGGCATCTGTGAGCCTCTT	121 YLGUILGGIYPREALAAASPIIGGLYALAALASEGGIYASPPIOThrG1 138 635AGGCCCTGGAGCTGCCACTGCTCATCCTGGCCGTGGGGCTGCTGGACTT 684 1::	685 CTGTGGCCAGGTGCTTCACTCCACTGGAGGCCCTGCTCTGACCTCTCCGGGA 741 158 lalaasnAsnThrLeuGlnGlyProCysArgalaLeuLeuAlaaspMetalaAlaGlySe 178 742 CCCGGACCACTGTCGCCAGGCCTACTGTCTATGCCTTCATGATCAGTCTTGGGGGCTG 801 178 rGlnThrLvsThrActVrAlaasnAlaPhaPhaPhaPhaPhaPhaPhaPhaPhaPhaPhaPhaPha	CCTGGGCTACCTCCTGCCATTGACTGGGACAC eGlyGlyTyralaAlaGlySerTyrSerArgLeuTyrThrValPheProPheThrLysTh CAGTGCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACC	-CTCATCTTCCTCACCTGCTAGCAGCCACCCCTGGTGCTGAGGAGGCAGCGCTGGG

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221 ysAspValTyrCysAlaAsnLeuLysSerCysPhePheIleSerIleValLeuLeuLeuS 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||:::|||
201 yrAlaAlaGlyAlaTyrThrHisLeuTyrLysLeuPheProPheThrLysThrThrAlaC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       846 TGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCTTCC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           906 TCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCCACCGAGC 965
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                                                                                                                                                                                                                                                                                                                                                                                                                           231 AGCAGITCIGGAGIGCCIGAACGGCCCCCT-----GAGCCCIACCCGCCIGGCCCACIA 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 MetValAlaGly-AlaAlaGlu---ProAsnSerSerPro-LeuArgLysValValMetV 41
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-May-2000 C;Accession: S43142
R;Weig, A; Komor, E.
submitted to the EMBL Data Library, March 1994
A;Description: A sucrose carrier from Ricinus communis.
A;Reference number: S43142
A;Accession: S43142
A;Accession: S43142
A;Accession: S43142
A;Accession: J-33-AWEI-
A;Accession: S43142
A;Accession: S43142
A;Accession: S43142
A;Accession: S43142
A;Accession: J-33-AWEI-
A;Cross-references: EWBL: Z31561; NID:9468561; PID:9468562
C;Superfamily: common tobacco sucrose transport protein
                                                                                                                                                                                                                                                               533
147
102
236
126
22
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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Figor-125/region: mella ttachment (R-G-D) motif
Figor-125/region: cell attachment (R-G-D) motif
Figor-1943/Region: cell attachment (R-G-D) motif
Figor-106/Region: cell attachment (R-G-D) motif
Filogr-106/Region: cell attachment (R-G-D) motif
Filogr-106/Region: cell attachment (R-G-D) motif
Filogr-105/Region: cell attachment (R-G-D) motified site: carbohydrate (Asn) (covalent) #status predicted
Filogr-105/Loleavage site: carbohydrate (Asn) (covalent) #status predicted
Filogr-105/Loleavage site: sarbohydrate (Asn) (covalent) #status predicted
Filogr-105/Loleavage site: sarbohydrate (Asn) (covalent) #status predicted
Filogr-105/Loleavage site: sarbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                     A;Cross-references: GB:J03051; NID:g179695; PIDN:AAA51858.1; PID:g179696
A;Note: the authors translated the codon GAA for residue 1460 as Gln, and GAG for res
C;Comment: Prolines and lysines at the third position of the tripeptide repeating uni
are 5-hydroxylated and subsequently 0-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 2q31-2q31 A;Ms48/3; 884/3; 902/3; 922/3; 974/3; 1046/3; 1064/3; 144 A;Introns: 33/1; 812/3; 830/3; 848/3; 884/3; 902/3; 922/3; 974/3; 1046/3; 1064/3; 144 C;Complex: type V collagen may be a homotrimer of alpha 1(V) chains (see PIR:CGHUIV), alpha 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among ength, is formed with desmosine cross-links made from lysine and allysine residues
                                                                                                                                                                                                                                                                                                                                                                                  Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
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                                         A; Molecule type: DNA
A; Residues: 1449-1463,'E',1465-1495,'A'
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Best Local Similarity:
A; Accession: A30017
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A. Residues: 1007-1226 <RE2>
A. Cross-references: GBM.10956; NID:q180427; PIDN:AAA52007.1; PID:q180428
A. Cross-references: GBM.10956; NID:q180427; PIDN:AAA52007.1; PID:g180428
A. Note: part of this sequence were determined by protein sequencing
A. Note: part of this sequence were determined by protein sequencing
A. Matl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A. Title: Human alpha 1(III) and alpha 2(V) Protocollagen genes are located on the long arm
A. Reference number: 159025, MUID:85216505; PMID:3858826
A. Status: translated from GB/EMBL/DDBJ
A. Molecule type: mRNA
A. Residues: GB.M11135; NID:q179693; PIDN:AA51887.1; PID:q179694
A. Note: part of this sequence were determined by protein sequencing
B. Myers: J.C.: Loidl. H. R. S. Seyer. J. M.: Dion, A.S.
J. Blod. Chem. 260, 11216-11222, 1988
A. Fille: Complete primary structure of the human alpha-2 type V procollagen COOH-termina
A. Reference number: A25374; MUID:85289337; PMID:2411731
                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Date: 31-Jul-1989 #sequence_revision 28-Jul-1995 #text_change 31-Dec-2000
C; Date: 31-Jul-1989 #sequence_revision 28-Jul-1995 #text_change 31-Dec-2000
C; Accession: A31427; A5455; S43643; A25874; I55239; I59025; A25374; A30017
R; Woodbury, D.; Benson-Chanda, V.; Ramirez, F.
J. Biol. Chem. 264, 2735-2738, 1989
A; Title: Amino-terminal propeptide of human pro-alpha2(V) collagen conforms to the struct A; Reference number: A31427; MUID:89123368; PMID:2914927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Cross-references: GB:J04478; NID:g179697; PIDN:AAA51859.1; PID:g179698
A)Experimental source: placenta
R;Greenspan, D.S.; Lee, S.T.; Lee, B.S.; Hoffman, G.G.
Gene Expr. 1, 29-39, 1991
A;Title: Homology between alpha2(V) and alpha1(III) collagen promoters and evidence for A;Reference number: A54555; MUID:92314691; PMID:1820205
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R;Moradi-Ameli, M.; Rousseau, J.C.; Kleman, J.P.; Champliaud, M.F.; Boutillon, M.M.; Ber
Ber J. Blochen. 221, 987-995, 1994
A)Title: Diversity in the processing events at the N-terminus of type-V collagen.
A;Reference number: S43642; MUID:94237164; PMID:8181482
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A; Residues: 288-291, P', 293-294, X', 296-297; 606, X', 608-617 <MOR>
A; Residues: 288-291, P', 293-294, X', 296-297; 606, X', 608-617 <MOR>
R; Well, D.; Bernard, M; Gargano, S.; Ramirez, F.
Nucleic Acids Res. 15, 181-198, 1987
A; Title: The pro alpha 2(V) collagen gene is evolutionarily related to the major fibrill
A; Reference number: A25874; MUID:87146331; PMID:3029669
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A.Residues: 1227-1417, T',1419-1437, S',1439-1496 <MYE>
A.Residues: 1227-1417, T',1419-1437, S',1439-1496 <MYE>
A.Gross-references: GB.M11718; NID:g180912; PIDN:AAA52058.1; PID:g180913
A.Experimental source: normal fibroblasts
R.Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F.
Genomics 3, 275-277, 1988
A.Title: Genetic distance of two fibrillar collagen loci, COL3A1 and COL5A2, located on A;Reference number: A30017; MUID:89138450; PMID:3224983
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R;Myers, J.C.; Loidl, H.R.; Stolle, C.A.; Seyer, J.M.
J. Biol. Chem. 260, 5533-5541, 1985
A;Title: Partial covalent structure of the human alpha 2 type V collagen chain.
A;Reference number: I55239; MUID:85182703; PMID:2985598
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                                                                                                                             collagen alpha 2(V) chain precursor - human
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A; Residues: 1-463 <WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-32 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A54555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A31427
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785 GluGlyThrAlaGlyAsnAs 1019 CCCGGCATGGACAGCAGTGG	Db Qy	ZUU3 GAGCGGGGGGTGGGGACCCAGTGAGGCGGCCCCCCCCCC	à d
9/	qa		a a
1139 TGAGTGCCATCCAGCTGCAC	Qy	0 4 0 4 4 m 0 0 0 0 0 m 4 0 0 0 0 0 0 0	À
763 GluArgGlyIleAlaGlyTh	qa		2 €
1184 ACAGC	QY		1 8
743 ProGlyProSerGlyThrPr	. qa	ZIOO CCICCAGICAGGCAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	දී සි
1214	ΟŻ	Tree interpretation	3 8
723 GlyLeuProGlyGluLysGl	qa	### A VSerAlaGlyPoproGlyCarproGlyProGlnGlySerThrGlyProGlnGly 462	3 A
1259 GGCTGCCCATCCGAACGC	Qy	ODER COMMUNICAR ENTRY TO THE CONTRACT OF THE C	Š
 704 LeuGlyProArgGlyGluAr	qa	2288 ACTAGGAGGCTAGCTGTAACCCTGAGCTAATCCACCTGCAGTTCCCCGCATTC 2229	Š €
1316 GCCGGTCCATGACCAGAGAG	Qy		QQ Q
GlyAspGlnGl	: <u>6</u>	GACTGAGTTTATCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCTCA 	δy
1364CTGCCACA	Qy	Thras	a a
674 GlnGlyHi	7 q	CCTAGAAACTCCCATGCAAGGTACATTAAACGAAGCTGCAGGTTAAGGGGCTTAGAGA	Οy
**************************************	ö	419 oGlyAlaIleGly 423	Q O
655 ProProGlyLeuArg-GlyG	ි සි	2468 CTCAGGACTCTTCCCCTACAAATAAGTCATATGTTCAAATCCCATGGAGGAGTGTTTCAT 2409	οy
1463 momentocomentalists	a ä	399 yProGlnGlyGlnArgGlyGluThrGlyProProGlyProValGlySerProGlyLeuPr 419	qq
	oy 1	2528 GGTGGATCAGCAAAAAGACAGTGCTGGGCTGAGGGGACCTGGTTCTTGTGTGTTGCCC 2469	Οy
	qa	:::	qq
1553 CACTGCTAGCACCTCCAGTG	QY	TGTCTCTGTGATGGCAACAGAAGGACCAACAGGCCACACATGAAAAGGTAAAGGGGG	ò
604 leLysGlyGlnProGlyThr	qa	s:::	qq
1605 AAGGGAGCTCCAGGC	QY	AATGGATTCCCTTCTACTTTGTTAAATAAATAAGTTAAATATTTAAATGCCTG	Οy
587 u-GlyAlaProGlyGluAsp	qa	 354 yGlnArgGlyAlaHisGlyMetProGlyLySProGlyProMetGlyProLeuGlyIlePr 374	qq
	Ολ	2669 TATTAGACACCAACACAGAA 2649	δy
	qa		q
1721 CCTCGGTGGGCTCACCACC	QY	AGCCCAATGACCAGCTATCTCAGGGGACCTGATTGTTGGGGATCCCCCACCCTACCCAAA	δ
555 Gly	qq	rGlyProMetGlyAlaMetGlyProLeuGlyProArgGlyMet	: <u>8</u>
1781 GGAAGGCACTATCCAGGATG	Qy	CACCCAGGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	ò
535 oLysGlyAlaGlnGlyGluA	qq		7 A
1834GCTGAGCTGGACA	Qy		2
:::::: 516 -GlyGluArgGlyAlaProG	qa	2004 ICLACCTICCTICAMCACCCTGGGTAACAGCATTTGGAATTATCATTTGGGAIG 2805	3 5
1886 TGGCGACCAGACCCAGGCCT	Qy		g (
111 513GlyP	g qa	AAGAGGGGTGGTTAGGGAAGCCGTTGAGACCTGAAGCCCCACCC	δi
1946 TCTACGCTGAGTATTGGCC	λĊ		

>-	1946	TACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAA 1	887
Ф	513	5	15
م ہ	1886	TGGCGACCAGCCCAGCCCTGCGGCAGACACCATATAGGCAGTGACAGACTG 18	835
	1834		7
۵	535	S	4
2 ~	1781	GGAAGGCACTATCCAGGATGGCGAGGTCCAGGCAGATGCCCGGGCCCGGAACCACCCTGG 17	1722
a >-	0		1665
. ۵	567		587
د .<	1664	AGAGCGCGGGTGGAGGGGGAGCACTGCCTCCAGCACCCACGTGTCCATTAGGG-16	1606
o >-	1605		1554
Ω	604	:::	23
>-	1553	CACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCT 15	1500
Q	624	ProGlyGluAlaGlyAsnProGlyVal	634
ъ Q	1499	CCAGTGTGTAGGGCAGGA LysValGlyProTyrGlyProProGly	1464 654
>-	1463		1404
Q	655	ProProGlyLeuArg-GlyGluArgGlyGluGlnGlyProProGlyProThrGlyPhe 67	73
λ.	1403	GGCATGTGGCACCGCCACCACAGGAAAG	1365
Ω	674	GlnGlyHisProGlyProProdlyProProGlyGluGlyGlyLysPro 68	83
> -	1364		1317
۵	069	GlyAspGlnGlyValProGlyGlyProGlyAlaValGlyPro 70	03
× Q	1316	GCCGGTCCATGACCAGAGAAGACCAGGGAGATGGCGCACTGCAGGAACAGCCCCA 12 	260
X	1259	1	215
Ω	723	Ser 7	42
*	1214		1185
	743	CO	62
γ	1184	ACAGCCCCTCGCCCAGGAAATCCGTGTAAAACÁGCGTGAAGGTCA 11.	140
Q	763		775
>-	1139	SGGCATGC	1080
۵	176		784
۸	1079	GGCAGCACAGCTGCAGCCGGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGG 10	1020
Ω	785		801
λ.	1019	CCCGGCATGGACAGCAGTGGGGCGACAAGGAGGGGGCCGACAGCCCTTCŢGCTGGCTCGG 96	096

Q	802 Pro 809	Db 1
ė		Qy
දි සි	939 TeleGeCCCCAGCGCCTCCTCAGCCACCAGGAGTGTGGTGTGG	Db 1
Qy		Qy
Dp		
Qy	869	RESULT 24 CGHUZE
QQ	841 AlaValGlyPheAlaGlyProGlnGlySerAspGļyGlnProGlyValLysGlyGlu 859	COLLAGEN A N;Alternat
δý	848 CCAGGGCACTGGTGCCCAGTCATGGCAGGAGGTAGCCCAGGCAGCCCCCAAGAC 789	C; Species:
qq	860 ProGlyGluProGlyGlnLysGlyAspAlaGlySerProGlyProGlnGly 876	C; Date: U/ C; Accessio
0.7	GACAGT	FEBS Lett.
qq	877	A;ricie: m hain.
Οy	740CCCGGAAGAGGT 729	A; Releicence A; Accessio
Db	892 LeuLysGlyGlyArgGlyThrGlnGlyProProGlyAlaThrGlyPheProGlySerAla 911	A; Residues
οy	728 CAGAGAGCAGGCCTCCAGTGGAGTGAAGCACACGTGGCCACAGAAGTCCAGCAGCCCCA 669	R;Kimura,
qq	oglyProAlaGlyAlaProGly	A;Title: T
QY	TGAGCAGTGCCAGCTCCAGGGGCCTGG	A; reletenc A; Accessio
Dp	929 LeuGlyGluProGlyLysGluGlyProProGlyProArgGlyAspProGlySerHisGly 948	A; Molecule A; Residues
ογ	614 CTGCTAGCCAGCCGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGTG 555	A; Cross·re A; Note: pa
QQ	949 ArgValGly 960	ed and sub
ογ	554 CCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTA 495	A; Genetics A; Gene: GD
qq	096 096	A; Map posi
QY	494 GGAGGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACGATGGTCATGAACT 435	A; Introns: A; Note: th
Op	::: :::	C;Complex: 3(XI) cha
δγ	TT	rmed with C;Function
qq		A; Descript A; Note: ma
ογ		C;Superfam C;Keywords
qa		F; 1-254/Do F; 1-187/Pr
Οy	344 CCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGGCGGC 306	F; 255-305/ F; 306-342/
q	::: ::: 1013 ProGlyLysValGlyProThrGlyAlaThrGlyAspLysGlyProProGlyProValGly 1032	F; 343-1356 F; 429-431/
Qy	305 TCACCCACACACATGGACCATAGTGGGCCAGGGGGGGGGG	F; 447 - 449/ F; 1257 - 125
QQ	1033 ProProGlySerAsnGlyPro-ValGlyGluProGlyProGluGlyProAlaGlyBanAs 1052	F;1357-138 F;1381-154
Qy	GAACTGCTTCGTCTCG	F; 1403-154 F; 109-163,
qa	1052 pGlyThrProGlyArgaspGlyAlaValGlyGluArgGly 1065	F; 319/MOD1 F; 426, 1266
δ	188 CTGCCGCCAACTGCCTAGGAATCAGCCAGCCGCCCATTTCTGCCAGCCCTTTGGTGCCGG 129	F; 927, 933,
QQ	1066	F;942/MODI F;942,1023 F:042,1023
ογ	128 TCCAGCTTCTCAGCCCATGCTCAACACCTGCTGCTGGGGCACCTCAGTGGGGACACGT 69	F; 1427, 143 F; 1460/Bin

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ferences: EMBL:L18987; NID:9306439; PIDN:AAA35498.1; PID:9306440
T.; Cheah, K.S.E.; Chan, S.D.H.; Lui, V.C.H.; Mattei, M.G.; van der Rest, M. Chem. 264, 13910-13916, 1989
The human alpha2(XI) collagen (COL11A2) chain. Molecular cloning of cDNA and connuber: A32645; MUID:89340485; PMID:2760050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tion: structural component of extracellular fibrous polymer associated with by play a role in controlling the lateral growth of collagen II fibrils nily: collagen alpha I(V) chain; fibrillar collagen carboxyl-terminal homolo sa: colled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxypr coduct: prollagenous (fragment) #status predicted <NC3> rocker, prolline/arginine-rich PARP protein (fragment) #status predicted <PAR Domain: collagenous, triple hellx #status predicted <COL2> Domain: non-collagenous #status predicted <NC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region: helical
(Region: cell attachment (R-G-D) motif
(Rogion: cell attachment (R-G-D) motif
(Rogion: carboxyl-terminal nonhelical telopeptide
(A-G-Momain: carboxyl-terminal propeptide (fragment) #status predicted
(A-G-Momain: fibrillar collagen carboxyl-terminal homology (fragment) #status
(A-G-Momain: fibrillar collagen carboxyl-terminal homology (fragment) #status
(A-G-Momain: fibrillar collagen carboxyl-terminal homology (fragment) #status
(A-G-Modified site: allysine (Lys) #status predicted
(A-Modified site: carbohydrate (Lys) #status predicted
(A-Modified site: carbohydrate (Lys) #status predicted
(A-Modified site: allysine (Lys) #status predicted
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1302/3: 1320/3; 1332/3: 1350/3; 1440/1; 1477/3

1- 1302/3: 1320/3: 1332/3: 1350/3; 1440/1; 1477/3

1- 1302/3: 1320/3: 1332/3: 1350/3; 1440/1; 1477/3

1- 1302/3: 1320/3: 1332/3: 1350/3; 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3: 1350/3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iferences: GB:J04974; NID:g180714; PIDN:AAA52034.1; PID:g180715 rrs of this sequence were determined by protein sequencing Prolines and lysines at the third position of the tripeptide repeating unisequently O-g1ycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fied site: 4-hydroxyproline (Pro) #status atypical 1,1299/Modified site: 5-hydroxylysine (Lys) #status experimental 1,1299/Modified site: carbohydrate (Lys) (covalent) #status experimental 13,1450,1459/Disulfide bonds: interchain #status predicted iding site: carbohydrate (Asn) (covalent) #status predicted
076 oGlySerGln-GlyAlaProGlyThrProGlyProValGly---AlaProGlyAspAlaG 1095
                                                                                                                                                                                                                                                                                                 095 lyGlnArgGlyAspProGlySerArgGlyProIleGlyHisLeuGlyArgAlaGlyLysA 1115
                                                                                                                                                    39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (man)
-Jun-1990 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
in: S34790; A32645
                                                                                                                             ------CGAGGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lpha 2(XI) chain precursor - human (fragment) e names: procollagen alpha 2(XI) chain proline/arginine-rich protein (PARP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e number: S34790; MUID:93314796; PMID:8325374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 rgGlyLeuProGlyProGlnGlyProArg 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                              38 GGCTGTCACCCGGAGCCAGCGCGTGCAGG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.I.; Brewton, R.G.; Mayne, R.
326, 25-28, 1993
                                                                                                                                                    68 CTCATCACTCAGATCCTGGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type: DNA; mRNA
586-1546 <KIM>
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 	qa 	2393GCAAGAGCIACATIAAACGAGCIGCAGGTTAAGGGGCTIAGA 2351	δλ
1439 CGGTGAGGGGGGCTGAAGCTGTCACCA	Qy	${\tt GlyProArgGlyProGlnGlyLeuThrGlySerLeuGlyLySAlaGlyArgArgGlyArg}$	qq
675 ProGlyAlaSerGly	qa —		Qy
	0	366	वृत
	qq	24	Λ0.
	óò	357 365	QQ
635 roThrGlyAspProGlyProProGlyL	73 aa	2522 TCAGCAAAAAGACAGTGTGTGGGCTGAGGGGACCTGGTTCTTGTGTGTTGCCCCTCAGG 2463	Οy
	a ô	351ThrGlyArgProGlyPro356	qa
1035 GTGGAGGTGGGAGGCCACTGCCTC 	y E	2582 TGTGATGGCAACAGACCAACAGGCCACATCTGATAAAAGGTAAGAGGGGGGGTGGA 2523	Oy
	a d	350 350	qq
	λ <i>λ</i>	2642 CAATGGATTCCCTTCTACTTTGTTAAATAAGTTAAATATTTTAAATGCCTGTGTCTC 2583	δλ
	2 2		qq
-cec	<u> </u>	2702 CCTGATTGTTGGGGGATCCCCCACCCTACCCAAATTAGACACCAACACAGAAAAGCTAG 2643	οy
55/ ThrLysGlybysProGlyProserGly	<u>a</u> .	::: ::::	qa
1787 ACAGCAGGAAGGCACTAICCAGGA	oy 1	2762 AGACCCCAGGAGAAGAAGATCTGGCAATGATCAGCCCAATGACCAGGTATCTCAGGGGA 2703	δλ
	qa	2816 TCATTTGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGGCATTTTGGGGGGCC 2/03 11 ArghedlyserGlyGlyGlyAspLysGlyProValVal 323	Qy QD
1847 CAGTGACAGACTGGCTGAGACAA	٥٧	Phe	q
	g qa	2876 GAAGCCCACCTCTACCTTCAACACCCTAACCTTGGGTAACAGCATTTGGAATTA 2817	Qy
1907 CHACCHGHGHACABARGHABATGGCGA	g è		QΩ
1967 ACCCCAATGTGCTGGAAGTTTTCTACG	δλ.	AGTGGGGGGAACCAGGCTGGGCCAAGAGAAGAGGGGTGGTTAGGGAAGCCGTTGAG	ζ,
	qa	299b GGGGAAATTTTGGGCAGTGCCTTCATCAGCTCTTAGAGAGAG	λo do
2024 GCAGCCCCATGGGGCTAACAGGAGCGG	QY	258 GlyProGluGlyProAlaGlyLeulleGlyProProProGlyIleGlnGlyAsnFroGly 2/0	g ,
	ද අධ	TGTGGAGCTGGTGGGGAAAGTTGGGGGTAGGGGAAAGTTGGGGGTA	δλ
	ì ò	239 GlyGluLysGlyGluProAlaValLeuGluProGlyMetLeuValGluGlyProPro 257	qq
9) f	3104 TGGACAAAGGCTTGGGAAACCGCACTTTGTGCTTCTGGTCCTGCAGTA 3057	Oy
439	g :		q
GGAAGGCCTCCAGTC	ΟŊ		ò
	QQ	3224 TTATTGCAAACGGCACTTAAACCCCCCTGAGAGATAAGACCTCCCTTAGCTCAGGCAGG	λο ·
2234 GCATTCCAGTGCATGGAGCCCTTCTGG	ΛÓ	US-09-759-143-110 (1-3410) x CGHUZE (1-1546)	60-SD
2294 GTCTCAACTAGGAGGCTAGCTGTTAACC	Qy Ph	5.21% Indels: 1 Gaps:	Query DB:
415 yPheAspGlyLeuProGly	qq	t Similarity: 28.85% Conservative: 58	Perce
2350GATGGGAAACCAGGTGACTGAGT	Qy	4.7e-12 Length:	Aligni Pred.
396 AlaGlyProAspGlyAlaArgGlyThrI	qa		

	396 AlaGlyProAspGlyAlaArgGlyThrLeuGl	yAspProGly-ValLysGlyAspArgGl 415
	GACTGAGTTT	ATTCAGCTCCCAAAAACCCTTCTCTAGGTGT 2295
•	415 yPheAspGlyLeuProGly	421
	4 GTCTCAACTAGGAGGCTAGCTGTTAACCCTG	GCAGAGTCCCC 22
	422	1 427
	2234 GCATTCCAGTGCATGGAGCCCTTCTGGCTCCCTGTATAAGTCCAGACTGAAACCCCCT	CCTGTATAAGTCCAGACTGAAACCCCCTT 2175
	74 G	21
	4.3	 spGlyGluArgGlyAspAspGlyGluIl 453
	, 5	-AGAGGACGCCCCAGCCCCAGCTGTGCAGCTACGCACCTCAGCAGCAGCGCAGGG 2079
	78 T	G 20
	466 yLeuLeuGlyProLySGlyProProGlyIleProGlyProProGlyValArgGlyMetA	ProGlyProProGlyValArgGlyMetAs 486
	2024 GCAGCCCATGGGGCTAACAGGAGCGGGGAGCTGGGACCCAGTGAGGCAGGCCCTC	TGGGACCCAGTGAGGCAGCCCTCC 1968
	1967 ACCCCAANGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAANA	STATTTGGCCAAGTCGCTCTTGTCAAATA 1908 ::: IyLeuProGlyPrqGlnGlyAlalle 522
	07	ACCCAGGCCTGCGGCAGACACCATATAGG 1848
	:::	 ysProGlyLeuProGlyMetProGlySer 542
	1847 CAGTGACAGACTGGCTGACAGAGAGGGGGCCCATAAACAGGGATGGGGCCACCTGGG	GCCCATAAACAGGGTGGGGCCACCTGGG 1788
	87 ACAGCAGGAAGGCA	CTATCCAGGATGGCGAGGTCCAGGCAGATGCCCCGGCCGGAA 1731
_	557 ThrLysGlyLysProGlyProSerGlyProG	inglyProLeuGlyTyrProGlyProGln 576
	0 CCAC	9
_	577 -GlyvalLysGlyValAsnGlyIleArgGly	sGlyGl 59
	1696ACGTACGGAGACATCACAGGCGGCGCCCGCAGACGCCCCGCAGACGCCCCGCAGACGCCCCGCAGACGCCCCGCAGACGCCCCGCAGACGCCCCCGCAGACGCCCCCGCAGACGCAGACGCAGACGCAGACGCAGACGCAGACGCAGACGCAGACGCAGACACGCAGACGCAGACGCAGACGCAGACGCAGACGCAGACGCAGACGCAGACGCAGACGCAGAC	ACAGGCAGAGGCCCCGCAGAGCGCGG 1656 ::: GlyvalLysGlyAspArgGlyGlu-ValG 616
	SAGGTGGGAGCAGGCCACTGCC	ACCCACGTGTCCATTAGGGAAGGGAGCTC 1596
_	616 lyValProGlySerArgGlyGluAspGl;	635
	95 CAGGCTTAGGGCCTGGCAGGAAGCTGGTCA	1
0	5 roThrGlyAspProGlyProProGlyLeuM	tGlyGluLysGlyLysLeuGlyValFroc 65
~ .	1535 TGTCCCTCGGTATTTGGCAGGAACA	vProLysGlySerLeuGlyPheProGlyPhe 674
	99 CCCGGTGGTAGAGGGAGGCCAGT	
. 0	675 ProGlyAlaSerGly	::: GluLysGlyAlaArgGlyLeuSerGly 688
~	/ 1439 CGGTGAGGCGGCTGAAGCTGTCACCACGG-	CTGAAGCTGTCACCACGGCCACACTGTGGGACAGGC 1392
c	0 689LysSerGlyProArgG	lyGluArgGlyProHisGlySerThrGly 703

^0	1391 ATGTGGCACAGAGAGAAAAGGAAAAAGGAAAAAAAAAAA
; <u>a</u>	
οy	
QQ	
Qy	
ДQ	lyProLysGlyPro
0y	1262 CCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAG 1203
qa	759 ProGlyHisProGlyGlnArgGlyGluValGlyPheGlnGlyLys***GlyPro 776
οy	1202 CTCTGGGCACGCCCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGG 1143
qa	777
ΟY	1142 TCATGAGTGCCATCCAGCTGCACAGCTCAGGAAGAGCCGGGGGCAGGGTGCGGGGGCA 1083
qq	779
0y	1082 TGGGGGAGCACAGGTGCAGCGGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGC 1023
qq	GlyProMet
Qy	1022 GGG
Dþ	808 GlyGluGlnGlyLeuProGlyThrAlaGlyLySGluGlyThrLySGlyAspproGly 826
٥y	CAGCCA
QQ	827 831
Qy	TGAGGGTGAGCAGGCCAA
Db .	832GlyLysAspGlyProAlaGlyLeuArgGlyDheProGlyGluArgGlyLeu 848
Qy	869 CCTGGGTGCCCAGGTAGGGGGCCAGGG
QQ	3lyAsnGluGlyProSerGlyProPro 867
0y	842CACTGGTGTCCCAGTCAATGGCAGGGAGGTAGCCCAGGCAGCCCCCAAGAC 789
Dp	868 GlyProAlaGlySerProGlyGluArgGlyAlaAlaGlySerGlyGlyProIleGly 886
Οy	729
QQ	887ArgGlnGlyArgProGlnGlyProGlnGlyProProGlyAlaAlaGly 901
Οy	CACAGAAGTCCAGCAGCCCCA 669
QQ	
Οy	TGAGCAGTGCCAGCTCCA 642
qa	915 ThrGlyArgAspGlyValGlnGLyProValGlyLeuProGlyProAlaGlyProPro 933
Qy	641 GGGGCC FGGGATCCGGGCACAGCCCTGCTAGCCAGCCGG 600
qq	934 GlyvalalaGlyGluAspGlyAspLySGlyGluValGlyValProGlyGlnLysGlyThr 953
Οy	591
Dp	954 LysGlyAsnLysGlyGluHisGlyProProGlyProProGlyProlleGlyProValGly 973
οy	590 TGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGGGC 531
DP	984

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!; Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Oji, O.; Kwan, A.; Liu, S.; tz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel ubmitted to the EMBL Data Library, July 1998
.; Description: Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequency, Reference number: 214202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: DNA; A7,492-512 <VYS>; Residues: 1-490, A7,492-512 <VYS>; Cross-references: EMBL:AC003979; NID:g3172156; PID:g3287687; GSPDB:GN00059; ATSP:T2; Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4) Alternate names: Sucrose proton symptories 0022

5) Species: Arabidopsis thaliana (mouse-ear cress)

5) Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 01-Dec-2000

6) Accession: S38196; T00773

1) Sauer, N.K.

1) Unbmitted to the EMBL Data Library, October 1993

1) Poscription: SUC1 and SUC2: two sucrose transporters from Arabidopsis thaliana.

1) Reference number: S38196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1025 GluThrGlyAspValGlyProMetGlyProProGlyProGlyProArgGlyProAla 1044
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530 CATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGA---GCGGGACACACAGA----- 480
                                                                                                                     -----CCAGGCCCA---GCACTGGACCAATGCCCAGCACCATGGTCATGAACTTCT 432
                                                                                                                                                                                                                                             374 -----ACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTT 327
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:Residues: 1-512 <SAU>
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995 TCGCCCCACTGCTGTCCATGCCGGCCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 ThralaLeuAsnTrplleAlaTrpPheProPheLeuLeuPheAspThrAspTrpWetGly 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 GlyAlaPheLysGluLeu-----LysArgProMetTrpMetLeuLeuIleVal 285
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PhePheMetAlaValGlyAsnValLeuGlyTyrAlaAlaGlySerTyrArgAsnLeuTyr 204
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                                                                              512
123
92
195
101
                protein
                                                                           Length:
Matches:
Conservative:
Mismatches:
A;Introns: 419/3; 441/1; 455/3
C;Superfamily: common tobacco sucrose transport
C;Keywords: sugar transport
                                                                                                                                          Indels:
                                                                                                                                                           Gaps:
                                                                                                                                                                                       US-09-759-143-110 (1-3410) x S38196 (1-512)
                                                                         5.4e-12
323.50
42.078
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Best Local Similarity:
                                                                 Alignment Scores:
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probable sucrose-proton symporter SUC2 protein T22J18.12 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C; Decies: Ara-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
C; Accession: G86380
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MuID:21016719; PMID:11130712
A; Molecule type: DNA
A; Residues: L-512 < RDA
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C;Genetics:
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                                                                                                                            346 MetSerLeuGlyValGluTrpIleGlyArgLySLeuGly---GlyAlaLySArgLeuTrp
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1175 GAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTÁT
                                 382 ThrLysGlnAlaGluAsnHisArgArgAspHisGlyGlyAlaLysThrGlyProProGly
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Length:

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Alignment Scores:

Pred. No.:

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		382	47	442	29	502	562	107	619	124	661	144	721	164	778	817	204	874	224	934	243	994	259	1054	269	-	2	1174	1234	325	1294
Matches: 123 Conservative: 92 Mismatches: 195 Indels: 101 Gaps: 18	60 (1-512)	CGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGTGTGTTTGGCC	ArgLeuArgLysIleIleSerValSerSerIleAlaAlaGlyValGlnPheGlyTrpAla	GCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAAGTTCATG	LeuGlnLeuSerLeuLeuThrProTyrValGlnLeuLeuGlyIleProHisLysTrpAla	ACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGGTCA ::::::::	GCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCCGC		TIGGGCATCCIGCTAGAGCCTCTTTCICATCCCAAGGGCCGGCTAGCAGGAGGCTG	GlyLeuValThrValAlaValPheLeuIleGlyTyrAlaAlaAspIleGly	AGGCCCCTGGAGCTGGCAC	HisSerMetGlyAspGlnLeuAspLysProProLysThrArgAlaIleAlaIlePheAla	CTGGGCGTGGGGGTGCTGGACTTCTGTGGCGAGGTGCTTCACTCCACTGGAGGCCCTG	LeuGlyPheTrpIleLeuAspValAlaAsnAsnThrLeuGlnGlyProCysArgAlaPhe	CTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCGGCCTACTCTGTCTATGCC	3CTGCCTGGGCTACCTCCTG	:::::::: PhePheMetAlaValGlyAsnValLeuGlyTyrAlaAlaGlySerTyrArgAsnLeuTyr	ACCAGTGCCCTGGCCCCTAGGAGGAG	LysValValPrOPheThrMetThrGluSerCysAspLeuTyrCysAlaAsnLeuLysThr	TGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG	<pre>nrLeuLeuLeuIleValThrPheValSerLeuCysTyr</pre>	GCTGAGGCAGCCCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCTCCTTG	ValLysGluLysProTrpThrProGluProThrAlaAspGlyLysAla	TCGCCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT	SerAsnValProPhePheGlyGlullePhe	CTGCCGCA	and towerst procuedated	GAGCTGTAGARCGGACTCATGACCTTCACGGTGTTTTACACGGATTTGTGGGG ThralaLeua::! :: ThralaLeuasnTrpTlacAlaTrpPheProPheLeuLeuPheAspThrAspTroHetGl	GAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTAT	:::: ArgGluValTyrGLyGLyAsnSerAspAlaThrAlaThrAlaAlaAlaSerLysLysLeuTyr	GATGAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTC
323.50 42.078 : 24.078 5.048	3410) x G86360	CCCAGCTCTTG	rgLysileile	TCACCTATGTG	euSerLeuLeu	TGCTGGGCATT(:: leTrpLeuCys(ACCACTGGCGTC	II spArgCysThr	rccrecreaecc	alThrValAlav)	etGlyAspGlnI	resserrecres	heTrplleLeuA	CTCTCTGACCTCTTCCGG- ::: LeuAlaAspLeuSerAlaG	CAGTCTTGGG	::::::: etAlaValGlyA	CCTGCCATTGACTGGGAC-	lProPheThr	rescerserea 	eLeuSerIleT	AGGCAGCGCTGG	uLysProTrpT	CTGCTGTCCAT		CCCCGGCTGCACCAGCTGTG ::: GlvalaPhetwsGluten		CAGCTGGATGG ::: ::: uAsnTrpIleA	GTACCAGGGCG	:::{	CGTTCGGATGG
rity: illarity	-110 (1-	CGGAAAG	ArgLeuA	GCAGGCA:	LeuGlnL	ACCATGG::::SerLeuI	GCCAGTG	Hissera	TTGGGCA'	GlyLeuV		HisSerM	CTGGGCG	LeuGlyP	CTCTCTG! ::: LeuAlaA	TTCATGA	 PhePheMe	CCTGCCA	Lysvalva	recerem	:ysPheP}	SCTGAGGAG	/alLysGl	rccccc.		CCCGGCT		AGCTGTG	SAGGGGCT	:: \rgGluVa	ATGAAGG
Score: Percent Similarity: Best Local Similarity: Query Match: DB:	-759-143-	323	28		48	443	503	88	563	108	620	125		145	722 (779	185	818	205 1	10		D.	244	995 1	260	1055 0		. 286 1	1175 G	306 ₽	1235 G
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procollagen type V alpha 2 - mouse
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
R;Andrikopoulos, K.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
Bev. Dyn. 195, 113-120, 1992
A;Title: Localization of pro-alpha 2(V) collagen transcripts in the tissues of the de A;Reference number: I49607; Mull:93214071; PMID:1297453
A;Reference number: I49607
A;Returs: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1497 RRES>
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C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homolo
F;39-98/Domain: von Willebrand factor type C repeat homology <VWC>
F;1270-1497/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                            1295 ITCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCC 1354
                                                                                                                                               1355 AGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTG 1414
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                                                                                                                                                                           365 GlyileValAsnPheIleLeu------AlaIleCysLeuAlaMetThrValValVal 381
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| 422 PheSer------IleProPheAlaLeuAlaSerIlePheSerThrAsnSerGly 437
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C;Genetics:
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Best Local Similarity:
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an an	4	GIYALARIOGIYLISALYGIYALARISGIYMGC 5555
Qy	2122	CAGCTACGCACCTCAGCAGACAGGGTGGCAGCAGA 20
Db	360	ProGlyLysProGlyProMetGlyProLeuGlyIleProGlySerSerGly 376
Qy	2068	AGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCT 20
Db	377	PheProGlyAsnProGlyMetLysGlyGluArgGlyProHisGlyAla 392
Qy	2008	AACAGGAGCGGGGAGCTGGGACCCAGTGAGGCAGGCCTCCACCCCAA 1961
QQ	393	yGlnAr
Qy	1960	TGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTG 1901
qq	409	GlyProAlaGlySerGlnGlyLeuPro- 417
Qy	1900	TGTAGCAAAGTAAATGGCGACCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGTGAC 1841
QQ	418	GlyAlaValGlyThrAspGlyThrProGlyArgLySGlyA 431
Qy	1840	AGACTGGCTGAGCTGGACATGGAGCCCATAAACAGGATGGGGCCACCTGGGACAGCAG 1781
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Qy	1780	GAAGGCACTATC 1769
Db	451	 1yProGlnGlySerThrGlyProGlnGlyIleArgGlyGlnSerGlyAspProGlyValP 471
QY	1768	CAGGATGGCGA
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Qy	1730	CCACCCTGGCCTCGGTGGGCTCACCACCAC 1697
Dp	491	GlyLysArgGlyProArgGl
Qy	1696	ACGTACGGAGACATCACAGGCAGAG
Db	510	111 lGlyProProGlyProMetGlyGluAr
QY	1642	CAGGCCACTGCCT
qq	530	raspGlyLeuproGlyProLysGlyAlaGlnGlyGluArgGlyProValGlySerSerGl 550
Qy	1597	TCCAGGCTTAGGG
qq	550	yProLysGlyGlyGlnGlyA
Qy	1546	AGCACCTCCAGTGTCCCCTCGGTATTTGGGCA
. qa	570	
Qy	1501	CTCCCGGTGGTAGAGGGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAA 1442
Db	590	
Qy	1441	CCCGGTGAGGGCGGCTGAAGCTGTCACCACGCCACACTGTGGGA 1397
Dp	609	ProGlySerMetGlyValProGlyProLysGlySerSerGlyAspLeuGlyLys
Qy	1396	CAGGCATGTGGCAC
Db	629	iii GlualaGlyAsnalaGlyValProGlyGlnArgGlyAlaProGlyLysAspGlyGluVal 64
Qy	1376	CCACAGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCT 13
Dβ	649	GlyProSerGlyProValGlyProProGlyLeuAlaGlyGluArgGlyGl
Qy	1322	GCACCAGCCGGTCCATGACCAGAGAGAGACCAGGGAGA 1284

Ор	 667 GlyF	
οy	1283, TGGC	TGGCGCACTGCAGGAACAGCCCCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCC 1224
Db	687 GlyG	GlyGlyLysAlaGlyAspGlnGlyValProGlyGluProGlyAlaVal 702
oy Op	1223 GGGCCT 703 GlyPro	GGGCCTCGGTGCCCGGCTCTGGGCACGCCCTGGTACAGCCCCTCGCCCACGAAAT 1164 UPProLeuGlyProArgGlyGluArgGlyAsnProGlyGluArgGlyGluArgGlyGluArgClyGluArgGlyGluArgClyGl
٥y	1163 CCGT	GAAGA
qa	721	
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ę ę	1064 GCAG 749 ThrI	GCAGCCGGGGAAGCAGGCCCCAGGTTCCGGAAAGCCAAGC
٥y	1022	5 E-
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٥y	971 CTG-	CTGGGTGGGGCCCAGCGCTCCTCCTCAGCCAGCA 927
QQ	789 AlaG	AlaGlyAsnAspGlyAlaArgGlyLeuProGlyProLeuGlyProProGlyProAlaGly 808
٥y	926 GTGT	GTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAGAGGCACT 873
qq	809 LeuLeu	
Qy	872 CCTCCTG	GGTGCCCAGGT
QQ	824 ProP	ProProdlySerArgGlyAsnProGlySerArgGlyGluAsnGlyProThrGlyAlaVal 843
٥y	848	0 84 0
qq	844 GlyP	GlyPheAlaGlyProGlnGlySerAspGlyGlnProGlyValLysGlyGluProGlyGlu 863
٥y	839 TGGT	TGGTGCCCAGTCAATGGCAGGCAGGAGCCCAGGCAGCCCCCAAGACTGATCATGA 780
qa	864	ProGlyGlnLysGlyAspAlaGlySerProGlyProGlnGly 877
Qy	779 AGGC	GACAGTG
qa	878	-LeuAlaGlySerProGlyProHisGlyVallyValProGlyLeuLysGly 895
Οy	740	CCCGGAAGAGTCAGAGA 720
Db	896 GLYA	GlyArgGlyThrGlnGlyProProGlyAlaThrGlyPheProGlySerAlaGlyArgVal 915
٥y	719 GGGC	GGGCCTCCAGTGGAGTGAAGCACCTGGCCACAGAAGTCCAGCAGCCCCCACGCCCAGGA 660
QQ	916 G1yP	oproGlyProAlaGlyAlaProGlyProAlaGlyProAlaGlyGluProGly 934
0y	659 TGAG	TGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCC
qa	935 LysG	LysGluGlyProFroGlyLeuArgGlyAspProGlySerHisGlyArgValGly 952
٥y	599 CCCT	CCCTTGGGATGAGAAGAGGCTCAGCAGGATGCCCAAAGGACAGTGCCCAGATGAAGGGCC 540
Db	953	:::
Qy	539 GGCG	GGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGGGGGGACACAGA 480
Db	963	::
δ	479 CCAGG	CCAGGCCCAGCACTGGACCAATGCCCAGCATGATGAACTTCTCCTCTACCCCA 420

967 GlyAspProGlyGluAspGlyGlnProGlyProAspGly981	CGGCCAAA	982 GlyProAlaGlyThrThrGlyGlnArgGlyIleValGlyMetProGlyGln 998	359 AGGTTAGCAGCTTGACCAGGAAGAGGTGGG 330	999 ArgGlyValThrGlyMetProGlyLeuProGlyProAlaGlyThrProGlyLySvalGly 1018	CTTTCGGTGCCGCAGCAGGC	ProfhrGlyAlaThrGlyAspLysGlyProProGlyProValGlyProFroGlySerAsn 10	zyv osaccaracisosCcadoccocaracaccarcacacaccaracaccaracacaracacaracaracaracaracaracaracaracaracaracaracaracacaracacaraca	233 GCTTGGTCTGGGTCTGCTCCAGAAGCTGGGGCCTCTCCTTGCTGCCGCCAACTGCC 174		TAGGAATCAGCCAGGCGCCCATTTCTGCC	067 pArgGlyAspProGlyProAlaGlyLeuProGlySerGln-GlyA 1082	113 CATGCTCAACACCTGCTGTGGGGCACCTCAGGGGACACGTCTCATCACACTCAGATC 54		order of the control	RESULT 28 522917 collagen alpha 5(IV) chain precursor, renal splice form - human NiAlternate names: procollagen alpha 5(IV) chain NiContains: collagen alpha 5(IV) chain NiContains: collagen alpha 5(IV) chain precursor, leukocyte splice form C;Species: Homo sapiens (man) C;Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 21-Jul-2000 C;Accession: S22917; A54365; A57079; A37122; I54317; A34850; S18850; I56971; I76598;		mplete amino acid sequence of the human alpha-5(IV) collagen chain and ide ndrome patient.	number: S22917; MUID:92316923; PMID:1352287 : S22917 type: mRNA 1.967 <zho></zho>	erences: GB:M90464; NID:9180826; PIDN:AAA52046.1; PID:9553234 Leinonen, A.: Tryggvason. K	em. 269, 6608-6614, 1994 ructure of the human type TV colladen COLAAS gene		type: DNA 1-922 <zh2></zh2>	erences: GB:U04470; NID:9463378; GB:U04520; NID:9463428; PIDN:AAC27816.1; Mochizuki, T.; Smeets, H.; Antignac, C.; Laurila, P.; de Paepe, A.; Trygg	letion of the paired alpha5(IV) and alpha6(IV) collagen genes in inherited number: A57079; MUID:93361972; PMID:8356449	: A57079 1-79: DNA 1-77: 7=14	erences: GB:237153; NID:9587203; PIDN:CAA85512.1; PID:9587204	A: Title: Complete primary structure of the triple-helical region and the carboxyl-ter	: A37122 Lype: mRNA
6	4	σ	m	6	m c	10	10:	7	10	н .	10	10.	-	, 110	LT 28 agen alk ternate ntains: ecies: 30-5 ces: 30-5	iol. Che	tle: Com port syr	<pre>Terence cession: lecule t sidues:</pre>	oss-refe	iol. Che tle: Str	ference	lecule t	oss-refe ou, J.;	tle: Del ference	dession: lecule t	oss-refe hlajanie	tle: Com ference	session: lecule t
QQ	Øγ	qa	δy	qq	oy d	g :	op Op	Qy	qq	Oy	qq	Oy Dp	ò	G Q	RESU S2290 C011 N; A1 N; C0 C; Sp C; Da	G. B	A; Ti	A; Ke A; Aç A; Mo A; Re	A; Cr. R; Zh	J. B.	A; Re	A; Mo	A; Cr. R; Zhc	A;Ti	A; AC	A;Crc R;Pil	A; Til	A; AC(A; Mo]

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A;Notes: permature termination mutation from a patient with Alport syndrome; one other muts. B;Lemmink, H.H.; Schroeder, C.H.; Brunner, H.G.; Nelen, M.R.; Zhou, J.; Tryggyason, K.; Genomics 17, 485-489, 1993
A;Title: Identification of four novel mutations in the COL4A5 gene of patients with Alpot A;Reference number: I54188; MUID:94010948; PMID:8406498
A; Residues: 84-439, 'GS', 442-624, 'LALQ', 629-666,'FR', 669-887,'R', 889-1264,1271-1691 <PIH)
A; Cross-references: GB:J05558; EMBL:M58526; NID:g1314209
A; Note: submitted to the EMBL Data Library, February 1991
A; Note: the authors translated the codon GCC for residue 115 as Val
R; Renleri, A: Seri, M: Myers, J.C.; Pihlajaniemi, T: Massella, L.; Rizzoni, G.; De Ma Hum. Mol. Genet. 1, 127-129, 1992
A; Title: De novo mutation in the COL4A5 gene converting glycine 325 to glutamic acid in A; Reference number: I54317; MUID:93244772; PMID:1363780
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A; Residues: 1284-1291, TFLGYLACLV <GU02>
A; Residues: 1284-1291, TFLGYLACLV <GU02>
A; Cross-references: GB:569169; NID:9546097; PIDN:AAC60613.1; PID:9545098
A; Note: frameshift mutation in patient with Alport syndrome
R; Myers, J.C.; Jones, T.A.; Pohjolainen, E.R.; Kadri, A.S.; Goddard, A.D.; Sheer, D.; Sc
R; Myers, J.C.; Jones, T.A.; Pohjolainen, E.R.; Kadri, A.S.; Goddard, A.D.; Sheer, D.; Sc
Am. J. Hum. Genet. 46, 1024-1033, 1990
A; Title: Molecular cloning of alpha5(IV) collagen and assignment of the gene to the regi
A; Reference number: A35335; MUID:90252791; PMID:2339699
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A; Residues: 1448-1477 < MYE>
R; Residues: 1448-1477 < MYE>
R; Nakazato, H.; Hattori, S.; Ushijima, T.; Matsuura, T.; Koitabashi, Y.; Takada, T.; Yos
Kidney Int. 46, 1307-1314, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:M63455; EMBL:M63456; EMBL:M63457; EMBL:M63458; EMBL:M63459; EMBL:M63470; EMBL:M63470; EMBL:M63471; EMBL:M63472; EMBL:M63473; NID:g177922; PIDN:AA51558.1; PID Riduo, T.; Van Damme, B.; Van Damme-Lombaerts, R.; Van den Berghe, H.; Cassiman, J.J.; M Kidney Int. 44, 1316-1321, 1993
A;Title: Differential splicing of COL4A5 mRNA in kidney and white blood cells: a complex A;Reference number: 156971; MUID:94133540; PMID:8301933
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A;Reference number: 156975; MUID:95156893; PMID:7853788
                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 313-324, Tg', 326-330 < REN
A;Residues: 313-324, Tg', 326-330 < REN
A;Cross-references: GB:S59334; NID:9299946; PIDN:AAD13909.1; PID:94261609
A;Cross-references: GB:S59334; NID:9299946; PIDN:AAD13909.1; PID:94261609
B;Hostikka, S.L.; Eddy, R.L.; Byers, M.G.; Hoeyhtyae, M.; Shows, T.B.; Tryggvason, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 1666-1610, 1990
A;Title: Identification of a distinct type IV collagen alpha chain with restricted kidne
A;Reference number: A34850; MUID:90160375; PMID:1689491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Zhou, J.; Hostikka, S.L.; Chow, L.T.; Tryggvason, K. Genomics 9, 1-9, 1991
Genomics 9, 1-9, 1991
A;Title: Characterization of the 3' half of the human type IV collagen alpha-5 gene that A;Reference number: A37969; MUID:91169491; PMID:2004755
A;Accession: S18850
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A;Molecule type: DNA
A;Residues: 1595-1602 <NAK>
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A; Residues: 1604-1607, 'VHDAYKC' <LEM>
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A; Residues: 924-1264,1271-1691_<ZH3>
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A; Residues: 914-1264,1271-1691 <HOS>
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A; Residues: 1258-1276 <GUO1>
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A;Cross-references: GB:S65767; NID:g425563; PIDN:AAD13967.1; PID:g4261667

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A; Description: minor structural component of extracellular basement membrane C; Superfamily: collagen alpha 1(IV) chain C; Superfamily: collagen basement membrane; coiled coil; extracellular matrix; gl F; 1-26/Domain: signal sequence #status predicted <SiG>F; 27-1691/Product: collagen alpha 5(IV) chain, renal splice form #status predicted <M F; 27-1464.1271-1691/Product: collagen alpha 5(IV) chain, leukocyte splice form #status F; 27-37-41/Domain: amino-terminal nonhelical, NC2 #status predicted <NC2>
                                                                                                                                                                                                                                        Amap position: Xq22-Xq22
A; Introns: 27/3; 47/3; 77/3; 92/3; 107/3; 128/3; 146/3; 155/3; 182/3; 182/3; 195/3; 2
A; Introns: 27/3; 47/3; 47/3; 92/3; 1006/1; 1036/1; 1085/3; 1125/1; 1152/1; 1185/1
A; 799/1; 837/1; 893/1; 93/4; 93/4; 1006/1; 1036/1; 1036/1; 1082/3; 1125/1; 1152/1; 1185/1
A; Note: the alpha 5(IV) and alpha 6(IV) chain genes are encoded on opposite strands w
C; Complex: This minor type IV collagen is thought to form a heterotriner of two alpha
mong trimer amino-terminal domains (with disulfide and desmosine cross-links), dimert
a ssociations in the interrupted helical domain (with disulfide and desmosine cross
A, Note: frameshift mutation from a patient with Alport syndrome; five other mutations C, Comment: Prolines and lysines at the third position of the tripeptide repeating uni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;125/Binding site: carbohydrate (Asn) (covalent) #status predicted F;1482-1570, 1515-1573/Disulfide bonds: (or 1482-1573, 1515-1570) #status predicted F;1527-1533, 1638-1644/Disulfide bonds: #status predicted F;1522-1684, 1626-1687/Disulfide bonds: (or 1592-1687, 1626-1684) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 CCAGGATCTGAGTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAG 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1463-1691/Domain: carboxyl-terminal nonhelical, NC1 #status predicted <NCl>
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F:1583-1687/Domain: collagen IV carboxyl-terminal repeat <CT2>
F:29,32,38,40,124,451,481,484/Disulfide bonds: interchain #status predicted
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Mismatches:
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                                                                                                                                                                    A;Gene: GDB:COL4A5; ATS
A;Cross-references: GDB:120596; OMIM:303630
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                                              C; Comment: Prolines and lysines at ed and subsequently O-glycosylated.
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ûy	398 GTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGAGAGATCATGACCATGGT 450	:	,
qa	622ProProGlyPheGlyProProGlyProvalGlyGluLysGlylleGlnG 638	QC .	
δy	451GCTGGGCATTGGTCCAGTGCTGGGCTGTGTGTCCCGCTCTAGGCTCAGCC 505	Oy.	1460 CAGATCO
QQ	638 lyValAlaGlyAsnProGlyGlnProGlyIleProGlyProLys 652	q _Q	901
Oy	506 AGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTG 565	٥y	1520 AAATACO
ΩD		Ωp	915 rg
δλ	566 GGCATCCTGCTGAGCCTCTTTCTCAAGGGCCGGCTGGCTAGCAAGAGACTAGTAGTAGAAGACTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGT	Qy	1580 CCAGGCC
QQ		qa	929
0y		Qy	1640 CTGCTCC
q 0 .	SpProGlyLeuProGlyG	qa	947 GlyLeuF
δλ		Οy	1700 GTGGTGG
QQ		qa	960 u-Glyse
δλ	CTATGCC	Qy	1739 CGGG
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0y	779 ITCATGATCAGTCTTGGGGGCTGCCTGGCTACCTCCTGCCTG	Qy	1784 CTGTCCC
Dp	722	qa	1000 lyLeupr
οy		Qy	1844 ACTGCCT
qq	::: :::	qa	1018
0y		Qy	1904 GTAGTAT
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ογ	938 GAGGAGGCAGCGCTGGGCCCACCGAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCG 997	Οy	1964 GGGTGGA
QQ		QQ	1030 lyAspMe
٥٧	998 CCCCACTGCTGTCCATGCCGGGCCCGCTTTCCGGAACCTGGGCGCCCTGCTTCCC 1057	δy	2024 CCGGGCT
QQ	:::	QQ	1050 ProglyG
Qy		ΟŊ	2084 TGCTGCT
QQ		Db	1061
Qy	1106 TICGIGGCIGAGCIGCAGCIGGAIGGCACCICAIGACCTICACGCTGIITIACACGGAT 1165	Οy	2144 GTCTCTA
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Qy	1286 TCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTC 1345	Οy	2297 ACCTAGA
QQ	::: 	qq	1121
٥'n	1346 TATTIGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCC 1399	Qy	2357 CCCCTTA
qa	882 euProGlyLysAlaGlyAlaSerGlyPheProGlyThrLysGlyGluMetGlyMet- 900	qa .	
å,	1400 CACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTG 1459	Ολ	2417 CTCCTCC

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	1460	CAGATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGAG
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	1520	AAATACCGAGGGA
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	1580	CCAGGCCCTAAGCTTGGAGCTCCCTTATGACACGTGGGTGCTGGAGGCAGTGGC 16
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	1640	CTGCTCCCACCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTG 16
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	096	VEGINGE GRACCCCACCCACCCACCCACCCACCCACCCACCACCACCA
	1739	GGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG
	980	
	1784	TTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 184
	9	
	84	CTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCGGTCGCCATTTACTTTGCTACACAG 190
	5	GlyLeuIleGlyProProGly
	1904	GTAGTATTTGACAAGGGGACTTGGCCAAATACTCAGGGTAGAAAACTTCCAGCACATTG 1963 ::: YThr11eG 1030
	1964	GGTGGAGGGCCTGCTCACTGGGTCCCAGCTCCCGGCTCCTGTTAGCCCCATGGGGCT
	1030	
	\sim	CGGGCTGGCCGCCAGTIT
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	2084	TGCTGCTGAGGTGCGTAGCTGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCT
	1061	GlnLysGlyAspLysGlyAspLysGlyIleSer 1071
	14	GGCCTTCCAAGGGGGTTTCAGTCTGGACTT
	07	-SerIleGlyLeuProGlyLeuProGlyProLysGlyGluProGlyLeuProGlyTyrPr 1091
	2201	AGGGAGGCCAGAAGGGCTCCATGCAGGATGCGG 2236
	2237	で
	11	rProGlyAlaLysGlyGlnProGlyLeu1120
	2297	GTTTTTGGGAGCTGAATAAACTCAG1
	1121	::: ProGlyPheProGlyThrProGlyProFroLyProLy 1133
	2357	CCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACA 2416
	1133	sglylleser-Gly 1137
	2417	CTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGAGTCCTGAGGGGCAACA 2476

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රු දි	253/ ACCITITATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGACACACAC	Aritle: The covalent structure of collagen. 2. The amino-acid sequence of alphal-CB7 A; Reference number: A91211; MUID:74086118; PMID:4359390
3 8	maaamammaacmmammmaacaaaggaagggaatccamgcagggg	A;Accession: A91211 A;Molecule type: protein
ž a	ייייין די	A Residues: 295-562 <fi3> A Experimental source: skin</fi3>
Qy	TTGGTGTCTAATATTTGGGTAGGGTGGGGGGATCCCCAACAATCA	R.Wendt, P.; Mark, K.V.D.; Rexrodt, F.; Kuenn, K. Eur. J. Biochem. 30, 169-183, 1972 A.mitle mhe constend structure of collagen. The amino-acid sequence of the 112 resid
qq	1164	
ογ	TGGTCATTGGGCTGATGATTGCCAGAATCTTCTCTCTGGGGTCTGG	A; Molecule type: protein A; Molecule type: protein A; Residues: 563-675
qq		R.Fietzek, P.P.; Rexrodt, F.W.; Wendt, P.; Stark, M.; Kuehn, K.
ç d	2765 CCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCCAAATGATAATTCCA 2824	<pre>Eur. J. Biochem. 30, 163-168, 1972 A;Title: The covalent structure of collagen. Amino acid sequence of peptide alpha1-CB A;Reference number: A91200; MUID:73042275; PMID:4343807</pre>
Qy	AATGCTGTTACCCAAGGTT	A.Accession: A91200 A;Molecule type: protein A.Residues: 676-758 <f14></f14>
qq	1196GlyLeuProGlyLeuSerGlyGlnLysGlyAspGlyG 1208	proline and the only hydroxylated pro
Qy	2879 GTCTCAACGGCTTCCCTAACCACCCTCTTCTCTTGGCCCAGCTGGTTCCCCCACTTC 2938	t, F.; Becker, U.; Stark, M.; Kuehn, K.
qa	ProGly11eProGlyAsnProGlyLeuPro	A; Title: The amino acid sequence of the carboxyterminal nonhelical cross link region A; Reference number: A43048
Qy Ph	2939 CACTCCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCAC 2980	A.Accesion: A43048 A.Molecule type: protein A.Residues: 759-779 <ra2></ra2>
07		A, Experimental source: skin control is a specific skin state of the hydron of the tripoptide repeating unit (G-X-Y) are comment. Despite at the third mostified of the tripoptide repeating unit (G-X-Y) are
Ωp	1237ProGlyProProBlySerProGlyProAlaLeuGluGlyProLysGly 1252	chain of
Qy	3041 CAACC 3046	C:Comment: The complete chain contains 1052 residues. C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo
qa	1253 AsnPro 1254	C, Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trime F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
RESULT CGBOIS COILage C; Speci C; Date: C; Acces R; Raute Eur. J.	RESULT 29 CGBOJS collagen alpha 1(I) chain - bovine (tentative sequence) (fragments) C;Species: Bos primigenius taurus (cattle) C;Species: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 31-Mar-2000 C;Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 31-Mar-2000 R;Renterberg, J; Timpl, R.; Furthmayr, H. Bur. J. Blochem. 27, 231-237, 1972	Alignment Scores: 7.65e-12 Length: 779 Pred. No.: 321.00 Matches: 229 Score: 31.12\$ Conservative: 38 Best Local Similarity: 26.69\$ Mismatches: 269 Query Match: 1.6\$ Indels: 324 DB: 6aps: 51
A;Title A;Refer	arr and	US-09-759-143-110 (1-3410) x CGBO1S (1-779)
A; Acces A; Molec A; Resic	ssion: A91193 cule type: protein tues: 1-19 CRAU>	Qy 2365 GTTAAGGGCCTTAGAGATGGGAAACCAGGTGACTGAGTTATTCA 2321 :::
A; Exper A; Note: R; Fietz	Inherical Source: SAIN : the epsilon carbon of Lys-9, by homology with the rat alpha 1(I) chain, is converge, P.P.; Kuehn, K. Dischem, 52, 77-82, 1075	2320 GCTCCCAAAAACCCTTCTCTAGGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGC
A;Title	. blocked. 34, 77.02, 137.5 e: The covalent structure of collagen: amino-acid sequence of the cyanogen-bromide	
A; Relei A; Acces A; Molec A; Resic	rence number: Agizes, Moior Cozzac, Fribritation Ssion: Aprize the Stone Stone Type: protein thes: 20-145 <fie></fie>	Qy 2260 CTGGGTAATCCACCTGCAGAGTCCCCGCATTCCAGTGCAGGAGCCCTTCTGGC 2207
A; Exper A; Note R; Fietz	A. Experimental source: skin short-short short short in 1971 103 is hydroxylated and binds glucosylgalactose R. Fietzek, P. P.; Wendt, P.; Kell, I.; Kuehn, K.	2206 CTCCCTGTATAAGTCCAGACTGAAACCCCTTGGAAGGCCTCCAGTCAGGCAGCAGCAGAAACCCCTTGGAAGGCCTCCAGTCAGGAAGCCCTAGAAACCCCTTGGAAGGCCTCCAGTCAGAAGGCCTAGAAGGCCTAGAAGGCCTAGAAGGCCTAGAAGGCCTAGAAGGCCTAGAAGGCCTAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA
FEBS L	FEBS Lett. 26, 74-76, 1972 A; Title: The covalent structure of collagen: amino acid sequence of alphal-CB3 from calf	Db 144 LeuProGlyPheProGlyProLysGlyAlaAlaGlyGluProGly 138

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o q	159 LysalaGlyGluArqGlyValProGlyProProGlyAlaVald vivs 177	qq	411 oProGl
δλ		Oy.	1146 AAGGTC
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qq	GluGlnGlyProAlaGly	qq	440 yAlaAl
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QQ	204 SerProGlyPheGlnGlyLeuProGlyProAlaGlyProProGlyGluAlaGlyLvs 222	qa	459Pr
ογ		Qy	972 TCTGCT
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Οy		Qy	912 CAGGTG
QQ	223 ProGlyGluGlnGlyValProGlyAspLeuGlyAlaPro235	qq	491
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٥y		Οy	848 -CCAGG
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q	380 yAlaAspGlyGlnProGly	QQ	664 *Gly***
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qq	411	
ολ.	1146	CGAAGAGCCGCCGCAGGGTGCG
qq	427	gGlySerAlaGlyProProGlyAlaThrGlyPhePro
Qy Db	1086	GGCATGCGGCACCACAGCTGGTGCAGCGGGAAGCAGGCGCCCAGGTTCCGG 1033
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Οy	912	CAGGTGAGGAAGATGAGGGTGAGGCCAAAGAGGCACTCCT 870
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Qy	795	Tegceacagregic
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Qy	735	AAGAGGTCAGAGAGCGGGGGGGGGGGGGGGAGCACCTGGCCACAGAAGTCCA 678
qq	552	aSerGlyGluArgGlyProProGlyProMetGlyProProGlyLeuAlaGlyProPr 571
Qy .	229	GCAGCCCCACGCCCAGGATGAGCAGTGCCAGGGGCCTGGGATCCGGG 625
Dp	571	3luGlyAlaProGlyAlaGluGlySerProG
٥y	624	CACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAGAGGCTCAGCAGGATGCCC 565
qa	587	yargaspGlySerProGlyalaLysGlyAspArgGlyGluThrGlyProAlaGlyAlaPr 607
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qq	664	*Gly***ArgGlyIleLysGlyHisArgGlyPheSerGlyLeuGlnGlyProProGlyPr 684
٥y	7	AGGGGCTCACCCACAGCCTCTGGACCATAGTGGG
qa	4	OProGlySerProGlyGluGlnGlyPro-SerGlyAlaSerGlyProAlaGlyProArgG 704
Yo	277	CCAGGGGGTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCGG 223

	GGCCAAGTGGCTCTTGTCAATACTGCTGTAGCAAAGTAATGGGGACCAGACCAGGCCAGGCCAGGCCAAGTAGTGGTTAGTAATGGGGACCAGACCAGGCCAGGCCAGGCAGG	Trocogregated and the process of the	
9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6			
Db 704 lyProProGlySerAlaGlySerProGlyLysAspGly	RESULT 30 B41182 collagen alpha 1(II) chain precursor (long splice form) - mouse c;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Accession: B41182 R;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E. S;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E. S;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E. S;Metsaeranta, M.; Toman, D.; de Cromplete nucleotide sequence, exon structure, and A;Reference number: A41182; MUID:9138489; PMID:1885613 A;Reference number: A41182; MUID:9138489; PMID:1885613 A;Residue; preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-1487 <met> A;Residues: 1-1487 <met> A;Cross-references: GB:M65161 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology <wcc> F;33-91/Domain: von Willebrand factor type C repeat homology <wcc> F;1259-1487/Domain: fibrillar collagen carboxyl-terminal homology <fcc></fcc></wcc></wcc></met></met>	Alignment Scores: 7.65e-12	0y 2440 ATATGTTCAAATCCCATGGAGGAGTGTTTCATCATCAAAACTCCCATGCAAGAGCTACAT 2381 Db 68 IleCysGluAspProAspCysLeuAsnProGluIleProPhe

qq	417 lyAlaLysGlySerAlaGlyAlaProGlyIleAlaGlyAlaProGlyPheProGlyP 436	
٥y	993	
QQ	436 roArgGlyProProGlyProGlnGlyAlaThrGlyProLeuGlyProLysGlyGlnA 455	
δλ	992AGGAGGGGCCGACAGCCCTTCTGCTGG 965	
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QY	CTGCCTCCTCAGCCACCAGGAGTGCTGCTACGCAGGTGAG 905	
qq	471 lyGluThrGlyProAlaGlyProGlnGlyAlaPro	
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ογ	873 873	
qa	503 leGlyProProGlyGluArgGlyAlaProGlyAsnArgGlyPheProGlyGlnAspGlyL 523	
٥y	824	31
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δλ	823 GGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATGAAGGCATAGAC 770 C.Accessio	: 27 ssic
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Qy	GCAGCAGAGGCGG 401	
qq	657 lyAlaProGlyProSerGlyPheGlnGlyLeuProGly 669	
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qq	683 lnGlyIleProGlyGluAlaGlyAlaProGlyLeuValGlyProArgGlyGluArgGlyP 703	
0y	311	·
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Oy to	GGCTCAGGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGGTCCAGAAGCT	
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205 GCGGCCTCTCCTCCTTGCTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGC 146
                      145 CAGCCCTTTGGT----- 113
                                                                                               782 AspGlyGlyArgGlyLeuThrGlyProIleGly-ProProGlyProAlaGlyAlaAsnGl 801
                                                                                                                                                                                                                                              278 CCCACTATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 TIGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTAT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 GIGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGC 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518 CGTGGACGCTATGGCCGCCGCCCTTCATCTGGGACTGTCCTTGGGCATCTGCTG 577
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                                                                                                                                                                                                                    76 GGACACGTCTCATCACTCAGATCCTGGC------CGAGGCGCGCGCGCGCTGTCACC 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transport protein - common tobacco
s: Nicotiana tabacum (common tobacco)
27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 26-May-2000
ion: S48789
- X.Y.Z.; Frommer, W.B.
It of the EMBL Data Library, October 1994
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ion: S48789
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126
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mily: common tobacco sucrose transport protein
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127	683	147	743	167	803	/81	839	207	896	777	245	1016	. 259	1076	276	1136	29	1196	31.	125	327	1316	137		1418	38:	1	40.		42.	150	44	15	
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A; Cross-references: GB:S63190; NID:9234368; PIDN:AAB19627.1; PID:9234369
A; Note: sequence extracted from NCBI backbone (NCBIN:63190, NCBIP:63192)
C; Superfamily: collagen alpha 1(I) ohain; fibrillar collagen carboxyl-terminal homolo C; Keywords: alternative splicing; colled coll; extracellular matrix; glycoprotein; tr F;1191-1419/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-1419 <MET>
A; Residues: 1-1419 <MET>
A; Cross.references: GB:M65161
B; Cheah, K.S.; Lau, E.T.; Au, P.K.; Tam, P.P.
Bevelopment 111, 945-953, 1991
A; Title: Expression of the mouse alpha 1(II) collagen gene is not restricted to carti A; Reference number: A44885; MUID:91347939; PMID:1879363
A; Accession: A44885
                                                                                                                                                                                                                                                                                                                        exon structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1894 AAAGTAAATGGCGACCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTG 1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1834 GCTGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGAAGGC 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1954 GGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGC 1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2104 CAGCTACGCACCTCAGCAGCACACAGGGTGGCAGAGAGCCACATTACTTTGGCAGCAAC 2045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2044 AGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAACAGGAGCGGGGGGGCTGGGA--- 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 ProGlyAsnProGlyProAlaGlyProProGlyProProGlyProProGlyLeuSerAla 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 GlyAsnPhe-----AlaAla 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
-CIGCICCCACCICCACCCGCG 1660
                                                                                                                                                                                C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999
C.Species: Al-1822, A44885
C.Species: A1-182, A44885
J. Biol. Chem. 266, 16862-16869, 1991
A.Title: Mouse type II collagen gene. Complete nucleotide sequence, exon strates commer: A1-182; MUD:91358489; PMID:1885613
A.Specession: A4-1182
A.Status: preliminary; not compared with conceptual translation
                           56 Gln------GlyProAlaGlyGluGlnGlyProArgGlyAspArgGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 LysGlyGluLysGlyAlaProGlyProArgGly-----ArgAspGlyGluProGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 GlnLysGlyGluProGlyAspIleArgAspIleIleGlyProArgGlyProFroGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                collagen alpha 1(II) chain precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-759-143-110 (1-3410) x A41182 (1-1419)
  1619 GTGGGTGCTGGAGGCAGTGGC
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318.50
31.66%
26.75%
5.12%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-28 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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--- CCAGGCAGATGCCCCGGCAGC 1730

1774 ACTAICCA---GGAIGGCGAGGI

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qq		è
οy	1729 CACCCTGGCCTCGGTGGGCTCACCCACCACGTACGGAGACATCACAGGCAGA 1673	S 1
Dp	169 lyProMetGlyProArgGlyProProGlyProAlaGlyLysProGlyAspAspGlyGl 188	gg
0y	1672 GGCCCGCAGAGCGCGGGTGGAGGT	δ t
Dp	188 uAlaGlyLysProGlyLysSerGlyGluArgGlyLeuProGlyProGlnGlyAlaArgGl 208	27
٥y	1636 ACTGCCTCCAGCACCCACGTGTCCATTAGGGAAGGGAGCTCCAGGCTTAGG 1586	Ολ
qq	208 yPheProGlyThrProGlyLeuProGlyValLysGlyHisArgGlyTyrProGlyTheu 227	QQ
οy	1585 GCCTGGCAGGAAGCTGGTCATCAGGCTGTCGTCACTGCTAGCACCTCCAGTGTCCCCTCG 1526	Qy
qq	228 -AspGlyAlaLys-GlyGlualaGlyAlaPro	đ
οy	1525 GTATTTGGGCAGGAACACCTGCTTCTCCCGGTAGAGGGAGG	Οy
qq	11::: 238 lyvalLysGlyGluSerGlySerProGlyGluAsnGlySerPro 253	qa
0y	1465 GATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGCTGAAGGTGTCACCACCACCACCAC 1406	Qy
qq	253 lyproMetGlyProArg-GlyLeuProGlyGluArgGlyArgThrGlyProAlaGlyA 272	qa
οy	1405 ACTGTGGGACAGGCATGTGGCACCGGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATA 1346	Qy
QQ	111 11 11 11 11 11 11 11	Ор
QY	1345 GACTECTCGAGTGCCGAATCGCTGCACCAGCCGGTCCATGACCAGAGAGAAGACCAGGGA 1286	QY
qq	283ProGlyProAlaGlyProProGlyP 290	qq
QY	1285 GATGGCGCACTGCAGGAACAGCCCCAGGCTGCCCATCCGAACGCCTTCATCATA 1232	οy
qq		qa
Oy	1231 GTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGCACGCCCTGGTACAGCCCCTCGCC 1172	Qy
Db	310 lyProThrGlyAlaArgGlyProGluGlyAlaGlnGlySerArgGlyGluP 327	qa
Qy	AGGTCATGAGTG	ΟŸ
Db	327 roGlyAsnProGlySerProGly·······ProAlaGlyAlaSerGlyAsnP 342	qa
Qy	1111 CACGAAGAGCCGGCGCAGGGTGCGGGCATGCGGCACAGCTGGTGCAGCCGGGAAG 1052	Qy
QQ	342 roGlyThrAspGlyIleProGlyAlaLySGlySerAlaGlyAlaProGlyIleA 360.	qa
۵y	1051 CAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGCATGGACAGCAGTGGGGGCGACA- 993	oy.
qq		qq
Oy	98	VO.
q	379 lyProLeuGlyProLysGlyGlnAlaGlyGluProGlylleAlaGlyPheLysGlyAspG 399	qq
٥y	ACAGCCCTTCTGCT	δλ
QQ		qq
٥y	928 CACTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAGAGGCACT 873	ΟŊ
qa	415GlyProAlaGlyGluGluGlyLysArgGlyAlaArgG 427	Dp
δλ	873 673	Qy
qo	427 lyGluProGlyGlyAlaGlyProIleGlyProProGlyGluArgGlyAlaProGlyAsnA 447	q _Q
λζ		RESULT 33 CGHU1E
ą	447 rgGlyPheProGlyGlnAspGlyLeuAlaGlyProLySGlyAlaProGlyGluArgGlyP 467	collagen a

Qy	847	,
Db	467	roSerGlyLeuAlaGlyProLysGlyAlaAsnGlyAspProGlyArgProGlyGluProG 487
Qy	793	AAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCGGGGTCCCGGGAA 734
qa	487	lyLeuProGlyalaArgGlyLeuThrGlyArgProGlyAspAlaGlyProGlnGlyL 506
oy G	733	GTCAGAGAGAGGCCTCCAGTGGAGTGAAGCACACGTGGCCACAGAAGTCCAGCAG 67
3 8) r	
3 A	526	Glyv
٥y	637	CCTGGGATCCGGGCACAGCAGCCCTGGTAGCCAGCCGGCCCTTGGGATGAGAAGAGGCT 578
qa	543	snGlyGluProGlyLysAlaGlyGluLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyL
٥y	577	CAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGCCATAGCG 524
qq	554	euAlaGlyAlaProGlyLeuArgGlyLeuPro564
٥y	523	TCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCA 468
qq	565	GlyLysAspGlyGluThrGlyAlaAlaGlyProProGlyProSerGlyP 581
2γ	467	CTGGACCAATGCCCAGCACCATGCTCATGAACTTCTCCTCTAC 425
qo	581	roAlaGlyGluArgGlyGluGlnGlyAlaProGlyProSerGlyPheG 597
λy	424	CCCCACTTCCAGCAGCAGAGGCGGCACATAGGTGATGCCTGCGGGCCAAACACACCTCCAG 365
qc	597	nglyLeuProGly
λy	364	CAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGC
qc	209	
Σλ	316	CAGCAGGCGGCTCACCACCTCTGGAC 287
qc	627	alGlyProArgGlyGluArgGlyPheProGlyGluArgGlySerProGlyAlaGlnGly- 646
λy	286	CATAGTGGGCCAGGCGGTAGGGGTCAGGGGCCGTTCAGGCACTCCAGAACTGCTT 230
qc	647	LeuGlnGlyProArgGlyLeuProGlyThrAspGlyProLysGlyAla 665
27	229	CGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAGG 170
q	999	lyLeuGl
λλ	169	AATCAGCCAGGCCCATTTCTGCCAGCCCTTTGGT
q	989	rgGlyAspVal
λ	130	
	902	
λ	100	GCTGCTGTGGGGGCACCTCAGTGGGGACACGTCTCATCACTCAGATCCTGGC 49
q	725	oproGlyproAlaGlyAlaAsnGlyGluLySGlyGluValGlyProFroGlyProSerGl 745
λγ	48	CGAGGCGCGCTGTCACCCGGA 25
	745	ySerThrGlyAlaArgGlyAlaProGly 754
ESULT 33 GHU1E collagen al	lpha snal	ESULT 33 GH01E Ollagen alpha 1(XI) chain precursor – human ;Atternate names: procollagen alpha 1(XI) chain

2954 AGACTAGAGGGGGAACCAGGCTGGCCCAAGAAAAGGGTTA 2895 460GlyProThrGlyProProGlyAspProGlyAspArgGlyProPro 474 2894 GGGAAGCCGTTGAGACCTGAAGCC	566 iGInGlyproprodiviringly-LysProGlyLysArgGlyArgProGlyAlaAsp 585 2537	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 00 00 00 00 00 00 00 00 00 00 00 00 0	6
C: Species: Homo sapiens (man) C; Date: 31-Mar-1990 #sequence_revision 03-oct-1995 #text_change 08-May-1998 C; Accession: A35239; A31795 C; Accession: A35239; A31795 B; Yoshioka, H.; Ramirez, F. J. Biol. Chem. 265, 6423-6426, 1990 A; Title: Pro-alphal(XI) collagen. Structure of the amino-terminal propeptide and express A; Reference number: A35239; MUID:9020294; PMID:1690726 A; Accession: A35239 A; Molecule type: mRNA A; Rossidues: 1-588 «XOS A; Rossidues: 1-588 «XOS A; References: GB:305407 B; Bernard, M.; Yoshioka, H.; Rodriguez, E.; van der Rest, M.; Kimura, T.; Ninomiya, Y.; D; Biol. Chem. 263, 17159-17166, 1988 A; Cross references: GB:305407 B; Bernard, M.; Yoshioka, H.; Rodriguez, E.; van der Rest, M.; Kimura, T.; Ninomiya, Y.; A; Hitle: Cloning and sequencing of pro-alphal(XI) collagen cDNA demonstrates that type X cartilagenous tissue. A; Molecule type: DNA; MRNA A; Residues: 538-1806 < RBR> A; Rocross-references: GB:304177 A; Accession: A31795 A; Rossious: 538-1806 < RBR> A; Residues: 538-1806 < RBR> A; Rocross-references: GB:304177 A; Gene: parts of this sequence were determined by protein sequencing C; Genefics: A; Gene: GDB:COLIIAI; COLL6 A; Gene: GDB:COLIIAI; COLL6 A; Gene: GDB:COLIIAI; COLL6 A; Molecues: GB:373; 618/3; 666/3; 681/3 A; Note: the list of introns is incomplete.	GXI) Chain (see PTR:CGHGC), initially linked by disulfide bonds among their carboxyl- rmed with desmosine cross-links made from lysine and allysine residues G; Function: G; Function: G; Function: G; Superfamily: G; Superfa	Alignment Scores: Pred. No.: Pred. No.: Pred. No.: 116.00 Matches: 315 Score: 116.00 Conservative: 61 Best Local Similarity: 26.03\$ Mismatches: 413 Query Match: 1.048 Mismatches: 413 Gaps: 106 Indels: 71 US-09-759-143-110 (1-3410) x CGHUIE (1-1806) Oy 3101 ACAAAGGCTTGGGAAACCGCACTTGTGCTTCTGGT

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QQ		qq	1044 ysGly(
Oy		Qy	1126 GCTGC
qa	GlyPheLysGlyAspMetGlyLeuLysG	q	1055 roval
οy		Oy	1066 GTGCAC
QQ	 796	qa	1069 lyPro]
VO		Qy	1006 GCAGTG
q	816 ysGlyArgAlaGlyProThrGlyAspProGlyProSerGlyG 830	QΩ	1089 ysGlyA
δ	AATGGCGACCAGAC	٥٧	946 TGCCTC
q 0	YLYSLeuG 838	qq	1102
Ολ	1874CCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAAT 1820	δλ	886 GCCAAA
qq	838 lyValProClyLeuProGlyTyrProGlyArgGln	qa	1108 ly
Qy		ζō	829 GTCAAT
qq	850pheprodiscription	qa	1119
οy		Qy	769 AGAGTA
q	 861 roGlyAlaAsnGlyGluLySGlyAlaArgGlyValAlaGlyLysProGlyProArqGlyG 881	qq	1131 leGlyG
Qy		ζō	709 TGGAGT
QΩ		qq	1150
οy		QY	649 CAGCTC
QQ		qq	1163 leAlaG
Qy		δλ	589 GAGAAA
q		qa	1172ProA
δy	1558 GICCICACIGCIAGCACCICCAGIGICCCCICGGIAITIGGGCAGGAACACCIGCIICIC 1499	Qy	529 ATAGCG
QQ		qa	1190 PhePro
ογ	1498 CCGGTGGTAGAGGGAGGCCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCC 1439	Qy	469 CACTEG
QΩ		qa	1206 roGlyG
ΟŅ	SCTGAAGCTGTCACCACGGCCA	Qy	421 CACTTC
qq		qa	1224 roglyp
οy	1378 AGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATGGCTGCAC 1319	Qy	361 AAAGGT
qq	977 Glu-ThrGly	qa	1244
Qy		δδ	301 CCACAG
qq		qa	1257 roglyG
Qy	1262 CCAGGCTGCCCATCCGAACGCCTTCATAGTGTCTCCGGGGCCTCGGTGCCCGGCTC 1205	δδ	244 ACTCCA
qq		qa	1277
Qy	1204 AGCTCTGGGCACGCCTGGTACA1176	δλ	187 TGCCGC
qq		qa	1295 AlaLys
ò	1175CGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCA 1127	Qy	147 -GCCAG
·		qq	1314 oGlyAsı

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1126	CTCAGCCACGAAGAGCCGGGGGCAGGGGGGGGGATGCGGCAGCACAGGT
1055	proglygludrgGlySerAlaGly
1066	GCCGGGGAAGCAGGCCCCAGGTTCCGGAAAGCCAAGCGGCCCGGCATGGACA 100
5	ıyrıdılesiylenargsiyargrrosiyrrosinsiyrroproglyproAlaGlyGl
1006	6 GCAGTGGGGGGGCAAGGAGGGGCCGACAGCCCTTCTGCTGGCTG
94	TGCCTCCTCAGCCACCAGCAGTGTGGCTGAGGTGAAGATGAAGATGAGAAGATGAGAAGATGAGAAGA
0	
886	GCCAAAGAGGCACTCCTCGGTGCCCAGGT AGGGGCCCAGGGCACTGGTGTCCCA 830
2 5	II TOTAL TOT
i Ai	
769	AGAGTAGGCCTGGCGACAGTGGTCCGGGACGGGAGGAGGTCAGAGAGAG
1131	
709	TGGAGTGAAGCACACGTGGCCACAGAAGTCCAGCAGCCCCACGCCCAGG
1150	
64	CAGCTCCAGGGGCCTGGGATCCGGGCACAGCAGCCCTGGTAGCCAGCC
۰	leAlaGlyGlyA
589	GAGAAAGAGGCTCAGCAGGATGCCCAAAGAACAGTGCCCAGATGAAGGCCCGCGGCGCGCC 530
1 6	riorigelyAlaArgely 11
1190	ATACCSTCCACGGGGGCCCAG 470 PheProGlyProPro-GlyProlleGlyLeuGlnGlyLeuProGlyProPro-
469	CACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCTCTTACCC 422
ō	roclyGluLysGlyGluAsnGlyAspValGlyProTrpGlyproproGlyProp 12
421	CTTCCAGCAGCAGAGGGGGCACATAGGTGATGCCTGCGGCCAAACACACCTCCAGGCC 362
7 7	Octyfiontgetyfioeinelyfronsholynaanspelyfroeinelyfroefy- 12
	AAANGATTAACAGGTGGCTTTTCGGTGCGCGGGGGGGGGG
301	AGGGCTCAGGGGGCCGTTCAGGC 24
1257	GlyGl
244	GCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGC 188
, ,	GiuargeiyeiuLyseiyeiuAlaGiyProProGiyAlaAlaGlyProProGiy 12
18	GCCGCCAACTGCCTAGGAATCAGCCGGCGCCCATTTCT 148
ა .	LaLysGlyProProGlyAspAspGlyProLysGlyAsnProGly-ProValGlyPhePr 1
14	GCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGCTGCTGGG 89
1314	oglygluLeuGlyP

CGA	\$ 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	320 CACCGGAA
C; Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999 C; Accession: 516366 R; Pettit, J.; Kingston, I.B. J. Biol. Chem. 266, 16149-16156, 1991 A; Title: The complete primary structure of a nematode alpha-2(IV) collagen and the parting A; Reference number: \$16366; MUID:91340768; PMID:1714907 A; Accession: \$16366 A; Motecule type: mRNA A; Residues: 1-1763 < JBI> A; Residues: 1-1763 < JBI> A; Cross-references: \$68:M67507; NID:9159648; PIDN:AAA18014.1; PID:9159649 C; Genetics: A; Introns: 229/3; 266/3; 305/3; 424/1; 489/1; 548/1; 656/3; 790/1; 891/1; 963/1;	0	559 InGlyGluArgGlyLeuProGlyIleProGlyAlaThrGlyAlaProGlyAspAspGlyL 579 482 TGTGTCCGCTCCTAGGCTGAGCCAGTGACCATGGCGGGGCGCGCGG 541
Superramnity: collagen alpha 1(N.) chain substance; cell binding; coiled coil; disulfid Keywords: alternative splicing; basement membrane; cell binding; coiled coil; disulfid 1-26/Domain: signal sequence #status predicted <sig> 27-1763/Product: collagen alpha 2(IV) chain #status predicted <mat> 27-42/Domain: non-collagenous NHI #status predicted <nhi> 43-1529/Domain: collagenous #status predicted <col/> 43-1529/Domain: cell attachment (R.G-D) motif 1530-1363/Domain: cell attachment (R.G-D) motif 1530-1363/Domain: repeat NCI #status predicted <ncii> 1530-1633/Domain: repeat NCI #status predicted <ncii> 1530-1350/Domain: repeat NCI #status predicted <ncii> 31, 34, 39, 41, 536, 539/Disulfide bonds: interchain #status predicted (R.G.D) motif (R.G.D) motifide bonds: interchain #status predicted (R.G.D) motifide Bonds: interchain #status predicted (R.G.D) motifide Bonds: interchain #status predicted (R.G.D) motifide Bonds: #status predicted (R.G.D) motifide Bonds: #status predicted (R.G.D) motifide (R.G.D) (R.G.D) motifical (R.G.D) (R.G.</ncii></ncii></ncii></nhi></mat></sig>		ThrLeukrgProGlyProCGTGGGGCTGCTGGA
Alignment Scores: 2.5e-11 Length: 1763 Pred. No.: 312.50 Matches: 315 Score: 31.65% Conservative: 60 Best Local Similarity: 26.58% Mismatches: 430 Query Match: 2 Best Local Similarity: 26.58% Mismatches: 430 Guery Match: 2 Gaps: 68 US-09-759-143-110 (1-3410) x S16366 (1-1763)	oy Oy Oy	GACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGC
CGCGCTGCCTCCGGTGACAGCCGCGCGCCTCGGCCAGGATCTGAG 	oy da oy oy	947 GCGCTGGGCCCCACCGAGCAGAGGCTGTCGGCCCCTCCTTGTCGCCCCATGC 1006 1111 715 etGlyProProValProdluSerGlnLeuargProGlyProProGlyLysAspGlyLeuP 735 1007 TGTCCATGCCGGGCCCGGTTGGCTTTCCGGAGCCCTGCTTCCCCGGCT 1062 735 roGlyLeuProGlyProLysGlyGlualaGlyPheProGlyAlaProGlyLeuG 753 1063GCACCAGCTGTGCCTGCCCCGG
116 CTGAGAAGCTGGACCAAAGGGTGGCAGAAATGGGCGCTGG 163 140 LeualaglyProProGlyalaLySG1/G1 161 141		753 InGlyProAlaGlyLeuProGlyMetLysGlyAsnProGlyLeuProGlyA 773 1097 CGCCGCTTTCTTCGTGGCTGAGCTGCAGCTGATCCTTCACGCTGTT- 1155 1097 CGCCGGCTTTCTTCGTGGCTGAGCTGACCTTCACGCTGTT- 1155 1111

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849	898	1402	888	1441	906	1473	926	1522	1558	964	1618	626	1678	996	1722	1009	1770	1029	1809	1046	1869	1060	1929	1062	1989	1081	2049	1090	2109	1090	2163	1107	2223
			ProGlyLeuAlaGlyAlaProGly	AGTGTGGCCGTGGT	YreuProGlyrysGluGlyProGlnGlyPro	TTCACCTTCTCAGCCCTGCAGATCCTGCCCTA		ysglyaspThrGlyLeuProGlyValProGlyLeuAladlyProProGlyClnFroGlyProGlyClnFroGlyLeuAladlyProProGlyClnFroGlyLeuAladlyProProGlyClnFroGlyClnFroGlyLeuAladlyProProGlyClnFroGlyLeuAladlyProProGlyClnFroGlyC		hePro-GlyGlnLysGlyGlnProGlyValAL				:::	TGTGATGTCTCCGTACGTGGTGGTGAGCCCACCGAGGC	IleProGlyAlaProGlyGlnAspGlyLeuProGlyLeu		ProGlyValLysGlyAspArgGlyPheAsnGlyLeuProGlyGluLysGlyGluProGly	TAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCTT	ProAlaAlaArgAspGlyGluLysGlyGluProGlyLeuProGlyGlnPro	TATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGG	ArgGlyProGlnGlyProProGlyLeuProGlyLeu	CCTGGGTCTGGTCGCCATTTACTTTGCTACAGGTAGTATTTGACAAGAGCGACTTGGC			 LeuLysGlyAspGluGlyGlnProGlyTyrGlyAlaProGlyLeu-MetGlyGluLy		sGlyLeuPro	TGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTAGCTGCACAG				GGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCATG 2
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2224 CACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTC 2283
                                                                     1121 lyLeuProGlyGlnAspGlyLeuProGlyLeuProGlyGlnLysGlyGluSerGlyPheP 1141
                                                                                                       2284 CTAGTTGAGACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTT 2343
1107 heProGlyLeuLysGlyGluAla--------GlyLeuPro---GlyAlaProG 1121
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                                                                                                                                         2344 TCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTT 2403
                                                                                                                                                                                                                1152 euProGlyLys------MetGlyAlaP 1159
                                                                                                                                                                                                                                                                                    1159 roGlyIleArg---GlyGluLysGlyAspAlaGlyLeuProGlyLeuProGlyGluArgG 1178
                                                                                                                                                                                                                                                                                                                          2460 -----AGTCCTGAGGGCAACACACAAAAACCAGGTCCCCTCAGCCCACAGACTGT 2511
                                                                                                                                                                                                                                                                                                                                                    1178 lyLeuAspGlyLeuProGlyGlnLysGlyGluAlaGlyPhePro------ 1192
                                                                                                                                                                                                                                                                                                                                                                                             2512 CTTTTTGCTGATCCACCCCCTCTTACCTTTATCAGGATGTGGCCTGTTGGTCCTTCTG 2571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2572 TTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAATTTAACAAAGTAGAAG 2631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2875 TCAGGTCTCAACGGCTTCCCTAACCAC--------CCCTCTTCTTGGC 2916
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|1326 ProGlyLeuSerGlyIleProGlyLysArgGlyAsnAspGlyIleProGlyLysProGly 1345
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| 1346 ProAlaGlyLeuProGlyLeuProGlyMetLysGlyGluSerGlyLeuProGlyProGln 1365
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collagen alpha 1(VII) chain precursor - human N'Alternate names: procollagen alpha 1(VII) chain C:Species: Homo sapiens (man) C:Species: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 20-Sep-1999 C:Accession: A54849; PH0844; S16316; I56328; A30296; I84686

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Best Local Similarity:
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A; Residues: 2395-2871, 'S', 2873-2944 <RE2>
A; Cross-references: GB:L06862; NID:9388713; PIDN:AAA89196.1; PID:9388714
A; Cross-references: GB:L06862; NID:9388713; PIDN:AAA89196.1; PID:9388714
B; Christiano, A.M.; Rynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A; Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser subs
A; Reference number: A55255; MUID:9424777; PMID:8170945
A; Contents: annotation
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
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A;Molecule type: mSNA
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A;Molecule type: mSNA
A;Molecule type: mSNA
A;Molecule type: mSS1236; NID:3262308; PIDN:AAB24637.1; PID:3262309
B;Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E.
A; Eltzer, J.L.; Edeavage of type VII collagen by interstitial collagenase and type IV collagena
A;Reference number: A30296; MUID:89139437; PMID:2537292
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A; Molecule type: protein
A; Molecule type: prote
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A; Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot A; Reference number: 156328; MUID:93107742; PMID:1469284
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary sequence of the alphal(VII
A;Reference number: A54849; MUID:94327588; PMID:8051117
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A;Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A;Reference number: S16316; MUID:91334380; PMID:1871109
A;Accession: S16316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;MOlecule type: mRNA
A;Residues: 'EFR',340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C',
A;Cross.references: DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:BAA02853.1; PID:g453699
A;Experimental source: keratinocyte
A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
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A;Residues: 815-892, 'E', 894-1439 <PAR>
A;Cross-references: GB:M65158; GB:S49017; NID:9180914; PIDN:AAA96439.1; PID:9180915
                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
Assaidues: 1-294 A CARPA
A; Gross-references: GB:LD2870; NID:9987124; PIDN:AAA75438.1; PID:9987125
A; Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
Biochien: Blobbys. Res. Commun. 183, 958-9587, 1992
A; Title: Molecular cloning and characterization of type VII collagen cDNA.
A; Reference number: PHO844; MUID:92231902; PMID:1567409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                     Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GDB:128750; OMIM:120120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: keratinocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: GDB: COL7A1; EBR1; EBD1; EB
                                                                                                                                                                                                                      A; Accession: A54849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: I56328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Function:
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F)1254-2783/Region: interrupted helical
F)1254-2783/Region: interrupted helical
F)1364-1336/Region: cell attachment (R-G-D) motif
F)2008-2010/Region: cell attachment (R-G-D) motif
F)2084-294-20main: carboxyl-terminal nonhelical #status predicted <NC2>
F)2864-2949/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F)2876-2999/Domain: animal Runitz-type proteinase inhibitor homology <BPI>F)2876-2999/Domain: animal Runitz-type proteinase inhibitor homology <BPI>F)2167,2186,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro) #status experimental
F)2625,2631/Modified site: carbohydrate (Lys) #status experimental
F)2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
F)2634,2802,2804/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1196 pProGluGlnLeuArgArgLeuAlaProGlyMetAspSerValGlnThrPhePheAlaVa 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 TCCCAAAAACCCTTCTCTA----GGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCT 2265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GlnLysGlyGluProGlyGl 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------CCCCTCAGGACTCTTCCCCTACAATAAGT 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2441 CATATGTTCAAATCCCATGGAGGAGTGTTTCATCCTAGAAACTCCCATGCAAGAGCTACA 2382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1177 IleArgGluAla-GlnAlaSerGlyLeuAsnValValMetLeuGlyMetAlaGlyAlaAs 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1236 aSerPheThrThrGlnProArgProGluPro---CysProValTyrCysProLysGly-- 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1261 uMetGlyLeuArgGlyGlnValGlyProProGlyAspProGlyLeuProGlyArgThrGl 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1281 yalapro-----GlyproGlnGlyPropro-----GlySer-AlaThrAlaLysGlyG 1297
                 F.17-1253/Lonain: amino-terminal appua 1(711) using $1.512.5100nain: amino-terminal nonhelical #status predicted (NCI) F.36-201/Domain: amino-terminal nonhelical #status predicted (NCI) F.36-201/Domain: ibronectin type III repeat homology (*VWAI) F.327-413/Domain: fibronectin type III repeat homology (*RN3) F.502/Domain: fibronectin type III repeat homology (*RN3) F.508-693/Domain: fibronectin type III repeat homology (*RN5) F.508-693/Domain: fibronectin type III repeat homology (*RN5) F.686-771/Domain: fibronectin type III repeat homology (*RN5) F.686-771/Domain: fibronectin type III repeat homology (*RN5) F.686-771/Domain: fibronectin type III repeat homology (*RN8) F.686-771/Domain: fibronectin type III repeat homology (*RN8) F.686-952/Domain: fibronectin type III repeat homology (*RN8) F.1170-1172/Region: cell attachment (*R-6-D) motifi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----CTTAGAGATGGGAAACCAGGT---GACTGAGTT----TATTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2264 GAGCCTGGGTAATCCACCTGCAGAGTCCCGGCATTCCAGTGCATGGAGCCCTTCTGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2204 CCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2144 CTGGGGAGAGAGAGAGA-----GGGACGCCCCAGCCCCCAGCTGTGCAGCTACGCACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2090 AGCAGCACAGGGGGGCAGCAGAGGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1158 ProGlyValMetValLeuLeuValAspGluProLeuArg------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1171 ------GlyAspilePheSerPro------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2944
260
37
362
291
53
collagen alpha 1(VII) chain #status
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
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31.26%
27.37%
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Db	1586		1603
Qy	926		936
Db	1604	 GlyProProGlyAspSerGlyProProGlyGluLysGlyAspProGlyArgProGlyPro	1623
٥y	935	CCACCAGCAGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAGAGGC	876
Db		ProGlyProValGlyProArgGlyArgAspGlyGluValGlyGluLysGlyAspGluGly	1643
Qy Db	875		846 1663
٥y	845	GGGCACTGGTGTCCCAGTCAATGGCAGGCAGGTAGCCCAGGCAGCCCCCAAGACTGA	786
qa	1664		1678
٥y	785	TCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAG	726
Ob	1679	GlyGluAspGlyArgAsnGlySerProGlySerSerGlyProLysGlyAspArgGlyGlu	1698
٥٧	725	AGAGCAGGGCCTCCAGGGCTTCA	702
qq	1699	ProGlyProProGlyProProGlyArgLeuValAspThrGlyProGlyAlaArgGluLys	1718
οy	701	CCAGGATGA	657
q	1719		1737
δy	656	(3	597
qq	1738		1743
λά	296	r) -	552
eg G	1744	GluargGlyIleGluGLyPheArgGlyProProGlyProGlaglyAspPro	1760
Σγ	551	•	492
. qo	1761		1769
λy	491	-	432
qc	1770		1781
λy	431		372
qc	1782	GlyLeuAspGlyLysProGlyAlaAlaGly	1794
λy	371		318
qC	1795	, y LeuArg	1814
λλ	317	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	278
q	1815	_	1834
λλ	277		231
ą	1834	LysProGlyLeuAsnGlyLysAsnGlyGluProGlyAspProGlyGluAspGl	1854
λy	230	TCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAG 1	171
q	1854		1874
λ	170	GAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCC	114
q	1874		1894
λλ	113	CATGCTCAACACCTGCTGCTGTGGGGCACCTCATGGGGACACGTCTCATCACTCG :	57

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A; Description: structural component of extracellular fibrous polymer associated with A; Note: may play a role in controlling the lateral growth of collagen I fibrils C; Superfamily: colled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxypr F; 1-26/Domain: signal sequence #status predicted <51G>F; 27-1250/Product: collagen alpha 2(V) chain #status predicted <AMT>F; 27-1250/Product: collagen alpha 2(V) chain #status predicted <AMT>F; 27-193/Domain: amino-terminal propeptide (uncleaved) #status predicted <NMP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;190-186/Region: helical
F;100-186/Region: helical
F;100-186/Region: helical
F;100-186/Region: helical
F;100-186/Region: helical
F;100-186/Region: cell attachment (R-G-D) motif
F;100-106/Region: cell attachment (R-G-D) motif
F;103-1135/Region: cell attachment (R-G-D) motif
F;103-1135/Region: cell attachment (R-G-D) motif
F;103-1135/Region: cell attachment (R-G-D) motif
F;113-1136/Pomain: carboxyl-terminal nonhelical telopeptide
F;125-1250/Region: cell attachment (R-G-D) motif
F;125-126/Region: cell attachment (R-G-D) motif
F;113-1136/Pomain: carboxyl-terminal nonhelical telopeptide
F;125-1250/Region: carboxyl-terminal homology <FCC>
F;27/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;104/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;290,293,296,608,614,1004,1007,1013,1028,1034/Modified site: 4-hydroxylysine (Lys) #status seperimental
F;290,293,296,608,614,1004,1007,1013,1028,1034/Modified site: 5-hydroxylysine (Lys) #status experimental
F;1250-1251/Cleavage site: 610-Asp (procollagen C-endopeptidase) #status predicted
F;1293,1299,1325/Disulfide bonds: interchalm #status predicted
F;1293,1299,1325/Disulfide bonds: #status predicted
F;1333-1494,1402-1447/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 2q31-2q31
A; Introns: 33/1; 812/3; 830/3; 848/3; 884/3; 902/3; 922/3; 974/3; 1046/3; 1064/3; 114
C; Complex: type V collagen may be a homotrimer of alpha 1(V) chains (see PIR:CGHUIV),
alpha 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among
ength, is formed with desmosine cross-links made from lysine and allysine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA A; Restaudes: 1449-1463, Ex,1465-1495, A' <TSI>A; Restaudes: 1449-1463, Ex,1465-1495, A' <TSI>A; Cestaudes: 1449-1463, Ex,1465-1495, PIDN: AAA51858.1; PID: 9179696 A; Cross-references: GB: J03051; NID: 9179695; PIDN: AAA51858.1; PID: 9179696 A; Note: the authors translated the codon GAA for residue 1460 as Gln, and GAG for rest c; Comment: Profiles and 1981nes at the third position of the tripeptide repeating unit are 5-hydroxylated and subsequently 0-91ycosylated.
C; Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
                                                                                                                                                                                                         R;Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F. Genomics 3, 275-277, 1988
A;Title: Genetic distance of two fibrillar collagen loci, COL3Al and COL5A2, located A;Reference number: A30017; WUID:89138450; PMID:3224983
A;Recession: A30017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -AGCCGCGCGCTCGG-----CCAGGA 55
                                                                         A; Residues: 1227-1417,'T',1419-1437,'S',1439-1496 <MYE>
A; Cross-references: GB:M11718; NID:g180912; PIDN:AAA52058.1; PID:g180913
A; Experimental source: normal fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;27-108/Region: nonhelical
F;40-99/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GDB:119064; OMIM:120190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-759-143-110 (1-3410) x CGHU2V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.68e-11
312.00
30.80%
26.46%
4.86%
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                                       A; Molecule type: mRNA
A; Residues: 1227-1417,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
A; Accession: A25374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB:COL5A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
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A; Residues: 1003-1034 <RES>
A; Cross-references: GB:M11135; NID:g179693; PIDN:AAA51857.1; PID:g179694
A; Cross-references: GB:M11135; NID:g179693; PIDN:AAA51857.1; PID:g179694
A; Note: part of this sequence were determined by protein sequencing
R; Myers, J.C.; Loidl, H.R.; Seyer, J.M.; Dion, A.S.
B. BAOL. Chem. 260, 112116-11222, 1985
A; Title: Complete primary structure of the human alpha-2 type V procollagen COOH-termina
A; Reference number: A25374; MUID:85289337; PMID:2411731
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A;Residues: 288-291, P', 293-294, X', 296-297;606; X', 608-617 <MOR>
A;Residues: 288-291, P', 293-294, X', 296-297;606; X', 608-617 <MOR>
K;Well, D.; Bernard, M.; Gargano, S.; Ramirez, F.
Nucleic Acids Res. 15, 113-198, 1987
Nucleic Acids Res. 15, 113-198, 1987
A;Title: The pro alpha 2(Y) collagen gene is evolutionarily related to the major fibrill
A;Reference number: A25874; MUID:87146331; PMID:3029669
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A; Note: part of this sequence were determined by protein sequencing
R; Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A; Title: Human alpha I(III) and alpha 2(V) procollagen genes are located on the long arm
A; Reference number: I59025; MUID:85216505; PMID:3858826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31-Jul-1989 #sequence_revision 28'-Jul-1995 #text_change 31-Dec-2000
C; Date: 31-Jul-1989 #sequence_revision 28'-Jul-1995 #text_change 31-Dec-2000
S; Accession: A31427; A5455; S413643; A25874; I55239; I59025; A25374; A30017
R; Woodbury, D.; Benson-Chanda, V.; Ramirez, F.
J; Biol. Chem. 264, 2735-2738, 1989
A; Title: Amino-terminal propeptide of human pro-alpha2(V) collagen conforms to the struct A; Reference number: A31427; MUID:89123368; PMID:2914927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:MS8529; NID:g180834; PIDN:AAC41699.1; PID:g553235
R;Moradi-Ameli, M.; Rousseau, J.C.; Kleman, J.P.; Champliaud, M.F.; Boutillon, M.M.; Bez R: U. D. Blochem. 221, 987-995, 1994
A;Title: Diversity in the processing events at the N-terminus of type-V collagen. A;Reference number: S43642; MUID:94237164; PMID:8181482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Greenspan, D.S.; Lee, S.T.; Lee, B.S.; Hoffman, G.G. Gene Expr. 1, 29-39, 1991
A;Title: Homology between alpha2(V) and alpha1(III) collagen promoters and evidence for A;Reference number: A54555; MUID:92314691; PMID:1820205
A;Accession: A54555
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                                                                                                                                              1894 rovalGlyProProGlyGlnGlyPheProGlyValProGlyGlyThrGlyProLySGlyA 1914
                                                                                        -CGAGGGGGGGGGC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A25874
A; Molecule type: mRNA; DNA
A; Residues: 398-1496 <WEI>
A; Cross-references: GB:X04758; NID:g29588; PIDN:CAA28454.1; PID:g1340175
A; Experimental source: rhabdomyosarcoma cell line
B; Myers, J.C.; Loidl, H.R.; Stolle, C.A.; Seyer, J.M.
J. Biol. Chem. 260, 5533-5541, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB:J04478; NID:g179697; PIDN:AAA51859.1; PID:g179698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collagen alpha 2(V) chain precursor - human
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                                                                                                                                                                                                                                                                                                                                                                 1934 lyGluProGlySer 1938
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                                                                                                                                                                                                                                                                             35 TGTCACCCGGAGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1002-1226 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-463 <WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-32 <GRE>
                                                                                   56 ATCCTGGC
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QQ	242 ProGlyAspProGlyProMetGlyProIleGlySerArgGlyProGluGlyProProGly 261
οy	CTGAGG
Ωþ	262 LysProGlyGluAspGlyGluProGlyArgAsnGlyAsnProGlyGluValGlyPheAla 281
ΟŻ	124
Db	282 GlySerProGlyAlaArgGlyPheProGlyAlaProGlyLeuProGlyLeuLysGly 300
0y	145
Db	301 HisArgGlyHisLysGlyCeuGluGlyProLysGlyGluValGlyAlaProGlySerLys 320
ð á	GCAGAAATGGCGCGTGGCTGATTCCTAGGCAGTTG
an ,	<pre>GlyGluAlaGlyProThrGlyProMetGlyAlaMetGlyProLeuGlyProArgGlyMet</pre>
දු පු	182 GCGCAGCAAGGAGGAGGGCGCAGCTTCTGGAGAGAGGCGAAGCAAGC
Qy	
QQ	ProMetGlyProLeuGlyIleProGlySerSerGlyPhePr 380
Qy	257
qq	380 oGlyAsnProGlyMetLysGlyGluAlaGlyProThrGlyAlaArgGlyProGluGlyPr 400
οy	292
qa	400 oGlnGlyGlnArgGlyGluThrGlyProProGlyProVal-GlySerProGlyLeuProG 420
Qy	340
ДQ	420 lyAlaileGlyThrAspGlyThrProGlyProLysGlyProThrGlySerProGlyThrS 440
٥y	400
Q	440 erGlyProProGlySerAlaGlyProProGlySerProGlyProGln 455
Qy	460
qq	456GlySerThrGlyProGlnGlyAsnSerGlyLeuProGlyAspProGlyPheL 473
ογ	461 GGTCCAGTGCTGGTCTGTGTCCCGCTCCTAGGCTCAGGCCAGTGACCACTGGCG- 519 11
q	493
Qy	537
qi	513
δ	538CCGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTT 586
Dp	513 lyProValGlyGluArgGlyAlaProGlyAsnArgGlyPheProGlySerAspGlyLeuP 533
Qy	587 CTCATCCCAAGGCCGGCTGGCTAGCAGGGCTGTGCCCGGATCCCAGGCCCTGGAG 646
Dp	533 roGlyProLysGlyAlaGlnGlyGluArgGlyProValGlySerSerGlyProLysG 552
δγ	647 CTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGTTCTGTGGCCAGGTGTGCTTC 703
qq	570
Qy	GCCCTGCT
Dp	570 lyLeuThrGlyAsnProGlyValGlnGlyProGluGlyLySLeuGlyProLeuGlyAlaP 590
٥y	790
qq	590 roGlyGluAspGlyArgProGlyProProGly
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Qy	791	GGGGCTGCCTGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCC	850
QQ	601		16
Qy	851	CCCTA	95
Dp	616	9	32
ΟŊ	6	CTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCGCTGGGC 9:	ນ
Dp	632	9	49
Qy	926	9	91
qa	649		299
Οy	992		1051
qq	899	GlnGlyHisProG 6	849
Οy	1052		1111
qq	678	lyProProGlyProProGly6	684
Οy	1112		1171
Db	685	::: GluGly	06
Qy	1172	GGCGAGGGGTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACAC 12:	231
QQ	069		907
٥y	1232	TGATGAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATC 1	285
Db	707	31yGluArgGlyAsnProGlyGluArgGlyGluProGlyIleThrGly	24
٥y	1286	- 1	336
QQ	724	euProGlyGluLysGlyMetAlaGlyGlyHisGlyProAspGly73	38
QY	1337	Ε	396
QQ	739		44
٥y	1397	TTCAGCCGCCTCACCGGGTTCACCTTCTCAGCC 1	456
Db	744	٠ ٦	25
QY	1457	1	516
QQ.	753	GlyProProGlyLeuGlnGlyMetProGlyGluArgGlyIleAlaGlyThrProG 75	771
Qy	1517		573
QQ	171	TysGlyAspArgGlyGlyIleGlyGluLysGlyAlaGluGlyThrAlaGly 7	68
٥y	1574	υ	1618
Db	790		808
٥y	1619	TGGGTGCTGGAGGCAGT	654
qq	808		828
Qy	1655	CCCCCTCTCCCCGGGCCTCTGCCTGTGTCTCCGTACGTGTG	1699
QQ	829	AsnProGlySerArgGlyGluAsnGlyProThrGlyAlaValGlyPheAlaGlyProGln 84	18
٥y	1700		738
QQ	849		898

GlyprowetGlyalametGlyProLeuGlyProArgGlyMetProGlyGluArg-GlyAr GGCCGCAGCTTCTGGAGCAGCAGCAGCAGCAGCAGTTCTGGAGTGCCTGAACGGCCC i:: gleuGlyProGlnGlyAlaProGlyLysArgGlyAlaHisGlyMetProGlyLysProGl yproMetGlyProLeuGlyIleProGlySerSerGlyPheProGlyAsnProGlyMetLy yproMetGlyProLeuGlyIleProGlySerSerGlyPheProGlyAsnProGlyMetLy sGlyGluArgGlyProHisGlyAlaArgGlyProGluGlyProGlnGlyGlnArgGlyGl	263 GCCCTACCCGCCACTATGGTCCAGAGGCTGT	518 CGTGGACGCTATGGCCGCGCCGGCCCTTCATCTGGCGCA 556 [11] 493 1y	
90 66 68 69	6y 6	67 COY COY COY	
OY 1739 CGGGGCATCTGCCTGGACCTCGC	Op 1955 AGCACATTGGGGTGGAGGGCCTGCTCACTGGGTCCCGGTCCTGTTAGCCCC 2014	A; Keterence number: 149607; MOLD: 93214071; FMLD: 12374333 A; Accession: 149607 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Mesidues: 1-1497 <res> A; Cross-references: GB: L02918; NID: 9309180; PIDN: AAA37440.1; PID: 9309181 C; Genetics: A; Genetics: A; Genetics: C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; F; 39-98/Domain: von Willebrand factor type C repeat homology <vwc> F; 1270-1497/Domain: fibrillar collagen carboxyl-terminal homology <fcc> Alignment Scores: Pred. No.: 2.88e-11 Length: 1497 Pred. No.: Soore: 2155 Percent Similarity: 30.034</fcc></vwc></res>	Mismatches:

Db 189	912 912	qq
Qy 1928 CCAAGTCGC	1889 TACTITGCTACACAGGTAGTATTTGACAAGAGGGACTTGGCCAAATACTCAGCGTAGAAA 1948	δy
Db 173 ProGlyLeu	901 lyProPro 912	Q O
Оу 1966	1829 CTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATT 1888	ογ
Db 153 GlySerThr	HisGlyValPro	qq
Qy 2017 CATGGGGCT	1781 CIGCIGICCCAGGGGCCCCATCCCTGTTATGGGCTCCATTGTCCAG 1828	ΟŊ
Db 147		qq
Qy . 2077 GGCAGCAGA		δλ
Db 130GlnAla	848 ProGlnGlySerAspGlyGlnProGlyValLySGlyGluProGlyGlu-Pro-GlyGlnL 867	qq
Qy 2137 GAGAGGAGA	1700	Οy
Db 118GlnLys	ArgGlyAsnProGlySerArgGlyGlu	q
QY 2197 TAAGTCCAG	1655CCCGCGCTCTGCGGGCCTCTGCCTGATGTCTCCGTACGTGTG 1699	οy
Db 102 ThrileGlu	808 GlyLeuLeuGlyAlaProGlyGluProGlyProArgGlyLeuValGlyProProGlySer 827	qq
Qy 2257 GGTAATCCA	1613 GGACACGIGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCA 1654	δ
Db 82 GlyProGly	789 AlaGlyAsnAspGlyAlaArgGlyLeuProGlyProLeuGlyProProGlyProAla 807	Op
Qy 2311 AACCCTTCT	1571 AGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTAAT 1612	Οy
62		qq
Qy 2368 CAGGTTAAG	ACT	οy
DB: US-09-759-143-110 (1-34	1431 TCAGCCTGCAGATCCTGCCCTACACTGGCCTCCCTCTACCACCGGGAGAAGCAGGTG 1510 	ž a
Best Local Similarity:	743 snProGlyProThrGlyThrIleGlyAspThr753	q
Score:	1391 TGCTGTCCCACAGTGTGGCCGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTC 1450	οy
Alignment Scores:	740 740 743	qa
A;Note: sequence extrac C;Superfamily: unassign	1331 GGCACTCGAGCACTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACA 1390	δŏ
A;Cross-references: GB: A;Experimental source:	723 hrGlyLeuProGlyGluLysGlyMetAlaGlyGlyHisGlyPioAspGly 739	qq
A; Residues: 1-920 <lii></lii>	1280 GCCATCTCCTGGTCTTCTCTCTGGGTCATGGACCGGCTGGTGCAGCGATTC 1330	δλ
A; Status: preliminary	708ArgGlyGluArgGlyAsnProGlyGluArgGlyGluProGlyIler 723	qq
A;Title: cDNA cloning a A;Reference number: A45	1226 AGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGC 1279	ΟŸ
R; L1, K.; Christiano, R Genomics 16, 733-739, 1	689 ysAlaGlyAspGlnGlyValProGlyGlyPlaValGlyProLeuGlyPro- 707	q
C;Date: 16-Feb-1994 #se C;Accession: A45748	1166 TTCGTGGCGAGGGCGTGTACCAGGCCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCGG 1225	О
collagen alpha 1(VII) c	686	qq
RESULT 38 A45748	1106 TICGIGGCIGAGCIGIGGAGCIGGAIGGCACTCAIGACCTICACGCIGITITACACGGAI 1165	Qy
Db 928 GlyProAle		qa
Qy 2009 AGCCCCATC	GCTGTGCCGCATGCCCCGCACCTGCGCCGGCTC	QY
Db 913		qq
Qy 1949 ACTICCAGO	986 CCCTCCTTGTCGCCCCACTGCTGCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGC 1045	QY

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and chromosomal mapping of the mouse type VII collagen gene (Co 5748; MUID:93315168; PMID:8325648
                                                                                                                                                                                                                                                                                  A.M.; Copeland, N.G.; Gilbert, D.J.; Chu, M.L.; Jenkins, N.A.;
CACATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCGGGCTCCTGTT 2008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3GGGCTTAGAGATGGG---AAACCAGGTGACTGAGTTTATTCAGCTCCCAAA 2312
                                CTA-----GGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCTG 2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCCTGTA 2198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGACGCCCCAGCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACAAGGGT 2078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||| ||| ||| |||||| :::
|GlyProProGlyProProGlyLeuProGlyArgThrGlyAlaPro----- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GlyProGlnGlyProPro 152
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|ProGlyValProGlySerProGlyIleLysGlySerThr------ 188
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-----GlyArgProGlyProArg 194
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s (house mouse)
equence_revision 18-Nov-1994 #text_change 20-Sep-1999
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| ArgLeuAlaProGlyThrAspProIleGlnAsnPhePheAlaValAspAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                            :S63654; NID:9386656; PIDN:AAB27492.1; PID:9386657 epidermal keratinocyte cted from NCBI backbone (NCBIN:135000, NCBIP:135001) end collagens
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31
319
235
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Matches:
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311.00
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Db 485 ProValGlyProArgGlyArgAspGlyGluAlaGlyGluLysGlyAspGluGly11ePro 504	Qy 869CCTGGGTGCCCAGGTAGGGGGCCAGGGCAC 840	Oy 839 TGGTGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCATGA 780	Oy 779 AGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGAAGAGGTCAGAGAGA 720	Qy 719GGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGAAGTCCAGCAGCCCCCACGC 666	Qy 665 CCAGGATGAGCAGTCCCAGGGGCTGGGGATCCGGGCACAGCCTGCTAGCC 606	605	545 AGGCCGGCGGCGATCACGCCAGCGCAGTGATCACGCTGAGCGAGC	485 CACAGACCAGGCCCAGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTCTA	Db 627 AspArgGlyProProGlyLeuAspGly	640 AspGlyLysProGlyAlaProGly	Qy 355 GGCCAAAGGTTAGCAGGTTGACCACCAAGAGCTTCCGGGCTTTCCGGGTCC 318 	Oy 317 GCAGCAGGCGCTCACCCACAGCCTTGGACCATAGTGGGCGGGGTAGGGCTC 261	260	satatiyaspaspelynysriotiynen	CGRIS COllagen alpha 1(I) chain - rat (tentative sequence) (fragments) C;Species: Rattus norvegicus (Norway rat)	C; Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000 C; Accession: A90559; A90552; A92029; A90353; A90566; A90357; A90362; A90379; A91209;	A; Bolustern, F. Biochemistry 8, 63-71, 1969 A:Pitle: Comparative sequence studies of rat skin and tendon collagen. II. The absence		A, Accession: A90559 A, Wolecule type: protein		A; Note: the amino-terminal tetrapeptide may be removed by limited proteolysis during R; Kang, A.H.; Bornstein, P; Piez, K.A. biochemistry A 782-705 1967	A.Title: The amino acid sequence of peptides from the cross-linking region of rat ski A.Reference number: A90552; MUID:67162268; PMID:5337886	A;Contents: CNBr1
1871 GGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACATGGAGCCCA 1812	TAAACAGGGATGGGGCCACCTGGACACCAGGAAGGCAC	IleThrGlyGlyGlyGlyProGlyPheProGlyLySLySGlyAspProGlyProSerGly TATCCAGGATGCCAGGTCCAGCCAGATGCCCGGCAACCACCCTGGCCTCGG	ProProGlySerArgGlyProValGlyAspProGlyProArgGlyPro-ProGlyLeuPr TGGGCTCACCCACCACACACACACACACACACACACACAC		274 lylleGlyAlaSerGluGlnGlyAspProGlyLeuProGlyLeuProGlySerProGlyP 294 1622 CCACGTGTCCATTAGGGAAG	294 roGlnGlyProAlaGlyArgProGlyGluLySGlyGluLySGlyAspCysGluAspGlyG 314 1598 CTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCTCTCAC 1551	ProGlyGlnPro CCAGTGTCCCCT	334 lyMetThrGlyProLysGlyAspArgGlyLeu-ThrGlyThrProGlyGluProGlyVal 353 1490 AGAGGGAGGCCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAGAGGTGAACCCGGTGAGGG 1431	354 LysGlyGlu356	CGGCIGAAGCIGICACCACACCACACACACACACCACCGCACCGCACCACACACACACACACACACACACACACACACACACAC	1370 GGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCGGGT 1311	1310 CCATGACCAGAGAGAGGGGGGGGGGGGCGCACTGCAGGAACAGCCCCAGGCTGCCCA	Т		1190 CCTGGTACAGCCCCTCGCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA 1131	1130 TCCAGCTGCACCAGCACGAGAGACCGGCGCGCGGGGGCGCGGGGCAGCA	407 GlyGlyAlaGlyAlaLysGlyGluLySGlyGlu	· 1070 GCTGGTGCAGCCGGGGAAGCAGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGCATG ::: :::	427 SerGlySerLysGlyGluGlnGlyAlaProGlyLeuAlaLeuProGlyAspProGlyPro	1010 GACAGCAGIGGGGCGACAAGGGGGGGGGACCACAGCCCTIGGTGGGTGGGTGGGGGC 954	953	465 ThrGlyAspSerGlyProProGlyGluLysGlyGluProGlyArgProGlySerProGly 484	929 GCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAGAGGCACTCCT 870
δ δ	ov .	Dρ	Db Qy	Oy Oy	ga Ko	Db Qy	qa Qy	DP Qy	qa i	i d	Qy Ph	Q V	Q V	qa	Qy	Οy	අ _ධ	Qy	qa d	qa Qa	Qy	qa	Qy

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ence studies of rat skin and tendon collagen. II. The absenc
3; MUID:69155173; PMID:5777344
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size (Norway rat)
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12; A92029; A90353; A90566; A90357; A90362; A90379; A91209;
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                                                                                                                                                                                                                                                          GTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGAGCA 720
                                                                                                                                                                                                                                                                                       CCAGTGGAGTGAAGCACACCTGGCCACAGAAGTCCAGCAGCCCCACGC 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCAGCCTGCTAGCC 606
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|IPProArgGlyProLysGlyAspProGlyProProGlyValSerGly 599
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ProGlyLeuAspGly------ArgSerGlyLeu 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCACCCACAGCCTCTGGACCATAGTGGGCCAGGCGGG---TAGGGCTC 261
JeuProGlyLysAlaGlyGluArgGlyLeuArgGlyAlaProGlyPro 524
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pGlyLysProGlyLeu 696
                                                                       GCCCAGGTAGG
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us-09-759-143-110.rpr

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3.55e-11
310.00
33.33%
28.63%
4.98%
                                                                                   A Molecule type: protein
A; Residues: 651-671 <ST2>
A; Experimental source: skin
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Best Local Similarity:
                                                  A; Accession: A91385
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A Molecule type: protein
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A Molecule type: Mole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. The cov
A:Reference number: A90566; MUID:70085124; PMID:5411206
A:Contents: CNBr5
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R;Stoltz, M.; Timpl, R.; Furthmayr, H.; Kuehn, K.
Biochem. 37, 287-294, 1973
A;Title: Structural and immunogenic properties of a major antigenic determinant in neutr
A;Reference number: A91209; MUID:74011954; PMID:4126850
A;Contents: CNBr6
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Blochemistry 13, 2946-2053, 1974
A;Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino
A;Centente number: A90379; MUID:74271984; PMID:4366532
A;Contents: CNBr3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rat skin collagen. Amino
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                                                                                                                                                                                                                                                  collagen.
                                                                                                                                                      R;Bornstein, P.
J. Blol. Chem. 242, 2572-2574, 1967
J. Blol. Chem. 242, 2572-2574, 1967
A;Title: The incomplete hydroxylation of individual prolyl residues in A;Feference number: A92029; MUID:67165368; PMID:4290711
A;Contents: CNBr2
                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 20-55 < B02>
A; Experimental source: 8.L.
Biochemistry 10, 2076-2081, 1971
A; Title: Chemical studies on the cyanogen bromide peptides of A; Reference number: A90353; MUID: 71263178; PMID: 4327399
A; Reference Number: A90353; MUID: 71263178; PMID: 4327399
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ERS Lett. 26, 61-65, 1972
A;Title: Non-helical regions in rat collagen alphal-chain.
A;Reference number: A91385; MUID:73049495; PMID:4636751
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R:Balian, G.; Click, E.M.; Bornstein, P.
Biochemistry 10, 4470-4478, 1971
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A;Residues: 56-102 <BU1>
A;Experimental source: skin
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A, Residues: 239-418 <BA2>
A, Experimental source: skin
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A; Residues: 568-651 <ST1>
A; Experimental source: skin
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A; Residues: 103-139 <BU2>
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A; Molecule type: protein
A; Residues: 419-567 <BU3>
                                     A; Molecule type: protein A; Residues: 5-19 <KAN>
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A;Accession: A90552
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A. Wote: the composition of peptides comprising residues 1-9 and 1-19 confirms the seq A. Note: this region (residues 651-671 above) probably corresponds to positions 1032-1 c. Comment: Prolines and lyshnes at the third position of the tripeptide repeating unled and subsequently 0-glycosylated.

C. Comment: The order of the nine CNBr peptides in the alpha 1(1) chain of rat skin co c. Comment: The complete chain contains 1052 residues.

C. Comment: The complete chain contains 1052 residues.

C. Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homolo C. Keywords: blocked amino end (Glx) (probably pyrrolldone carboxylic acid) #st F. 1/Modified site: blocked amino end (Glx) (probably pyrrolldone carboxylic acid) #st F. 9404/Almiding site: carbohydrate (Lys) (covalent) #status experimental F.103/Modified site: 5-hydroxylysine (Lys) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2071 AGAGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGG 2012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1949 ------TITICIACGCIGAGIATTIGGCCAAGTCGCTCTIGTCAAATACTACCT 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1844 TGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAACAGGGATG-------- 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GGGCCACCTGGGACAGCAGGAAGGCACTATCCAGGATGGCGAGGTCCAGGCAGA 1746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1745 TGCCCCGGCCCGGAÁCCACCCTGGCCTCGGTGGGCTCACCCACCACCACGTACGGAGA 1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1685 CATCACAGGCAGAGGCC---CCGCAGAGCGCGGGTGGAGGT--------GGGAGCA 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1640 GG-----CCACTGCCTCCAGCACCCACGTGTCCATTAGGG---AAGGGAGCTCCAGGCT 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 ProProGlyProGlnGlyAlaArgGlyLeuProGlyThrAlaGlyLeuProGlyMetLys 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 GlyGluAsnGlyAlaProGlyGlnMetGlyPro---ArgGlyLeuProGlyGluArgGly 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 -----GlyAlaLysGlyAsnThrGlyProAlaGlyProLysGlyGluProGlySerPro 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 ArgProGlyProProGlySerAlaGlyAlaArgGly-AspAspGlyAlaValGlyAlaAl 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 aGlyPro-ProGlyProThr---GlyProThrGlyProProGlyPheProGlyAlaAlaG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 ProGlyLysAsnGlyAspAspGlyGluAlaGlyLysProGlyArgProGlyGlnArgGly 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 ArgGlyLeuProGlyProProGlyAlaPro---GlyProGlnGlyPheGlnGlyProPro 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 GlyGluProGlyGluProGlyAlaSerGlyProMetGlyProArgGlyProProGlyPro 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-759-143-110 (1-3410) x CGRT1S (1-671)
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Oy	1589 TAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAG 1536	
£		:
3 .		Qy 581 GGCTCAGCAGGATC
Qy	TGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGG	Db 524 GlyValGlnGlyPr
QΩ		Ov 524 GTCCACGCCAGTGC
Qy	1475 TGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGCGGCGGCTGAAGCTGTCA 1416	5.44
셤	255ProSerGlyPro-GlnGlyProSerGlyAlaProGlyProLysGlyAsnSerGlyGl 273	167
δλ	⋖	, T
qa		
ογ	1355 TGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCAGCCGGTCCA 1308	77 0
q		00 0
οy	. 1307 TGACCAGAGAGAAGACCAGGAGAGATGGCGCACTGCAGGAACA	303
ą	 299 GlyProalaGlyGluGluGlyLysArgGlyAlaArgGlyGluProGlyProSerGlyLeu 318	את ה ה
Óy	TGCCCATCC	305
q		613
è		Qy 248 AGGCACTCCAGAAO
7 t		Db 631 rGlyProPro
a	ValAlaGlyProbySGlyProAlaGlyGluArgGlySerFroGlyFroAlaGlyFroLyS	RESULT 40
ολ	CGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACAGCTCAGCCA :::	A40333 collagen alpha 1'(II) chain
qq	359 GlySerPro 361	C;Species: Xenopus laevis (C:Date: 16-Sep-1992 #sequen
δλ	1109 CGAAGACCGGCGCAGGGTGCGGGCATGCGGCAGCAGCTGGTGCAGCGGGGAAGCA 1050	C; Accession: A 40333 R: Su. M.W.: Suzuki H.R.: B
qa	rgPro(J. Cell Biol. 115, 565-575,
Oy	1049 GGGCCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGCATGGACAGCAGT 1002	A; Reference number: A40333;
QQ		A; Accession: A40333 A; Status: nucleic acid sequ
δλ		A; Molecule type: mkNA A; Residues: 1-1492 <sua></sua>
qd		A;Cross-references: GB:M635 A;Note: this sequence is pr
à	CTICAGCCACCAGCAGTGTGGCTGCTACGCTGAGGAAGGAAGATGAGGGTGAAGCAAAAAAAA	es they replace; the approp C;Superfamily: collagen alp
3 2		C; Keywords: coiled coil; ex F:37-96/Domain: von Willebr
2 6	The Laboratory Carbo annual Lab	F;1263-1492/Domain: fibrill
Š i	Addiscreticularia and a second	Alignment Scores:
QQ	MetGlyPheProGlyProLysGlyThrAlaGlyGluProGlyLysAlaGlyGluArgGly	
. 60	836 TGTCCCAGTCAATGGCAGGCAGGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGG 777	Percent Similarity: 32. Best Local Similarity: 27.
qa	ProAlaGlyLysAspGlyG	
Οy	776 CATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGA 723	115-00-759-143-110 (1-34)
q	455 GlyalaGlnGlyAlaProGlyProalaGlyProAlaGlyGluArgGlyGluGlnGlyPro 474	245 AALC
Qy	722GCAGGGCCTCCAGTGAAGC 699	
qa	475 AlaGlySerProGlyPheGlnGlyLeuProGlyProAlaGlyProFroGlyGluAlaGly 494	r
Qy	698 ACACCTGGCCACAGAAGTCCAGCGCCCACGCAGGATGAGCAGGTGCCAGCTCCA 642	
qq	495 LysProGly************************************	204
Qy	641 GGGGCCTGGGGATCCGGGCACAGCAGCCCTAGCCAGCCGGCCCTTGGGATGAGAAGA 582	XX

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nonallelic type II procollagen genes during Xenopus laevis; MUID:92011898; PMID:1918153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         presented as substitutions relative to another sequence in a opriate interpretation of the sequence figure was reconstruction at 1.1) chain; fibrillar collagen carboxyl terminal homolo extracellular matrix; glycoprotein; trimer; triple helix brand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCAGCCGGCCATGGGCTAACAGGAGCGGGGAGCTGGGA--- 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JICAGCAGCACAGGGTGGCAGCAGAGCCCACATTACTTTGGCAGCAAC 2045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523
                                                                                                          ProproGlyProAlaGlyProArgGlyAsnAsnGlyAlaProGly*** 543
                                                                                                                                                          SGTCACTGGCTGAGCCTAGGAGCG---GGACACAGACCAGGCCCAGCA 468
                                                                                                                                                                                     ------CCAGCACCATGGTCATGACTTCTCCTCTA 426
                                                                                                                                                                                                                                                                                                                                                  GCAGCAGAGGCGCACATAGGTGATGCCTGCGGCCAAACACACCTCCA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGCGGCGC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||| ||| ::: |||||| ||| ||| AlaGlySerProGlyLys***GlyLeu***GlyLeu***619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :TCTGGACCATAGTGGGCCA---GGCGGGTAGGGCTCAGGGGCCGTTC 249
                                                                                                                                                                                                                                                                                                     SerGlyLeu***GlyProProGlyProProGlySerProGly***** 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleGlyPro-ProGlyProArgGlyArgThrGly***AlaGlyProSe 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| ||||||
------GlyProProGlyProProGlyProPro 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTCT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n precursor - African clawed frog
(African clawed frog)
ence_revision 16-Sep-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                            AlaSerGlyProAla------GlyProArgGlyProPro
TCCCCAAGGACAGTG----CCCAGATGAAGGGCCGGCGGCGCCCATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bieker, J.J.; Solursh, M.; Ramirez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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2.52%
7.41%
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දි දි	198/CCCAGTGAGGCCGTCCCAATGTGCTGGA 1952	•	
qq		40	
	163 ProGlyAsnProGlyProAlaGlyProProGlyProProGlyProProGlyLeuGlyGly 182	a a	
0y	1951 AGTITICTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAA 1892	QY	985 GGCCGACAGCCCTTC
QQ		Dp	473 lyProLysGlyGlu
ογ		Qy	938
qq		QQ	492 luGluGlyLysArgG]
٥y		δλ	904 GAAGATGAGGGTGAGG
qq	207 roMetGlyProMetGlyProArgGlyProProGlyProSerGlyAlaproG 224	Dβ	512 lyGluArgGlyAlaPı
οy	1775CACTATCCAGGATGCCGAGGTCCAGGCAGTGCC 1742	Οy	868 CTGGGTGCCCAGGT
QQ	224 lyProGlnGlyPheGlnGlyAsnProGlyGluProGlyGluSerGlyAlaglyGlyProM 244	Db	532 ysGlyAlaProGlyGl
Qy	1741 CCGGCCCGGAACCACCCTGGCCTCGGTGGGCTCACCCACCACCTACGGAGAC 1685	. KO	814 GAGGTAGCCCAGG
qq	259	qa	552 spProGlyArgProGl
οχ	SCAGGCCACTGCCTCCAGC	Οy	757 GCGACAGTGGTCCG
qa	259 pGlyGluAlaGlyLysProGlyLysSerGlyGluArgGlyProProGl 275	qa	572 lyAspalaGlyProGl
Qy	1624 ACCCACGIGICCATTAGGGAAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGT 1568	ολ	721 CAGGGCCTCCAGTGGP
QQ	275 yProGlnGlyAlaArgGlyPheProGlyThrProGlyLeuProGlyValLys 292	DD	592 roGlyProPro
Qy	1567 CATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACAC 1508	δλ	
qa	293ArgGlyTyrP 298	qq	603 InProGlyvalMetGl
οy	1507 CIGCITCICCCGGTGGTAGAGGGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAA 1448	δy	625 GCACAGCAGCCCTGCT
Op		qa	620 lyLysAlaGly
Qy	1447 GGTGAACCCGGTGAGGCCGGCTGAAGCTGTCACCACGCCCACACTGTGGGACAGGCATGT 1388	Οy	565 CAAGGACAGT
qa	314 GlyGluSerGlyAlaSerGly-GluAlaGlyAlaProGlyProMetGlyProArgGlyLe 333	qa	631 roGlyLeuArgGlyLe
0y	1387 GGCACCGGCAGCCACAGGAAAGCTGCCACACTGGCCAAATAGAC 1343	Qy	511 GTCACTGGCTGAGCCT
QQ	:	. qa	647 lyProAsnGlyProAl
0y	1342 TGCTCGAGTGCCGAATCGCTGCACCAGCGGTCCATGACCAGAGAGAAGACCAGGGAGAT 1283	ογ	469 CACIGGACCAAIG
qq	353GlyLeuProGlyProAlaGlyPro	qq	667 erGlyPheGlnGlyLe
Qy	1282 GGCGCACTGCAGGAACAGCCCCAGGCTGCCCATCCGAACGCCTTCATCATAGTG 1229	ΟŊ	412 CAGCAGAGGCGGCACA
qq		QQ	
Οy	1228 TUTUCGGGCCTCGGTCCCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCCCCTCGCCCAC 1169	δλ	367 CAGGCCAAAGGTTAGC
QΩ		qa	AspG
δy.	1168 GAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACAGCTCAGCCAC 1109	Óγ	311GGCGGCTC
qq		qa	703 rgGlyGluArgGlyPh
οy	1108 GAAGAGCCGGCGCAGGGTGCGGGGATGCGGCAGCAGCTGGTGCAGCCGGGGAAGCAG 1049	Qy	262 TCAGGGGGCCGTTCAG
qq		QQ	
Qy	1048 GGCGCCCAGGTTCCGGAAAGCCAAGCGGCCCGGCATGGACAGCAGAGGGGGCGACA 993	ΟŊ	220TCTG
ź		40	738 Alambroland

Qy	693	AGGAGGG 986
qa	453 roLeuGlyProLysGlyGluThrGlyAspProGlyIleAlaGlyPheLy	l ysGlyGluHisG 473
Qy	GCCGACAGCCCTTCTGCTGGCTCGGTGGGGCCCAGCGCTGCCTCC	686
QQ	473 lyProLysGlyGlulleGlySerAlaGlyProGlnGlyAla-ProGl	lyProAlaGlyG 492
ΟŶ	938CAGCCACCACCACCAGGAGTGTGGCTACGCAGGT	racccaggreag 905
qq	492 luGluGlyLysArgGlyAlaArgGlyGluProGlyAlaAlaGlyProl	euGlyProProG 512
Qy	AAGATGAGGGTGAGC	ACTCCTC 869
Dp	ArgGlyAlaProGlyAsnArgGlyPheProGlyGlnAspGly	LeuAlaGlyProL 532
٥y	68 CTGGGTGCCCAGGT AGGGGG CCAGGGCACTGGTGTCCCAGT	CAATGGCAGGCAG 815
Dp	31yAlaProGlyGluArgGlyValProGlyLeuGlyGlyProLys	GlyGlyAsnGlyA 552
٥٨.	TAGCCCAGGCAGCCCCAAGACTGATCATGAAGGC	AGAGTAGGCCTG 758
qq	ArgProGlyGluProGlyLeuProGlyAlaArgG	ArgPro
٥y	7 GCGACAGTGGTCG	SAGGTCAGAGAG 722
qq	yAspAlaGlyProGlnGlyLysValGlyProSerGlyAlaAla	GlyGluAspGlyArgP 592
Οy	721 CAGGCCTCCAGIGGAGTGAAGCACACCIGGCCACAGAAGTCCAGCAGCC	3CCCACGC 666
Dp	lyProProGlyProG	AlaA
Qy	665GAGGATGAGCAGGTGCCAGGGG	CTGGGATCCGG 626
Db		:::[snGlyGluProG 620
Qy	TGCTAGCCAGCCGGCCCTTGGGATGA	AGCAGGATGCC 566
Db	620 lyLysAlaGlyGluLysGlyLysGlyL	euGlyGlyAlaP 631
Οy	565 CAAGGACAGİTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCG	CCACGCCAGTG 512
qq	GlyLeuArgGlyLeuProGlyLysAs	pGlyGluThrGlyAlaGlnG 647
Qy	511 GTCACTGGCTGAGCCTAGGAGCGGGACACAGAGA	-ccaggcccag 470
. qa	647 lyProAsnGlyProAlaGlyProAlaGlyGluArgGlyGluGlnGlyProProGlyProS	oProGlyPros 667
. оу	- ;	CCCACTTCCAG 413
οp	667 erGlyPheGlnGlyLeuProGlyPro	675 675
Qy	412 CAGCAGAGGGGGCACATAGGTGATGCCTGCGGCCAAACACACT	998 5
Db	676	l uGlyGlyLysP 685
δÿ	CAAAGGTTAGCAGGTTGACCAGCAAGGAGCTGGGCTTTCCGGT	GCCGCAGCA 312
Db	GlyValProGlyGluAlaGlyAlaAlaGlyL	euValGlyProA 703
Qy	311GGCGGCTCACCCACAGCCTCTGGACCATAGTGGGCCAGGCGGG	TAGGG
Db	703 rgGlyGluArgGlyPheProGlyGluArgGly-SerSerGlyProGln	ly LyLeuGlnGly 722
Οy	262 TCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGC	221
Db	erArgGlyLeuProGlyThrPro	lyProLysGly 737
Qy	220TCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCGCCCAACTGCCT	GCCAACTGCCT 173
Db		:: :::

122 yGlyLeuLeuGlyAspThrAlaAspAsnLysThrMetAlaIleValAlaPheValIleGl 142 667 CGTGGGCCTGCTGGACTTCTGTGGCCAGTGTGCTTCACTCCACTGGAGGCCTGCTCT 726 11	191 11 11 11 11 11 11 1
90	8 3 8 3 8 3 8 3 8 3 8 3 8 3 8 3 8 3 8 3
Qy 172 AGGAATCAGCCCCAGTTTCTGCCAGCCCTTTGGT	RESULT 41 **Atternate names sucrose/Protein - carrot **Control of the protein transport protein - carrot **Control of the protein transport protein - carrot **Control of the protein transport protein 20-Sep-1999 #text_change 21-Jul-2000 **Control of the protein of sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 **Control of the protein of sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 **Control of the protein of sequence and sink-specific sucrose/H+ symporters from carrot **Attle of characterization of source and sink-specific sucrose/H+ symporters from carrot **Attle of characterization of source and sink-specific sucrose/H+ symporters from carrot **Attle of characterization of source and sink-specific sucrose/H+ symporters from carrot **Attle of characterization of source and sink-specific sucrose/H+ symporters from carrot **Attle of characterization of source and sink-specific sucrose/H+ symporters from carrot **Attle of characterization of source and sink-specific sucrose/H+ symporters from carrot **Attle of characterization of source and sink-specific sucrose/H+ symporters from carrot **Attle of characterization of source and sink-specific sucrose/H+ symporters from carrot **Attle of characterization of source and sink-specific sucrose/H+ symporters from carrot **Attle of characterization of source and sink-specific sucrose/H+ symporters of characterization of source and symporters of sucrol symporters of sucrol symporters of source and symporters of sucrol sy

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US-09-759-143-110 (1-3410) x CGHU3B (1-1670)
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                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
DB:
                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Function:
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A; Residues: 1-1670 < WARS
A; Cross-references: G8 128031; NID:9577563; PID:9577564
A; Cross-references: Ridney
A; Cross-references: Ridney
B; Turner, N.; Mason, P.J.; Brown, R.; Fox, M.; Povey, S.; Rees, A.; Pusey, C.D.
J. Clin. Invest. 199, 529-601, 1992
A; Title: Molecular cloning of the human Goodpasture antigen demonstrates it to be the all A; Reference number: A43928; MUID:92147878; PMID:11737849
A; Accessation: A43928
A; Molecule type: mRNA
A; Residues: 1331-1524, I',1526-1670 < TUR>
A; Molecule type: mRNA
A; Residues: GB: M81379
A; Cross-references: GB: M81379
A; Experimental source: Kidney
B; Outlones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 267, 19780-19784, 1992
A; Title: Exon/intron structure of the human alpha 3(IV) gene encompassing the Goodpasturent of the human alpha 3(IV) gene encompassing the second of the human alpha 3(IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 3(IV) chain precursor, long splice form - human NiAlternate names: Goodpasture antigen; procollagen alpha 3(IV) chain long splice form C; Species: Benociting man)
C; Date: 28-Oct.1994 #sequence_revision 03-Oct.1995 #text_change 22-Jun-1999
C; Accession: A54763; A43928; A44043; A45971; A39786
C; Accession: A54763; A43928; A44043; A45971; A39786
J; Mariyama, M; Leinonen, A; Mochizuki, T; Tryggvason, K; Reeders, S.T.
J; Biol. Chem. 269, 23013-23017, 1994
A; Title: Complete primary structure of the human alpha3(IV) collagen chain. Coexpression A; Reference number: A54763; MUID:9436494; PMID:8083201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1427-1444 <BER>
A;Note: sequence extracted from NCBI backbone (NCBIP:133363); sequence incorrectly ident
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A. Reference number: A44043; MUID: 93015826; PMID: 1400291
A. Reference number: A44043; MUID: 93015826; PMID: 1400291
A. Reference number: A44043; MUID: 93015826; PMID: 1400291
A. Molecule type: DNA; MRNA
A. Residues: 1386-1670 <QUI>
A. Cross-references: GB: MS2993; NID: 9177895; PIDN: AAA21610.1; PID: 9177896
A. Note: sequence extracted from NCBI Deckbone (NCBIP: 115597)
B. Outnones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
A. Reference number: A44738; MUID: 94274734; PMID: 8006044
A. Contents: annotation; erratum; correction to intronic sequence in A44043
A. Chontents: annotation; erratum; correction to intronic sequence in A44043
A. Fille: The human mRNA encoding the Goodpasture antigen is alternatively spliced.
A. Reference number: A45971; MUID: 93280184; PMID: 8505332
   CTGTGATGTCTCCGTACGTGTGGTGGTGGTGGCCCACCGAGGCCAGGGTG---GTTCC 1734
                                                                                                                                 ------GGCCGGGCATCTGCCTGGACCTCGC 1761
                                                                                                                                                                                                                                                     1762 CATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCCATCCCTGTTTATGGGCTCCAT 1821
                                                                                                                                                                                                                                                                                                                                                                                    ----AGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGC 1866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1867 AGGCCTGGGTCTGGTCGCCATTTACTTTGCTACAGGTAGTATTTGACAAGAGCGACTT 1926
                                                           399 eSerAlaLeuIleValPheAlaIleLeuGlyIleProLeuAlaIleThrTyrSerValPr 419
                                                                                                                                                                                   419 oTyrAlaLeuValSerThrArglleGluSerLeuGlyLeuGlyGlnGlyLeuSerMetGl 439
                                                                                                                                                                                                                                                                                                                                                                                                                               459 pAspGlnLeuPheGlyGlyGlyAsnSerProAlaPheValValAlaAlaLeuSerAlaPh 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A45971
A; Status: nucleic acid sequence not shown
                                                                                                                          1735 G-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1927 G 1927
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C;Superfamily: collagen alpha 1(IV) chain
E;1.28 Domain: signal sequence #status predicted <SIG>
F:29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <MA
F:29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <MA
F:29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <MA
F:29-1670/Product: collagen collattachment (R-G-D) motif
F:31-1797/Region: cell attachment (R-G-D) motif
F:1154-1156/Region: cell attachment (R-G-D) motif
F:1143-1147/Region: cell attachment (R-G-D) motif
F:143-1147/Region: cell attachment (R-G-D) motif
F:143-1157/Domain: carboxyl-terminal nonhalical, NCl <NCl>
F:143-1157/Domain: carboxyl-terminal nonhalical, ncl 
F:143-1165/Domain: collagen IV carboxyl-terminal repeat <CT2>
F:141-1155/Domain: collagen IV carboxyl-terminal repeat <CT2>
F:151-1655/Domain: collagen IV carboxyl-terminal repeat <CT2>
F:151-1651/Domain: collagen IV carboxyl-terminal repeat <CT2>
F:151-1651/Domain: collagen IV carboxyl-terminal repeat <CT2>
F:151-1651/Disulfide bonds: (or 1460-1551, 1493-1548) #status predicted
F:150-1511,1616-1652/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted
F:1570-1662,1604-1665/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Access-references: GDB:128351; OMIN:120070
A;Cross-references: GDB:128351; OMIN:120070
A;Map position: 2q36-2q37
A;Map position: 2q36-2q37
A;Introns: 1385/1; 1418/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete
A;Note: the alpha 3(1V) and alpha 4(1V) chain genes are encoded on opposite strands w
A;Note: the alpha 3(1V) and alpha 4(1V) chain genes are encoded on opposite strands w
C;Complex: This minor type IV collagen is thought to form a heterotrimer of two alpha
mong trimer amino-terminal domains (with disulfide and desmosine cross-links), dimeril
er associations in the interrupted helical domain (with disulfide and desmosine cross
                                                                                                                                                                                                                                                                                        A; Residues: 1453-1593, 'A', 1595-1670 <MOR>
A; Cross-references: GB:S55790; NID:g224418; PIDN:AAB19637.1; PID:g234419
C; Comment: Prolines and lysines at the third position of the tripeptide repeating unied and subsequently O-glycosylated.
C; Comment: In Goodpasture's syndrome, an autoimmune response develops against an epit
R;Morrison, K.E.; Mariyama, M.; Yang-Feng, T.L.; Reeders, S.T.
Am. J. Hum. Genet. 49, 545-554, 1991
A;Title: Sequence and localization of a partial cDNA encoding the human alpha3 chain A;Reference number: A39786; MUID:91353570; PMID:1882840
is Accession: A39786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3071 TCTGGTCCTGCAGTAGCTCCAAACAGGGTTGTGGAGCTGGTGGGGAAAGTTGGGGGTAGG 3012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1930 GGGAACCAGGCTGGGCCAAGAGAGAGGGGTGGTTAGGGAAGCCGTTGAGACCTGAAGCC 2871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1870 CCACCCTCTACCTTCCTTCAACACCCTAACCTTGGGTAACAGCATTTGGAATTATCATTT 2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------AGTGGAAGTGGG 2931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3011 GGAAAGTTGGGGGTAGGGGAAATTTTGGGCAGTGCCTTCATCAGCCCAGTCCTAGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 GlyGluGlnGlyPheProGlyLeuProGlyThrLeuGlyTyrPro-----
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278
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Mismatches:
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GGGATGGGTAGGATTTCGAGGTCCTGGGTTAGGCATTTTGGGGGGCCCAGGGG 275:	1901 GTGTAGCAAGGAAGCAGACCAGGCGTGCGCGCAGACACC 1855 348 pThrTyrGlnGluLysGlyAspGluGlyThrProGlyProProGlyProArg 365 1854 ATATAGGCAGTGACAGCTGGCTGACATGGACACATGAACAGGGATGGCCC 1795 1854 ATATAGGCAGTGACAGTGGACAATGGACACATGAACAGGGATGGCCC 1795 11
	oy by oy

collagen alpha 1(III) chain - bovine

RESULT 43

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A; Residues: y467-1049 xAblu>
A; Residuental source: skin
B; Henkel, W.
B; Het type: Int collagen molecule is a trimer of identical chains. Introduce comment: The type III collagen molecule is a trimer of identical chains. Introduce collagen alpha I(I) chain; fibrillar collagen carboxyl-terminal homolocy collagen alpha I(II) chain; fibrillar collagen carboxyl-terminal homolocy F; Hough F; Hou
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A; Residues: 243-422 CDEW1>
R; Behtz, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
A; Title: The covalent structure of calf skin type III collagen. III. The amino acid s
A; Reference number: A38002; MUID:80026028; PMID:488908
C;Species: Bos primigenius taurus (cattle)
C;Date 04-Dec-1986 #text_change 07-May-1999
C;Date 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 07-May-1999
C;Accession: A02862; A38001; A38003; A38004; A38005; S71946
R;Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehn, K.
Hoppe-Seyler, S. Z. Physiol. Chem. 360, 809-820, 1979
A;Title: The covalent structure of calf skin type III collagen. I. The amino acid seq
A;Reference number: A02862; MUID:80026026; PMID:488906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Readdues: 423-571 CBEN>
A; Readdues: 423-571 CBEN>
R; Lang, H; Glanville, R.W.; Fletzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A; Title: The covalent structure of calf skin type III collagen. IV. The amino acid se
A; Reference number: A38003; MUID:80026029; PMID:488909
A; Accession: A38003
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A; Noblecule type: protein
A; Residues: 809-947 < CDEW2>
R; Railmann, H; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.
Hopper-Seyler's 2. Physiol. Chem. 360, 861-868, 1979
A; Fitle: The covalent structure of calf skin type III collagen. VI. The amino acid A; Reference number: A38005; MUID:80026031; PMID:488911
A; Moccession A38005
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 948-1049 < ALL>
                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: protein
A; Residues: 1-242 *CFIE>
R:Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
A; Title: The covalent structure of calf skin type III collagen. II. The amino acid
A; Reference number: A38001; MUID:80026027; PMID:488907
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A; Residues: 572-808 < LAN>
R; Dewes, H.; Fietzek, P.P.; Kuehn, K.
HOppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A; Title: The covalent structure of calf skin type III c
A; Reference number: A38004; MUID:80026030; PMID:488910
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Pred. No.:
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Db	407ProGlyPro	
Oy	887 CTGCT	891
qq	425 roGlyProLysGly	yAsnAspGlyAlaProGlyLysAsnGlyGluArgGlyGlyProGlyG 445
Qy	892CACCCTCATO	CACCCTCATCTTCCTCACCTGCGTAGCAGCCACTGCTGGTGGCTGAGGAG 943
qa	445 lyProGlyProGlnGlyProAl	llyProAlaGlyLysAsnGlyGluThrGlyProGlnGlyProProG 465
Oy da	44	GCAGCGCTGGGCCCCACCGAGCAGCAGAGGCTGTCGGCCCCCTTGTCGCCCCAC 1003
2	J IYFI	, ,
Qy	04 TGCT	GTCCATGCCGGGCCCGCTTGCGGAACCTGGGCGCCCTGCTTCCCGG 1060
Q C	t encī	106 304
QY	1061 CTGCACCAGCTGTG	CACCAGCTGTGCTGCCCGCATGCCCCGCACCTTGCGCGCTCTTCGTGGCTGAGCTG 1120
Dp	504 ly	ProLysGlyGluAlaGlyAlaProGlyIleBroGly 516
Qy	1121 TGCAGCTGGATGGC	GGATGCCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAG 1177
Dp	517Giy	-GlyLysGlyAspSerGlyAlaProGlyGluArgGlyProProGlyAlaG 533
Qy	1178 GGGCTGTACCAGGG	ACCAGGCGTGCCCAGAGCTGAGCCGGCACCGAGGCCCGGAGACACTATGAT 1237
pp	533 lyGlyProProGly	ProArgGlyGlyAlaGlyProProGlyProGluGlyG 550
Οy	ο,	
qa	550 lyLysGlyAlaAla	: :::
Qy	1283 ATCTCCCTGGTCTT	ATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGCÁGCGATTCGGC 1333
qq	570 lyMetProGlyGlu	ArgGlyGlyProGlyGlyProGlyProLysGlyAspLysGlyGluP 590
Qy	1334 ACTCGAGCAGTCTA	ACTCGAGCAGTCTATTTGGCCAGTGTGGCCAGCTTTCCCTGTGGCTGCCGGTGCCATGC 1393
qa	590 roGlySerSer	GlyvalaspGlyAla
Οy	1394 CTGTCCCACAGTGT	CTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCA 1453
Dβ	599 roGlyLysAspGly	ProArgGlyProThrG 609
Qy	1454 GCCCTGCAGATCCT	SCCTGCAGATCCTGCCCTACACACTGGCCTCTCTACCACCGGGAGAAGCAGGTGTTC 1513
Db	- 0	roGlyProAlaGlyGlnProGlyAspLysGlyGluSerGlyAla
Qy	1514 CTGCC	CAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGC 1561
ρp	629 roGlyValProGly	yllealaGlyProArgGlyGlyProGlyGlua 644
Oy	1562 CTGATGACCAGCTT	GCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGA 16
QQ	644 rgGlyGluGinGly	Phe ProGlyAla ProGlyGl
QY	1616 CACGTGGGTGCTGG	GIGGGIGCTGCAGGCAGTGCCTGCTCCCACCTCCACCC 1657
Db	664 GluProGlyAlaLy	GlyGluLysGlyGluGlyGl
Qy	IGCG	GGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGGTG
qq	laGl	roAlaGlyGlySerGlyPro
Qy	1718 G	AGGCCAGGTGGTTCCGGCCCGGGGCATC 1747
Dp	698 oGlyProGlnGlyV	alLysGlyGluArgGlySerPro-GlyGlyProGlyAlaAlaGlyP 718
δλ	1748 IGCCIGGACCICGC	CTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCC 1798

yo g	2765 CCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCA 2824
ċ	о полити в
S 6	2023 AAIGCLIGITACCCAAAGGITAGGGTGTTGAAGGTGGAAGGTGGGGTGG
Qy	2885 ACGCCTTCCCTAACCACCCCTTTCTTGGCCCAGCTTGGTTCCCCCACTTCCACTCC 2944
QQ	1000HisProGlyProlleGlyPro-ProGlyProArgGlyAsnArgGly 1014
QY	CTAGGACTGGCTGATGAAGGC
qa	1015 GluArgGlySerGluGlySerProGlyHisProGlyGlnPro 1028
λο d	ACTITCCCCACCAGCTC
a a	1029 GIYFIOFIOGLYFFOFFOGLYFFOGLYFFOCKYS 1040
RESUI B4033 colls C;Spe C;Dat	RESULT 44 B40333 collagen alpha 1(II) chain precursor - African clawed frog C; Species: Xenopus laevis (African clawed frog) C; Species: Xenopus Psequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Acc R; Su,	h, M.; Ramirez, F.
J. CE A;Tit	111 Biol. 115, 565-575, 1991 Lie Expression of two nonallelic type II procollagen genes during Xenopus laevis
A; Acc	careuce number: A40333, MOID:92011096; PMID:1918133 Session: 840333 thus: oreliminary
A; Mol A; Res	ecule type: mRNA sidues: 1-1486 <sua></sua>
A;Crc C;Sup C;Key F;37-	Cross-references: GB:M63595 Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo Keywords: colled coll; extracellular matrix; glycoprotein; trimer; triple helix 37-96/Domain: von Willebrand factor type C reneat homology cyun.
F; 125	1-terminal homo
Aligr Pred. Score Perce Best	Alignment Scores: Pred. No.: 4.69e-11 Length: 1486 Score: 308.00 Matches: 277 Percent Similarity: 33.50% Conservative: 54 Best Local Similarity: 28.04% Mismatches: 362
Query DB:	4.95% Indels:
0S-09	1-759-143-110 (1-3410) x B40333 (1-1486)
Qy	2569 GAAGGACCAACAGCCACATCCTGATAAAAGGTAAGAGGGGGGTGGATCAGCAAAAAGAC 2510 :::
Qy	2509 AGTGCTGTGGGCTGAGGGGACCTGGTTCTTGTGTTGCCCCTCAGGACTCTTCCCCTAC 2450
Db	
Qy	2449 AAATAAGTCATATGTTCAAATCCCATGGAGGAGTGTTTCATCCTAGAAACTCCCATGCAA 2390
QO	155 155
Qγ	2389 GAGCTACATTAAACGAAGCTGCAGGTTAAGGGGCTTAAGAGATGGGAAACCAGGTGACTGA 2330
Db	156161
Qy	2329 GTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCTCAACTAGGAGGCTAGCTGTA 2270
Db	162ThrProGlyAsnProGly
Qy	2269 ACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCGCATTCCAGTGGAGGCCCTTCT 2210

168 209 188
2155AGCCCTAGAGACTGGGGAAGAGAGAGACCCCCCCTAGAGCCCCTAGAGCCCCTAGAGGGGAAGAGAGAG
. ~ @
1987 CCCAGT
1951 AGTTTCTACGCTGAGTATTGGCCAAGTCGCTCTTGTCAAA 1910 11
1909 TACTACCTGTGTAGCAAAGTAAAATGGCGACCAGCCCAGGCCTGCGGCAGACACATATA 1850
1849 GGCAGTGACAGACTGGCTGACCAATGGAGCCCATAAACAGGGATGGGGCCA 1794
1793CCTGGGACAGCAGGAAGG
0 0
1700 CCACACGTACGGAGACATCACAGGCAGAGGCC
1661 GCGCGGGTGGAGGTGGGAGCAGCCACTGCCTCCAGCACCCACGTGTCCATTAGGGA 1605
1604 AGGGAGCTCCAGGCTTAGGGCCTGGCAGGAGCTGGTCATCAGGCTGTCCTCAC 1551
1550 TGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGCCAGGAACACCTGCTTCTCCCGGTGGT 1491
1490 AGAGGGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGG 1446
ın ee
1391 ATGTGGCACCGGCAGCCACAGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAG 1335
1334 TGCCGAATGGCTGCACCAGCCGGTCCATGACCAGAGAGAGA

82	::: ProAsnGlyGluLysGlyGluSerGlyProP	8
36.	GAGGCGCACATAGGTGATGCCTGCGGCCAAACACACTC	94
• 00	464 GACCAATGCCCAGGACCATGGACTTCTCCTATAGGACTCTATAGGACTAGACTTCTATAGACTAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	46
4	ArgGlyAspThrGlyGlubysclyriociuciyaiasero	769
465	1	51
76	:: 9 GlyLeuGl	74
516	3	299
748		73
564	3 ACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCA	62
733		718
624	5	99
717	9 GOOGLE CONTROLL	69
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720 697	3 AGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGGAGAGAGAGAGAGAGAGAGAGAG	77
678	:::	9
774	:InGlyProProGly	65,
83	GCCAGGGCACTGGTGTCCC	88
, LO	CCTCAGCCACCACCAGTGTGGCTGCTACGCAGGTGGGGGGGG	941
643	LeuvalGlyAlaProGlyLeuArgGlyLeuProGlyLysAspGlyGluThrGlySerGln	624
942	CTTCTGCTGGCTGGGTGGGGCCCAGCGCTGCCT	974
623	MetGlyPheProGlyProLys6lyAlaAsnGlyGluProGlyLySAlaGlyGluLysGly	604
975	TITEL TO THE TOTAL OF THE TOTAL	, ,
1011 603	GGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGG	1058
1059 583	GCTCAGCCACGAGGCGGCGCAGGGTGCGGCATGCGGCAGCAGCAGCTGGTGCAGCC 1::::	1118
- 9	CCAGCTGCACA GlyLeuThr	1178
20	valProGlyLeuGlyGlyProLysGlyGlyAgnGlyAspPro 55	537
· -	PheproGlyGlnAspGlyLeuAlaGlyProLySGlyAlaProGlyGluArgGLy 3	21
239 36	CCAGGGAGATGGCGCACTGCAGGAACAGCCCCAGGCTGCCCATCCGAACGCCTT 1	σ,

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349 CCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGCCATCACCTATGTGCCGCCTCT 408 :::			UGLYTYRALAALAGLYSerTyrThrasnLeuHisLysMetPheProPheThrMe CACCAGTGCCCTGCCCCTACCTGGGCACCCAGGAGAGAGA		1071 TGTGCTGCGCGACCCGGCCGGCTCTTCGTCGCTGAGCTGCAGCTGGA 1130 11		1311 ACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCC 1370 i::::::::::::::::::::::::::::::::::::
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	oy Oy Oy	' qa 60 qa 60	40 40 40	qa , , , , ,	9y 9y 9y	oy Oy
362 821 344 841 311	257 880 197 899 137 919	UY B9 GGCACCTCAGTGGGGACACGTCTCATCAGATCCTGGCCGAGGCGCGGGTGT 33 Db 934 rgGlyAspAlaGlyProProGlyArgAlaGlyAspProGlyLeuGlnGlyAlaAlaGlyA 954 Qy 32 CACCGGA 25 :: Db 954 laProGly 956 RESULT 45 P96741	probable sucrose transport protein F17M19.4 (imported) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: F96741 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000	A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. Rizzo, M.; Rooney, T.; Kowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon, A; Title. Sequence and analysis of chromosome l of the plant Arabidopsis. A; Reference number: A86141; MuID:21016719; PMID:11130712 A; Reters preliminary A; Redeutes: preliminary A; Redeutes: DNA A; Residues: 1.512 csro>	A.Cross_references: GB:AE005173; NID:g6978914; PIDN:AAF34306.1; GSPDB:GN00141 C.Genetios: A.Genetios: A.Map position: 1 C.Superfamily: common tobacco sucrose transport protein A.lignment Scores:	Fores. No.: 5.39e-11 Length: 512 Score: 5.30e-12 Length: 512 Score: 5.307.00 Marches: 128 Percent Similarity: 42.15% Conservative: 92 Best Local Similarity: 24.52% Mismatches: 208 Query Match: 4.78% Indels: 95 DB: 759-143-110 (1-3410) x F96741 (1-512)	Oy 289 CCAGAGGCTGTGGCTGCTGCTGCTGCGGAAAGCCCAGCTCTTGCTGGTCAA 348 ::: :::

qq	371	:::
٥y	1424	
Db	388	388 isHisArgGluIleAlaGlyProLeuAlaGlyProSerSerGlyIleLysAlaGlyValP 408
Οÿ	1449	1449 TCTCAGCCCTGCAGATCCTG
Db	408	
Qy	1479	1479 TGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTG 1538
qa	428	eualaSerllePheSerThrAsnSerGiyAlaGlyGlnGlyLeuSerLeuGlyValLeuA 448
Qy	1539	1539 GAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCT 1594
qq	448	snilealaileCysileProGlnMetileValSerPheSerSerGlyProLeuAspAlaG 468
QY	1595	.595GGAGCTCCCTTCCCTAATGGACACGTGGGTGGTGGAGCAGGCAGTG 1637
Db	468	InPheGlyGlyGlyAsnLeuProSerPheValValGlyAlaIleAlaAlaAlaValSerG 488
Oy	1638	1638 GCCTGCTC
Dp	488	lyvalLeualaLeuThrValLeuProSerProProProAspalaProAlaMetSerGlyA 508
Qy	1671	1671 CC 1672
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Sequence 708, App
Sequence 852, App
Sequence 706, App
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Sequence 21, Appl
Sequence 159, Appl
Sequence 36, Appl
Sequence 56, Appl
Sequence 547, App
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Sequence 547, App
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Sequence 113, Application US/09232880

publication No. US20020182596A1

SEMERAL INFORMATION:

APPLICANT: W., Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: Ocnepounds FOR IMMUNODIAGNOSIS OF

TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE

FILE REPREBENCE: 210121.428C6

CURRENT APPLICATION NUMBER: US/09/232,880

CURRENT FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 338

SOFTWARE FALSEQ for Windows Version 3.0

LENGTH: 553
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Mismatches:
           0 US-09-745-288-101

0 US-09-788-785-2

0 US-09-789-789-113

0 US-09-780-669-113

0 US-09-105-66-113

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US-10-00-036-159
US-10-096-986-103
US-10-096-986-103
US-09-919-497-56
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-MAXLEN=200000000 -USER=USO9759143_@CGN_11_92_@runat_05052003_11331_23172
-NCPU-6 -LCDOM_MAPP-LARGEQUERY -NG_SCORES=0 -WAIT -DSPBLCCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 113,
Sequence 113,
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11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
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                                                Compugen Ltd
                                                                                                               protein search, using frame_plus_n2p model
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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Vinals de Bassols, Carlota
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Publication No. US20020183251A1
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Wantanabe, Yoshihiro
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Matches:
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Mismatches:
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FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 113
LENGTH: 553
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
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APPLICANT: Carter, Darrick
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APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Hang, Aljun
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Houghcon, Robert A.
APPLICANT: Houghcon, Robert A.
APPLICANT: Houghcon, Raymond L.
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Panger, ComPoSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT APPLICATION NUMBER: 2001-06-29
NUMBER OF SED ID NOS: 982
SOFTWARRE: FastSEQ for Windows Version 3.0
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Matches:
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Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
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Best Local Similarity:
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APPLICANT: HALLOCKEr, Susan L.
APPLICANT: HALLOCKEr, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John W.
APPLICANT: Stolk, Thomas S.
APPLICANT: Oavier, Thomas S.
APPLICANT: Wang, Aljun
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APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Winals de Bassols, Carlota
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICANTON: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT FILING DATE: 2001.06-29
NUMBER OF SEQ ID NOS: 990
SSOTUMRE: FastSEQ for Windows Version 3.0
SEQ ID NO 113
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US-09-759-143-110 (1-3410) x US-09-895-814-113 (1-553)
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Mismatches:
Indels:
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Matches:
                                                                   Sequence 113, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION:
                                                                                                             APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Best Local Similarity:
Query Match:
DB:
                                                        US-09-895-814-113
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| Publication No. US20030088062A1
| GENERAL INFORMATION:
| APPLICANT: W. Jiangchun
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Harlocker, Susan Louise
| APPLICANT: Harlocker, Susan Louise
| APPLICANT: Rados, Atchael
| APPLICANT: Rados, Michael
| APPLICANT: Fanger, Gary
| APPLICANT: Fanger, Gary
| APPLICANT: Cappositions and Methods For THERAPY AND
| APPLICANT: Cappositions of INVENTION: Compositions of INVENTION: Cappositions of Inventions of Inven
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1604 TTCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCCTCCACCCCCCCC	TTGCTACACAG	TTLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE CURRENT APPLICATION NUMBER: US/09/745,288 QY CURRENT FILING DATE: 2000-12-19 Db CURRENT FILING DATE: 2000-12-19 Db SOFTWARE: FastSEQ for Windows Version 3.0 QY SOFTWARE: FastSEQ for Windows Version 3.0 Db SOFTWARE: FastSEQ for Windows Version 3.0 QY SOFTWARE: FastSEQ for Windows Version 3.0 Db SOF	44.58% Indels: 10 3410) x US-09-745-288-101 (1-553) AGAGGCTGTGGGTGAGCCGCTGCTGCGGCACC

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Qy 1664 TGCGGGGCCTCTGCTGTGATGTCTCCGTACGTGGGTGGTGGCTGGC	Oy 1724 AGGGTGGTTCCGGGCCGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1783	Qy 1784 CTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCAGCTCAGCCCAGTCTGTC 1843	Oy 1844 ACTGCCTATATGGTGTCTGCCGCGGGCCTGGGTCGGCCATTTACTTTGCTACACG 1903 .	Oy 1904 GTAGTATTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942	RESULT 7 US-09-838-785-2 . Sequence 2 Annitation IC (Adda28785	Sequence 4, Application US/09838/83 ; Patent No. US/2002009455Al ; GENERAL INFORMATION:	; AFFLICANT: Lau, red ; AFFLICANT: Lin, Rick ; AFFLICANT: Parkes, Debbie	APPLICANT: Parry, Gordon APPLICANT: Schneider, Douglas APPLICANT: Stainbrecher, Renate APPLICANT: Van Hanit Pam T	; APPLICANT: Wu, John ; TILLE OF INVENTION: DNA Encoding a No. US20020009455Alel PROST 03	FILE REFERENCE: 51431ADGMI ; CURRENT APPLICATION UNMBER: US/09/838,785 ; CURRENT FILING DATE: 2001-04-20	; PRIOR APPLICATION NUMBER: 60/200,065 ; PRIOR FILING DATE: 2000-04-27 ; NUMBER OF SEO ID NOS: 26	SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LEMETH. 65.3	TYPE: PRT ORGANISM:	785-2 Scores	3.32e-151 Length: 2861.00 Matches:	ocal Similarity: 100.00% Conservative: 0 Local Similarity: 100.00% Mismatches: 0 Match: 44.58% Indels: 0 10 Gaps: 0	US-09-759-143-110 (1-3410) x US-09-838-785-2 (1-553)	Oy 284 ATGGTCCAGAGGTGTGGGGCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTGCTG 343	344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCG	Db 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40	Oy 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGGCGGCATTGGT 463	Qy 464 CCAGTGCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGA 5.23 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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Qy 1604 TTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGCTCCCACCCCCCCC	OY 1784 CTGTCCCAGGTGGCCCATCTTATGGGCTCCATTGTCCAGCTCAGCTGTC 1843	3-113 13, Applid US2002000 FORMATION XU, Jii XU, Jii Mitchar Mitchar Harlocl H	APPLICANT: STOLK, JOHN A. APPLICANT: Day, Craig H. APPLICANT: Carter, Darrick APPLICANT: Carter, Darrick APPLICANT: Li, Samuel APPLICANT: Wang, Aljun APPLICANT: Wang, Aljun APPLICANT: Hepler, William TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C23 CURRENT PELLING DATE: 2001-01-12 CURRENT FILING DATE: 2001-01-12 CURRENT PLING DATE: 2001-01-12 CURRENT PLING DATE: 2001-01-12	ogt cch sma sma sma sellel	Oy 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCGGCACCGGAAAGCCCAGCTCTTGCTG 343

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Mismatches:
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                                                   210121.428C3
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
                                                  REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1543
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               GTTCGGATGGGCAGCCTGGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTG 1303
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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Patent No. US20020081580A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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δy	944	GCAGCGGTGGGCCCCACCAGCAGAAGGGCTGTCGCTCTCTTTTTTTT	
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Qy Dp	1004	TGCTGTCCATGCCGGGCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG	0 9
δ d		CCAGCTGTGCTGCCGCATGCCCCGCACCTGCGCCGGCTCTTTGTTGGTGCTGTGCTGCGCTGCGTGCGTGCGCTGCGTGCGTGCGTGCGTGCGTGCGTGCTTTTTT	о н.
α :	26	isGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
a d	1124	AGCTGGATGGCACTCATGACGTTCACGCTGTTTACACGGATTCGTGGCGAGGGGCTG	1183
oy .		SACACTATGATGAAGGC	
QQ	301	GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	3.20
oy Op	1244 321	GTTCGGATGGCAGCCTGGGGCTGTTCTGCAGTGCGCCATCTCCTGGTCTTCTTCTG 1	η,
ò	ò	47GGACGGCTGGTGCAGCGATTCGCAATTCAACAAAAAAAAA	40
qq	341		1363 360
Qy	1364	TTTCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCGCGTGGTGACAGCT	4
QQ	361		80
٥y	1424	GCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC	4
qq	381	erAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	00
δλ	1484	TTCCTGCCCAAATACCGAGGGGACACTGGAGGT	1543
qq	401	erLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	~
οy	1544	CTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTC	1603
Dp	421	- ŭ	. 4
οy	1604	TCCCTAATGGACACGTGGTGCTGGAGGCAGGTGGCCTGCTCCCACCTCCACCGGGCT	1663
Dp	441	ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu 4	.0
٥y	1664	SGGGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAGGCC 1	1723
QQ	461	CysGlyalaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 4)	æ
οy	1724	GTGGTTCCGGGCCGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG	1783
qa	481	JValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 5	ō
Οy	1784	37CCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1	1843
QQ	501		C.
Qy	1844	CTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1	1903
qq	521	hralaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGIn 5	240
οy	1904	SAGCGACTTGGCCAAATACTCAGC	
Dp	541	alvalPheAspLysSe	
RESULT 11 US-09-822 ; Sequence	-827- e 113	113 , Application US/09822827	

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APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SEG ID NO 133
LENGTH: 553
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Best Local Similarity:
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Sequence 113, Application US/09822827 Patent No. US20020081680A1 GENERAL INFORMATION:

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                                           TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT
            CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu
                                  CACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCCGGCTCTTCGTGGCTGAGCTGTGC
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
TITLE OF INVENTION: METHODS FOR THEIR USE
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CURRENT APPLICATION NUMBER: US/09/115,453B
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       CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version
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US-09-115-453-113
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APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vials de Bassols, Carlota
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT APPLICATION NUMBER: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARR: FastsEQ for Windows Version 3.0
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Matches:
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Mismatches:
Indels:
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Vedvick, Thomas
Carter, Darrick
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Best Local Similarity:
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Pred. No.:
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                                                                                                                         VENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND VENTION: DIAGNOSIS OF PROSTATE CANCER NCE: 210121.534C1
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'alvalPheAspLysSerAspLeuAlaLysTyrSerAla 1079
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Matches:
Conservative:
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ING DATE: 2001-03-28
EQ ID NOS: 982
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                                                              Application US/09822827
$20020081680A1
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2861.00
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lAlaAlaThrLeuLeuValAl	GCTGTCGGCCCCCTCCTTGTC 	GAACCTGGGCGCCCTGCTTCC 	CGGCT 	TTACACGGATTTCGTGGGCGA 	GAGGCCCGGAGACACTATGA: 	GCGCCAT	CGAGCAGTCTATTTGGCCAGT 	CACAGTGTGGCCGTGGT 	CTGCAGATCCTGCCCTACAC	CCCAAATACCGAGGGGACAC 	CCTGCCAGGCCCTAAGCCTGGA 	TGCTCCCACCTCCACC	GTGGTGGGTGAGCCCACC 	CTCGCCATCCTGGATAGTGCC 	TCCATTGTCCAGCTCAGCCAG 	CTGGTCGCCATTTACTTTGCT 	TCAGCG 1942 SerAla 1079	
uThrLeullePheLeuThrCysVa	3GGCCCCACCAAGCAGCAGAAGG 	ATGCCGGGCCCGCTTGGCTTTCCG 	GTGCTGCCGCATGCCCCGCACCCT 	3GCACTCATGACCTTCACGCTGTT 	CGTGCCCAGAGCTGAGCCGGGCACCC 	GGGCAGCCTGGGGCTGTTCCTGCAGT 	CCGGCTGGTGCAGCGATTCGGCACTC 	TGTGGCTGCCGGTGCCACATGCCT 	CCTCACCGGGTTCACCTTCTCAGC	CCACCGGAGAAGCAGGTGTTCCTGG 	GAGGACAGCCTGATGACCAGCTT 	3ACACGTGGGTGCTGGAGGCAG 	CTCTGCCTGTGATGTCTCCGTACGTC 	CCGGGCCGGGCATCTGCCTGGACCTC 	GGGCCCCATCCCTGTTTATGGGC 	ATGGTGTCTGCCGCAGGCCTGGGT 	GACAAGAGCGACTTGGCCAAATAC 	tion US/09895793
GlyLeuLe	GCAGCGCT(TGCTGTCC,	CACCAGCT	AGCTGGAT(TACCAGGGG	GTTCGGAT(GTCATGGA(ValmetAsp	GCTTTCCC	TCAGCCGCC	TCCCTCTAC	GCTAGCAGT	TTCCCTAATG(TGCGGGGCC 	AGGGTGGTT(CTGTCCCAG 	ACTGCCTATA 	GTAGTATTT 	974 , Applica
727	944	1004	1064	1124	1184	1244	1304	1364	1424	1484	1544	1604	1664	1724	1784	1844	1904	T 15 -895-793- uence 974
qa	Oy Dp	Qy Db	Qy	Qy	Qy	Oy Op	Qy Dp	Oy Db	Oy Dp	Qy Db	Qy Dp	Oy Dp	Qy pp	Oy Dp	Qy Db	Qy Db	Qy Dp	RESUL US-09

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284 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTG 343
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT APPLICATION NUMBER: US/09/895,793
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches:
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                Harlocker, Susan L.
Jiang, Yuqiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
Bay, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
Wang, Aljun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
        GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
US20020192763A1
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Best Local Similarity:
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LENGTH: 359
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Db 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40	QY 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGAAGTTCATGACCATGGTGCTGGCCATTGGT 463 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 464 CCAGTGCTGGGCCTGGTCTGTGCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGA 523	OY 524 CGCTATGGCCGCCGCCGCTTCATCTGGCACTGTCGGCATCCTGCTGAGCCTC 583	Qy 584 TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCTG 643	Qy 644 GAGCTGGCACTGCTCATCCTGGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGTTC 703	0y 704 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC 763	Oy 764 TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG	Qy 824 ATTGACTGGGACACCAGTGCCCTACCTAGGCACCCAGGAGGAGTGCCTCTT 883	Oy 884 GGCCTGCTCACCTCATCTTCCTCACGTAGCAGCCACACTGCTGGTGGCTGAGGAG 943	0y 944 GCAGCGCTGGGCCCACCGAGCAGCAGCAGCGGCCCCCTCCTTGTCGCCCCAC 1003	Qy 1004 TGCTGTCCATGCCGGCCCGCTTGCGGAACCTGGGCGCCCTGCTTCCCGGCTG 1063	0y 1064 CACCAGCTGTGCTGCCGCATGCCCGGACCTGGCCGGCTCTTCGTGGCTGAGCTGTGC 1123	Qy 1124 AGCTGGACGCACTCATGACCTTGTTTTACACGGATTTCGTGGGCGAGGGCTG 1183	Oy 1184 TACCAGGCGTGCCCAGAGCTGAGCCGGGCACCGGGAGACACTATGAAGGC 1243	SULT 17 -10-012-896- Sequence 708 Publication GENERAL INFC	APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer	; APPLICANT: Harlocker; Susan L.; APPLICANT: Jiang, Yuqiu ; APPLICANT: Kalos, Michael D. ; APPLICANT: Retter, Marc W.	APPLICAN APPLICAN APPLICAN
Db 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140	Oy 704 ACTCCACTGGAGGCCCTGCTCTGACCTTCCGGGACCCGGACCACTGTCGCCGAGGCC 763	Oy 764 TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGCTGCCTGGCTACCTGCCTG	Oy 824 ATTGACTGGGACACCAGTGCCCTGGCCCTGGGCACCCAGGAGGAGTGCCTCTTT 883	Oy 884 GGCCTGCTCACCTCATCTTCCTCACCTGCGCACACTGCTGCTGGTGGCTGGGGG 943	Oy 944 GCAGCGCTGGGCCCCACCGAGCAGAGAGGCTGTCGGCCCCTTGTCGCCCCCAC 1003	Qy 1004 TGCTGTCCATGCCGGCCCGCTTGCCTACGGACCTGGGCGCCCTGCTTCCCGGCTG 1063	0y 1064 CACCAGCTGTGCTGCCGCATGCCCTGCGCCGGCTCTTCGTGGCTGTGC 1123 	0y 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTCGTGGGCGAGGGCTG 1183 	Oy 1184 TACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGATGAAGGC 1243	RESULT 16 US-09-822-827-974 ; Sequence 944 Application US/09822827	; FACENT NO. USZUZZUGUSTOWAI ; APPLICANT: Xu, Jiangchun ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	; FILE OF THE NETICION: DIAGNOSIS OF FROSIALE CANCER; CURRENT APPLICATION NUMBER: US/09/822,827; CURRENT FILING DATE: 2001-03-28	NUMBER OF SEQ 1D NOS: 982 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 974 LENTH: 359) TIPE: FRI) ORGANISM: Homo sapiens US-09-822-827-974	Alignment Scores: 1.35e-86 Length: 359 Pred. No.: 1696.00 Matches: 320 Bercent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Mismatches: 0 Description of the conservation	US-09-759-143-110 (1-3410) x US-09-822-827-974 (1-359)	Oy 284 ATGGTCCAGAGGCTGTGAGCGCCTGCTGCGGCACCGGAAGCCCAGCTTGCTG 343	Qy 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGCCATCACCTATGTGCCG 403

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RESULT 18
US-09-895-793-708
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LENGTH: 371
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SerLeuValProLeuProLeuAlaLeuTyrLeuSerGlnProLeuThrHisThrThrSer 28
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                                                                                                                               APPLICANT: Fanger, Gary R.
APPLICANT: Wantenabe, Yoshihiro
APPLICANT: Meather Gary R.
APPLICANT: Meather Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.427027
CURRENT APPLICATION UNBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
SOFFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 708
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Mismatches:
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Matches:
                                                                      Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                         Henderson, Robert A.
Hural, John
                                   Skeiky, Yasir A.W.
Hepler, William T.
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1420.50
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Carter, Darrick
Li, Samuel X.
                         Wang, Aijun
                                                                                                                       Foy, Teresa
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Best Local Similarity:
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                         887 CTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACCTGCTGGTGGCTGAGGAGGCA 946
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APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT APPLICATION NUMBER: US/09/895,793
SOFTWARE: FASTSEO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 708, Application US/09895793; Publication No. US20020192763A1; GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Hepler, William T.
Henderson, Robert A.
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Jiang, Yuqiu
Kalos, Michael D.
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McNeill, Patricia
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Vedvick, Thomas S.
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Stolk, John A.
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US-09-895-793-708
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1307 ATGGACCGGC 1316 : :::||| 315 aValSerGly 318

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1067 CAGCIGIGCIGCCGCAIGCCCCGCACCCIGCGCCGGCTCTICGIGGCTGAGCTGIGCAGC 1126
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SOFTWARE: FastSEQ for Windows Version 3.0
         Sequence 708, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION:
                                       APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqiu APPLICANT: Kalos, Michael D.
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LENGTH: 371
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Patent No. US20020022248A1
GENERAL INFORMATION:
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Skeiky, Yasir A.W.
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Vedvick, Thomas S
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                                           FastSEQ for Windows Version 3.0
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
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1420.50
88.58%
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                                                                                    ORGANISM: Homo sapiens
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Pred. No.:
                                                    SEQ ID NO 708
LENGTH: 371
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                                                             327 TATGGCCGCCGCCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTTTT
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Fatent No. US20020081680A1

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C1

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SEQ ID NO 708
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Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: 05/09/780,669
CURRENT FILING DATE: 2001-02-09
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
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McNeill, Patricia D.
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Hepler, William
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Li, Samuel
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315 aValSerGly 318
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SOFTWARE: FastSEQ for
SEQ ID NO 708
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315 aValSerGly 318
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                                                                                       Conservative:
Mismatches:
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Matches:
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                                                          2.57e-71
1420.50
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                    ; ORGANISM: Homo sapiens
US-09-822-827-708
                                                                                  Percent Similarity:
Best Local Similarity:
                                                     Alignment Scores:
LENGTH: 371
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIGNOSIS OF PROSTATE CANCED
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CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
Sequence 852, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
                                               APPLICANT: Xu, Jiangchun C, APPLICANT: Dillon, Davin C, APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
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Hepler, William T.
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                                            AGGCCCGCTGGCTAGCAGGCCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 852, Application US/09895793; Publication No. US20020192763A1; GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Mitcham, Jennifer L.; APPLICANT: Harlocker, Susan L.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Kalos, Michael D.
Retter, Marc W.
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Hepler, William T.
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Li, Samuel X.
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Conservative:
  DIAGNOSIS OF PROSTATE CANCER
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TITLE OF INVENTION: DIAGNOSIS OF PROSTATE FILE REPERBYCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 852
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                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-793-852
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CURRENY PEPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
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EDENERAL INFORMATION: APPLICANT: APPLICANT: Xu, Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
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ORGANISM: Homo sapiens
US-09-759-143-852
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APPLICANT: FOY, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427026
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 852
LENGTH: 400
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Matches:
Conservative:
Mismatches:
Indels:
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Wang, Aljun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
                                                                                     Sequence 852, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION:
                                                                                                                             APPLICANT: Xu, Jiangchun
APPLICANT: Xi, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carler, Day, Craig H.
APPLICANT: Carler, Day, Craig H.
APPLICANT: Carler, Darrick
APPLICANT: Carler, Darrick
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207 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 226
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APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Hural, Dahn
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT FILING DATE: 2001-02-09
CURRENT FILING DATE: 2001-02-09
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Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
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Vedvick, Thomas S.
Carter, Darrick
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Hepler, William T.
Henderson, Robert A.
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Wantanabe, Yoshihiro
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
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Kalos, Michael D.
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR T
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
KUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
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Patent No. US20020081680A1
GENERAL INFORMATION:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
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CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASELSEQ for Windows Version 3.0
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Vinals de Bassols, Carlota
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Publication No. US20020183251A1
GENERAL INFORMATION:
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FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                        SEQ ID NO 571
LENGTH: 84
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Conservative:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
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Retter, Mark
Solk, John
Day, Craig
                              ; ORGANISM: Homo sapiens
US-10-012-896-1011
                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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 LENGTH: 355
TYPE: PRT
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Washer, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
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Conservative:
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Vinals de Bassols, Carlota
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McNeill, Patricia D.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Kalos, Michael D.
Retter, Marc W.
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Hepler, William T.
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Query Match:
                 ; ORGANISM: HOMO
US-10-010-940-571
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.53462 CURRENT APPLICATION NUMBER: US/09/895,793 CURRENT FILING DATE: 2001-06-29
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Mismatches:
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Matches:
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SSOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 706
LENGTH: 123
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Jiang, Yuqiu
Kalos, Michael D.
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Skeiky, Yasir A.W.
Hepler, William T.
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Vedvick, Thomas S.
Carter, Darrick
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Stolk, John A.
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US-10-012-896-706
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1250 ATGGCCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATG 1309
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 21012.1.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT APPLICATION NUMBER: US/09/895,814
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches:
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 706
LENGTH: 123
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Vinals de Bassols, Carlota
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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McNeill, Patricia
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Vedvick, Thomas S.
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Hepler, William T.
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Stolk, John A.
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                                                                         ORGANISM: Homo sapiens
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                                                                                           us-09-895-793-706
                                                                                                                                Alignment Scores:
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CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
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Skeiky, Yasir A.W.
Hepler, William
Hural, John
McNeill, Patricia D.
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
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Kalos, Michael D.
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Stolk, John A.
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DAGNOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DAGNOSITIONS AND METHODS FOR THE THERAPY AND
CURRENT FILING DATE: 2001.01-12
NUMBER OF SEQ ID NOS: 934
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Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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Jiang, Yuqui.
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Dillon, Davin C.
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US-09-895-814-706
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            Sequence 706, Application US/09822827
Sequence 706, Application US/09822827
Betent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEO ID NOS: 982
SOFTWARE FELSE FESTSEQ for Windows Version 3.0
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Causey, Stuart
Pollock, Thomas J.
Cappello, Joseph
Crissman, John W.
TITLE OF INVENTION: No. US20030083464Alel Peptides Comprising Repetitive
Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2347 GGGAAACCAGGTGAGTTTATTCAGCTCCCAAAAACCCTTCTTAGGTGTGTCTCAA 2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2287 CTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGGCATTCC 2228
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                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: I EACHY ULSA
COMPUTER: I EACHY ULSA
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,986
FILING DATE: 12 AMAR-2002
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/44,791
FILING DATE: 22-No. US/2003/008446A1-1999
APPLICATION NUMBER: US 08/482,085
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 29-OCT-1987
APPLICATION NUMBER: US 06/27,258
FILING DATE: WINDRAMER: US 06/27,258
FILING DATE: US 06/27,258
FILING DATE: OTT-1986
ATTORNEY/AGENT NUMBER: US 06/27,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET UNBER: A-55186-11/RFT/BTC
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
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                                     APPLICANT: Ferrari, Franco A. Richardson, Charles Chambers, James
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear

MOLECULE TYPE: peptide

: SEQUENCE DESCRIPTION: SEQ ID

US-10-096-986-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 837 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 103:
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                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
Publication No. US20030083464A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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356.50
35.16%
31.35%
5.73%
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                       GENERAL INFORMATION:
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Best Local Similarity:
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73	AGTGCATGGAGCCCTTCTGGCTCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGC 2168 DD	CTCCAGTCAGCCCTAGAGACTGGGGAGAGGGACGCCCCAGCCCCAGCT 2108 CTCCAGTCAGCCCTAGAGACTGGGGAGAGAGGGACGCCCCAGCCCCAGCT 2108 Db	7	GlyLeuProGlySerProGlyAlaProGlyThrProGlyP 116 Ov	1.988	laProGlyThrProGlyProGlnGlyLeuProG 136 Ov	TGTGCTGGAAGTTTTCTACGCTGAGTATTTGGC 1928	144	IGTAGCAAAGTAAATGGGGACCAGGCC 1868	GlySerProGlyA 155	AGACTGGCTGAGCTGGACAATGGAGCCCATAAA 1808	euProGlySerPro 168	SAAGGCACTATC 1769	GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaP 186	C	laProGlyThrProGlyProGlnGlyLeuProG 226	16	lyProGlnGlyLeuProGlySerProGlyAlaP 246	CATTAGGGAAGGGAGCTCCAGGCTAGGGCTGGCAGGAAGCTGGTCATCAGGCTGTCCT 1554	ProGly-SerProGlyAlaProGlyThrPro 264	15	ProGlnGlyLeuProGlySerProGlyAlaProGlyThr 278	AGGGCAGGATCTGCAGGGCTGAGAGGTGAACC		CACACTGTGGGACAGGCATGTGGCACC	AlaProGlyThrPr	-GGCAGCCACAGGGAAAGCTGCCACACACGGCGAAATAGACTGCTCGAGTGCCGAATCGCT 1323	SerProGly 319	12	LeuProGlySerProGlyAlaProGlyThrPro 339	GCCCCAGGCTGCCCATCCGAACGCCTT 1239
σ	227			ProGln						'n		ın	CAGGGA	:							53	5 Gly		on.				oglyProglagly			1265

340	GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 359
1238	CATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCC 11
360	 SlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro
-	CTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGC 11
379	lyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGly 394
rà c	TGCACAGCTCAGCCACGAAGAGCCGGCGCAGGGTGCGGGGCATGCGGCACA 1
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	SECTOR TO CONTROL OF THE SECTOR OF THE SECTO
43	 nGlyLeuProGlySerPro 45
959	GGCTGCTACGCAGG
454	 hrProGlyProGln
902	AGATGAGGGTGAGCCAAAGAGGCACTCCT
464	48
857	GGTAGGGGCCCAGGCACTGCTGTCCAGTCAATGGCAGGCA
484	GlyAlaproGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 50
797	CCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGT
501	ProglyThrProGlyProGlnGlyLeuProGly 51
4	CCCGGAAGAGGTCAGAGAGGCCTCCAGTGGAGTGAAGCACACAGGCACAGA 68.
512	SerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGly 32
683	AGTCCAGCAGCCCCACGCCCAGGATGAGCAGTGCCAGGGGCCTGGGGATCCGGGC 624 :::
623	
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572	SerProGlyAlaProGlyThrProGlyProGlnGl
446	6 TGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAGGGGGGCA 399
586	6 GlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 605
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179	ALarrocly:iiirricelyricelyricelricelycelricelycelricelyricely
287	1 TGGGCCAGGGGGGTAGGGCTCAGGGGGCGGTTCAGGCACTCCAGAACTGCTTCGTCT 225
3	COTY FLOORING 1 PEGG 1 COTY COTY 1 CO

###	180 GinMetGlyProArgGlyLeuProGlyGluArgGlyArg	394 rodiyalaiys-GlyAiaAsndiyAlaPro
Oy 224 CGGCTCTGCTCCAGAAGCTGCGGCCTCTTGCTGCCGCCAACTGCCTAGGAATCA 165 Db 659 uProGlySalaproGlyThrProGly	Application US/10216705 No. US20030096973A1 No. US20030096973A1 Meriatem Therapeutics, S.A. WENTION: Recombinant Collagens and Derived P. WENTION: Obtaining Such and Their Uses NUCE: 1149-3 DIV LICATION NUMBER: US/10/216,705 LICATION NUMBER: US/02-08-09 IG DATE: 1999-08-17 EQ ID NOS: 22 atentIn version 3.1 64 Homo sapiens	Alignment Scores: Series: Societ: Societ: 347.00 Matches: Societ: 1464 Score: Score: 137.00 Matches: 1367 Best Local Similarity: 13.428 Conservative: 137.00 Mismatches: 138.028 Mismatches: 138.028 Mismatches: 139.00 Mismatches: 130 Mismatches Mismatches 130 Mismatches Mismatches 130

Dp	524GlyGluAlaGlyArgProGlyGluAlaGlyLeuProGlyAlaLysGlyLeuThrGly 542	Qy 242 TCCAGAA
Qy	1031 AAGCCAAGGGGCCCGGCAIGGACAGCAGGGGGGGGGACAGGGGGGGCCGACAGCCCIT 972	Db 864 a
QQ	543 SerProGlySerProGlyProAspGlyLysThrGlyProPro 556	188
Qy	971 CIGCIGGCICGGGGCCCAGCG	879
qq	557GlyProAlaGlyGlnAspGlyArgProGlyProProGlyProPro 571	128
δý	929GCAGTGGCTG 918	000
qq	572 GlyAlaArgGlyGlnAlaGlyValMetGlyPheProGlyProLysGlyAlaAla 589	7.4
δ	917 CTACGCAGGTGAGGAAGATGAGGTGAGCAGGCCAAAGAGGCACTCCTCCTGGG 864	912
qq	590GlyGluProGlyLysalaGlyGluArgGlyValProGlyProFroGly 605	VV
Qy	863 TGCCCAGGTAGG 852	44 GCGCGCC : :
qa	606 AlaValGlyProAlaGlyLysAspGlyGluAlaGlyAlaGlnGlyProProGlyProAla 625	30 6 1113
δλ	GGGCACTGGTGTCCAGTCAATGGCAG	US-10-060-036-159
q		; Publication No. US;
Qy	CAAGACTGATCATGAAGGCATAGACAGAGTAGG	
qq		
Qy	755 GACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGAGCAGGGCCTCCAGTGGAG 705	APPLICANT: Persing APPLICANT: Heple:
qq		
δy	704 TGAAGCACACTGGCCACAGAAGTCCAGCACCCCAAGGATGAGCAGTGCCA 648	; FILE REFERENCE: 2
ΩD		CURRENT APPLICATION CURRENT FILING DA
ογ	99	SOFTWARE: FastSEQ
QQ		; SEQ ID NO 159 ; LENGTH: 1464
Qy	614 CTGCTAGCCAGCCGTCCTTGGGATGAGAAAGAGGCTCAGGAGGATGCCCAAGGACAGTG 555	CRGANISM: HOMO S
qq	::: :::	SCT-050-001-01-50
Οy	554 CCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTA 495	Alignment Scores: Pred. No.:
· £	:::	Score: Percent Similarity:
20	rionysatyaspangatyaspangatyrionysatyanaaspary	Best Local Similarit
ΟŅ	CIGGAC	Query match: DB:
qa	GlyLysAspGlyValArgGlyLeuThrGlyProIleGlyProProGlyPróAla	US-09-759-143-110 (1
δλ	461 CAATGCCCA 453	Qy 2353 AGAGAT
qa	776 GlyAlaProGlyAspLysGlyGluSerGlyProSerGlyProAlaGlyProThrGlyAla 795	
Οy	452GCACCATGGTCATGAACTTCTCCTCTACCCCACTTCCAGCAGCAGAGGGGGGA 399	2299
οp	796 ArgGlyAlaProGlyAspArgGlyGluProGlyProProGlyProAlaGlyPheAlaGly 815	
Qy		QY 2242 GAGTCC
qq		Db 171 SerThr
οy	GGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGGCGGCTCACACAGCCTCT	QY 2182 ACCCC
q O	GlyGluProGlyAspAlaGlyAlaLySGLyAspAlaGlyProProGlyProAla	Db 183
Qy		Qy 2122 CCCCAG
qq	845 Glypro-AlaGlyproProGlyproIleGlyAsnValGlyAlaProGlyAlaLysGlyAl 864	=

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GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCT-----TCTCTA 2300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGGGAGAGGGACG 2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCCCCAGCTGFGCAGCTACGCACCTCAGCACAGGGTGGCAGCAGCAGAGACCCA 2063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------ArgGlyPro------ArgGlyLeu 189
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|GlylleproGlyGlnProGlyLeuProGlyProProGlyProProGlyProPro 150
                                                                                                                                             lyProAlaGlyArgProGlyGluValGlyProProGlyProProGlyProAlaG 932
                                                           CCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGG 129
                                                                                     CTGCTTCGTCTCGGCTCTGCT----CCAGAAGCTGCGGCCTCTCCTTG 189
                                                                                                                                                                                         CATCACTCAGATCCTGGCCGA-----G 45
                                                                                                                            TCTCAGCCCATGCTCAACACCTGCTGCTGTGGG-----GCACCTCAGTGGGG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : ||| ||| ||| cGlyGlyIleSerValProGlyProMetGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NI: COMPOSITIONS AND METHODS FOR THE THERAPY
NI: AND DIAGNOSIS OF PANCREATIC CANCER
1.10121.566
ON NUMBER: US/10/060,036
TTE: 2002-01-30
NOS: 4560
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                        ication US/10060036
20030073144A1
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s, Michael D.
s, Michael J.
ing, David H.
er, William T.
g, Yuqiu
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Dp	190	ProGlyProProGlyAlaProGlyProGlnGlyPheGlnGlyProProGlyGluPro 208	_
Qy	2062	CATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAACAGG 2003	
qq	209	GlyGluProGlyAlaSerGlyProMetGlyProArgGlyProProGlyProProGlyLys 228	
QY	2002	AGCGGGGAGCTGGGA1967	
QQ	229	nGlyAspAspGlyGluAlaGlyLysProGlyAr	
οy	1966	AGTTTTCTACGCT	
DP	249	ProGlnGlyAlaArgGlyLeuProGlyThrAlaGlyLeuProGly 263	
0y	1927	CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGGGACCAGACCCAGGCC 1868	
qq	264	 MetLysGlyHisArgGlyPheSerGlyLeuAspGlyAlaLysGlyAspAlaGlyProAla 283	
οy	1867	TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAA 1808	
QQ	284	GlyProLysGlyGluProGlySerProGlyGluasnGlyAlaProGly 299	
δo :		CAGGGATGGGGCCACCTGGGACAGCAGGAGGACTATCCAGGATGGCGAG 1757	
qq		GlnMetGlyProArgGlyLeuProGlyGluArgGlyArgProGlyAlaProG 317	
Qy Dp	317	GTCCAGGCAGATGCCCGGCCGGGA	
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3		nrolykroalaglykrokroglyknekroglyalavalGlyalaLysGlyGluAlaGlyP 357	
٥y	1679	GGAGCAGG	_
qq	357	roGlnGlyProArgGlySerGluGlyProGlnGlyValArgGlyGluProG 374	
٥y	1634	TGCCTCCAGCACCCACGTGTCCATTAGGGAAAGGGAGCTCCAGGCTTAGGGC 1584	-
qq	374	lyProProGlyProAlaGlyAlaAlaGlyProAlaGlyAsnProGlyAlaAspGlyGlnP 394	
Qy	1583 (CTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGT 1524	
Db	394	roGlyAlaLys-GlyAlaAsnGlyAlaPro	
Oy	1523 /	ATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGG	
Db	405	i:: IleAlaGlyAlaProGlyPheProGlyAlaArgGlyProSerGly 419	
Οy	1463 1	TCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGCTGAAGCTGTCACCACGGCCACAC 1404	
Db	420 1	Pro-GlnGlyProGlyGlyProProGlyProLysGlyAsnSerGlyGluProGlyAl 438	
Οy	1403 1	GTGGGACAGGCATGTGGCACCGGCAGCACAGGGAAAGCTGCCACACTGGCCAAATAGA 1344	
ρp	438 8	aProGlySerLysGlyAspThrGly-AlaLysGlyGluProGlyPro 453	
Qy	1343 (CTGCTCGAGTGCCGAATCGCTGCAGCCGGTCCATGACCAGAGAGAAGACCA 1290	
QQ	454	.:: Val-GlyValGlnGlyPrOProGlyProAlaGlyGluGluGlyLySArgGly 470	
Οy	1289	iggagargecgcacrecaggaacagccccaggcrecccarccgargec 1242	
qa	471 4	AlaArgGlyGluProGlyProThrGlyLeuProGlyProProGlyGluArgGlyGlyPro 490	
Qγ	1241 -	TCITCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTC 1200	
Dp	491 G	GlySerArgGlyPheProGlyAlaAspGlyValAlaGlyProLysGlyProAlaGlyGlu 510	
Qy	1199 1	TGGGCACGCCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCA 1140	
qq •	511 A	rgGlySerProGlyProAlaGlyProLysGlySerPro 523	

Qy	1139	TGAGTGCCATCCAGCTGCAGGCTCAGCCACGAAGAGCCGGCGCGAGGGTGCGGGGGCATGC	108
Db	523		523
ΟY	1079	GGCAGCACAGCTGGTGCAGCCGGGGAAGCAGGGCGCCCCAGGTTCCGGA	103
Db	524	::: GlyGluAlaGlyArgProGlyGluAlaGlyLeuProGlyAlaLysGlyLeuThrGly	542
Qy	1031	AAGCCAAGCGGGCCCGGCATGGACAGCAGTGGGCGACAAGGAGGGGCCGACAGCCCTT	972
QQ	543	SerProGlySerProGlyProAspGlyLysThrGlyProPro	556
Qy	971		930
Db	557	spGlyArgPr	571
Qy	929		918
qa	572	ProLy	589
Qγ	917	GCAGGTGAGGAAGATGAGGGTGAGCCAAAGAGAGGCACTCCTCCTGG	864
qa	290	 yGluProGlyLysAlaGlyGluArgGlyValPro	605
οy	863	TGCCCAGGT-2AGG	852
qq	909	Pro	625
Qy	851		813
Db	626	erPro	645
Qy	812	GGTAGCCCAGGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGC	756
qq	646	ProGlyProAlaGlyProProGlyGluAlaGlyLysProGlyGluGlnGlyValProGly	665
Qy	755	-ccgggrccc	705
Db	999	AspLeuGlyAlaProGlyProSerGlyAlaArgGlyGluArgGlyPheproGlyGlu	684
Qy	704	TGAAGCACACCTGGCCACAGAAGTCCAGCAGCCCCAGGATGAGCAGCA	648
Db	685	 ArgGlyvalGlnGlyProProGlyProAlaGlyProArgGlyAlaAsnGlyAlaProGly	704
Óy	647	U	615
Db	705	>-	722
Oy	614		555
Db	723	AlaProGlyLeuGlnGlyMetProGlyGluArgGlyAlaAlaGlyLeuProGly	740
Qy	554	4	495
qq	741	0	757
Qy	494	SACACAGACCAGGCCCAGCACTGGAC	462
qq	758		775
Qy	461		453
QQ	176	GlyAspLysGlyGluSerGlyProSerGlyProAlaGlyProThrGlyAla	795
Qy	452		399
Db	796	ArgGlyAlaProGlyAspArgGlyGluProGlyProProGlyProAlaGlyPheAlaGly {	815
οy	398		351
Db	816		826

QY Db

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                                                                                                                                                                                                                                                                                                           912 luThrGlyProAlaGlyArgProGlyGluValGlyProProGlyProProGlyProAlaG 932
                                                                     242 TCCAGAACTGCTTCGTCTCGGCTCTGCT-----CCAGAAGCTGCGGGCCTCTCCTCCTTG 189
                                                                                                                                                                   188 CTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGG 129
GGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGGCGCCTCACACCACAGCCTCT 291
                          844
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-16-114
                 290 GGACCATAGTGGGCCA------GCCGGGTAGGGCTCAGGGGCCCGTTCAGGCAC
                                                                                                                                                                                                                        128 TCCAGCTTCTCAGCCCATGCTCAACACCTGCTGCTGTGGG-----GCACCTCAGTGGGG
                                                                                                                                                                                                                                                                                74 ACACGTCTCATCACTCAGATCCTGGCCGA-----G
                                                                                                                                     864 a-------ArgGlySerAlaGlyProProGlyAlaThrGlyPheProGlyAl
                                                                                                                                                                                       379 aAlaGlyArgValGlyProProGlyProSerGlyAsnAlaGlyProProGlyProProGl
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Mismatches:
Indels:
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
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899 yProAlaGlyLysGlu------
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                                                                                                                                                                                                                                                                                                                                       GCGCGCGCTGTCACCCGGAGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36, Application US/10171311 Publication No. US20030087270A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Chen, Xumel
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Ganavarapu, Manjula
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343.00
32.32%
27.91%
5.51%
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LENGTH: 1464
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APPLICANT:
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2063 ------CCACCCTGGCCTC 1718 -----GCAGAGGCCCCGCAGAGCGCGGTGGAGGTGGGAGCAGGCCAC 1635 -----CCCAGTGAGGCAGGCCCTCCA--- 1967 1966 ------CCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGC 1928 .867 TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAA 1808 .807 CAGGGATGGGGCCA-----CCTGGGACAGCAGGAAGGCACTATCCAGGATGGCGAG 1757 1634 TGCCTCCAGCACCCACGTGTCCATTAGGG---AAGGGAGCTCCAGGCTTAGGG-----C 1584 CTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTAGCACCTCCAGTGTCCCCTCGGT 1524 1463 TCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGGGGGCTGAAGCTGTCACCACGGCCACAC 1404 .403 TGTGGGACAGGCATGTGGCACCGGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGA 1344 2242 GAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCTGTATAAGTCCAGACTGAA 2183 2062 CATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGGCTAACAGG 2003 2299 GGTGTGTCTCAACTAGGAGGCTAGCTGTTA---ACCCTGAGCCTGGGTAATCCACCTGCA 2243 248 263 roGlyAlaLys-GlyAlaAsnGlyAlaPro------Gly 404 183 ------ArgGlyLeu 189 264 MetLysGlyHisArgGlyPheSerGlyLeuAspGlyAlaLysGlyAspAlaGlyProAla 283 317 357 roGlnGlyProArgGlySerGluGlyProGlnGlyValArgGly------GluProG 374 131 ArgAspGlyIleProGlyGlnProGlyLeuProGlyProProGlyProProGlyProPro 150 420 Pro-GlnGlyProGlyGlyProProGlyProLysGlyAsnSerGlyGluProGly---Al 2122 CCCCAGCCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAGAGAGCCA |||| |||||| 190 ProGlyProProGlyAlaPro---GlyProGlnGlyPheGlnGlyProProGlyGluPro 209 GlyGluProGlyAlaSerGlyProMetGlyProArgGlyProProGlyProProGlyLys 249 ProglnGlyAlaArgGlyLeuProGlyThrAlaGly------LeuProGly 284 GlyProLysGlyGluProGlySerProGly------GluAsnGlyAlaProGly 151 GlyProProGlyLeuGlyGlyAsnPheAlaProGlnLeuSerTyrGlyTyrAspGluLys 2182 ACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGGAGAGGGACG 1927 CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGGCC 438 aProGlySerLysGlyAspThrGly-AlaLysGlyGluProGlyPro ||| |||||| ||| 405 Ile---AlaGlyAlaProGlyPheProGlyAlaArgGly-----171 SerThrGlyGlyIleSerValProGlyProMetGly---1756 GTCCAGGCAGATGCCCCGGCCCGGAA----2002 AGCGGGGAGCTGGGA-1679 AG---g

APPLICATION NUMBER: US/10/096,986		
; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFWARE: Patentin Release #1.0, Ve	534 CCCMAATGARGGCCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTA 495 111:::1	යි යි
; MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE	ProGlyGluArgGlyAlaAlaGlyLeuProGly	q :
COMPUTER READABLE FORM:	614 CTGCTAGCCGGCCCTTGGGATGAGAAGAGCTCAGCAGGATGCCCAAGGACAGTG 555	δλ
STATE California	705 AsnAspGlyAlaLysGlyAspAlaGlyAlaProGlyAlaProGlySerGlnGly 722	qa
ADDRESSEE: Flehr Hohbach Test Albri STREET: Four Embarcadero Center, St.	647	Qy
; NUMBER OF SEQUENCES: 117 ; CORRESPONDENCE ADDRESS:		QQ
; TITLE OF INVENTION: No. US20030083464A1.	704 TGAAGCACACCTGGCCACAGAAGTCCAGGAGCCCCAGGCCCAGGATGAGCAGTGCCA 648	ογ
; Cappello, Joseph ; Crissman, John W.	666 AspLeuGlyAlaProGlyProSerGlyAlaArgGlyGluArgGlyPheProGlyGlu 684	qq
causey, Stuart Pollock, Thomas J.	755 GACAGTGGTCGGGTCCCGGAAGAGGTCAGAGAGCAGGCCTCCAGTGGAG 705	Qy
Chambes	646 ProGlyProAlaGlyProProGlyGluAlaGlyLysProGlyGluGlnGlyValProGly 665	qq
APPLICANT: Ferrari, Franco A.	812GGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGC 756	Oy
; Sequence 103, Application US/10096986 ; Publication No. US20030083464A1	626 GlyProAlaGlyGluArgGlyGluGlyProAlaGlySerProGlyPheGlnGlyLeu 645	qq
RESULT 41 US-10-096-986-103	851 GGGCCAGGGCACTGGTGTCCCAGTCAATGGCAGGA	Qy
Db 932 lyGluLysGlySerProGlyAla 939	 606 AlaValGlyProAlaGlyLysAspGlyGluAlaGlyAlaGlnGlyProProGlyProAla 625	qq
Oy 44 GCGCGCGCTGTCACCGGAGCC: 22	863 TGCCCAGGTAGG 852	οy
51	917 CTACGCAGGTGAGGAAGATGAGGGTGAGCCCAAAGAGCACTCCTCCTGGG 864 590GlyGluProGlyLySAJaGlyGluArGGlyValProGlyProProGly 605 .	oy da
DD 899 yProAlaGlyLysGlu	572 GlyAlaArgGlyGlnAlaGlyValMetGlyPheProGlyProLysGlyAlaAla 589	qq
128	929GCAGTGGCTG 918	Qy
Db 879 aAlaGlyArgValGlyProProGlyProSerGly		qa
OY 188 CTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCC		Qy
864 aArgGlySerAlaG	1031 AAGCCAAGCGGGCCGGCATGGACAGCAGTGGGGGGGACAAGGAGGGGGCGACAGCCCTT 972 543 SelPtoGlySerProGlyProAspGly	g d
DD 845 GlyPro-AlaGlyProProGlyProlleGlyAsn	524GlyGluAlaGlyArgProGlyGluAlaGlyLeuProGlyAlaLysGlyLeuThrGly 542	qa
	1079 GGCAGCAGCTGGTGCAGCCGGGGAAGCAGGCGCCCAGGTTCCGGA 1032	Qy
827	523 523	QQ
Qy 350 GGTTGACCAGCAAGAGCTGGGGTTTCCGGTGCCG	1139 TGAGTGCCATCCAGCTGACAGCTCAGCACGAAGAGCCGGCGCAGGGTGCGGGGCATGC 1080	ογ
DD 816ProProg		qa
QY 398 CATAGGTGATGCCTGCGGCCAAACACACCTCCAG	1199 TGGGCACGCCTGGTACAGCCCCTCGCCCACGAATCCGTGTAAAACAGCGTGAAGGTCA 1140	٥y
196	491 GlySerArgGlyPheProGlyAlaAspGlyValAlaGlyProLysGlyProAlaGlyGlu 510	qq
452	1241	δλ
Db 776 GlyAl		qa
461	TGCCCATCC	ΟY
758	:::!!! luGlyLysArgGly	Db
	1343 CTGCTCGAGTGCCGAATCGCTGCACCAGCCGGTCCATGACCAGAGAGAAGACCA 1290	οy

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el Peptides Comprising Repetitive
s and DNA Sequences Encoding the Same
erGlyProAlaGlyProThrGlyAla 795
                                                                                                                                                                                                                                                             TAGGGCTCAGGGGGCGTTCAGGCAC 243
|||::: |||
|ValGlyAlaProGlyAlaLysGlyAl 864
                                                                                                                                                                                                                                                                                                                                                                     CATTTCTGCCAGCCCTTTGGTGCCGG 129
                                                                                                       CCCCACTTCCAGCAGCAGGCGGCA 399
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|IyAlaAspGlyGlnProGlyAlaLys 826
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                                                                                                                                                                                                            CAGCAGGCGCTCACCCACAGCCTCT 291
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|ProGlyAlaThrGlyPheProGlyAl 879
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AsnAlaGlyProProGlyProProGl 899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCT-- 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 GCCG----CCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 GGTGCCCCACAGCAGCAGGTGTTG-----AGCATGGGCTGAGAAGCTGGACCGGCACCA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 AAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTGGCGGCAGCAAGGAGGA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-781-1989
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHRRACTERISTICS:
                                                      FILING DATE: 22-NG. U$20030083464A1-1999
APPLICATION NUMBER: U$ 08/482,085
FILING DATE: 07-UN-1995
APPLICATION NUMBER: U$ 08/175,155
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: U$ 08/053,049
FILING DATE: 22-APF-1993
APPLICATION NUMBER: U$ 07/114,618
FILING DATE: 29-OCT-1987
APPLICATION NUMBER: U$ 06/927,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-759-143-110 (1-3410) x US-10-096-986-103 (1-837)
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Mismatches:
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Matches:
                              APPLICATION DATA:
APPLICATION NUMBER: US/09/444,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-096-986-103
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FILING DATE: 12-Mar-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                            FILING DATE: 04-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 837 amino acids
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION
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323.00
30.52%
26.29%
5.03%
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Best Local Similarity:
Query Match:
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1482 CCTCCCTCTACCACCGGGAGAGCAGGTGTTCCTGCCCAA-----ATACCGAGGGGACA 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1089 GCACCCTGCGCCGGCTCTTCGTGGCTGTGCAGCTGGATGGCACTCATGACCTTCA 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1149 CGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGC 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1209 CGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGGT-- 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [267 ----GIICCIGCAGIGCGCCAICTCCCTGGICITCTCTCTGGICATGGACCGGCTGGIGC 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1323 AGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCG 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1383 GTGCCACATGCCTGTCCC---------ACAGTGTGGCCGTGGTGACAG 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1422 CTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGG 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  972 AAGGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTT 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1032 TCCG----GAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCGCGATGCCCC 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 oGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly-- 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 o---GlyAlaProGlyThrProGly----- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 ------GlyProGlnGlyLeu------ProGlySerProGlyAlaPr 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 ySerProGlyAlaPro----------GlyThrProGlyProGlnGlyLe 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 oGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPr 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      912 GCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCCACCGAGCCAGCAG 971
                                                                                                                           182 rProGlyAlaProGlyThrProGlyProGlnGlyLeu-----ProGlySerProGlyAl 200
                                                                                                                                                                                                                                                                                CACTGGAGGCCCTGCTCTGACCTCTTCCGGGA---CCCGGA---CCACTGTCGCCAGG 761
                                                                                                                                                                                                                                                                                                                                                                                -----GlyAlaProGlyThrPro-----GlyProGl 162
                                                                                                                                                                                     648 IGGCACIGCICAICCIGGGCGIGGGGCIGCIGGACIICIGIGGCCAGGIGTGCIICACIC 707
537 GCCGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             822 CCATTGACTGGGACACCAGTGCCCTGGCCCC-----CTACCTGGGCACCCAGGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 ------ProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro------
                                                                                                                                                                                                                                                                                                              597 GGGCCGGCTGGCTAGCAGGGCTGCT----GTGCCCGGATCCCAGGCC---CCTGGAGC
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Qy	1536 CTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAG 1591	
q a		
δò	1592	Qy 2607 ACTTATTTATTAACAAAGTA
qa	449 euProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProG 469	Db 675
λō ·	1632 GCAGTGGCCTGCTCCCACCTCCACCGGGGTCTGCGGGGCCTCTGCCTGTGATG 1685	OY 2667 ATATTTGGTAGGGGGGA
QQ	469 lyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrP 489	Db 676GlySerProGlyAl
ΛO	1686 TCTCCGTACGTGGTGGTGGGTGAGCCCACGAGGCCAGGGTGGTTCCGGGCCGGGGCA 1745	QY 2727 GCTGATCATTGCCAGAATCTT
qa	489 roGlyProGlnGlyLeuProGly-SerProGlyAlaPro-GlyThrProGlyProGlnGl 508	Db 687
οy	1746 TCTGGCTGGACCTCGCCATCCTGGATGCCTTCCTGCTGTCCCAGGTGGCCCCATCCC 1805	QY 2787 GACCTTGGAAATTCTACTCAT
Dp		Db 697 yThrProGlyProGlnGlyLei
ζO	1806 TGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATA 1853	Qy 2847 GTGTTGAAGGAAGGTAGAGGG
qa		Db 715
οy	1854 TGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTG 1913	Qy 2907 TTCTTTGGCCCAGCCTGGTTC
qa	540 oGlySerProGlyAlaProGlyThrPro	Db 727 yThrProGlyProGlnGlyLe
Qy	1914 ACAAGAGGACTTGGCCAAATACTCAGGGTAGAAAACTTCCAGGACATTGGGGTGGAGGG 1973	Qy 2964 TGGGCTGATGAAGGCACTGCCC
qa		
Qy	1974 CCTGCCTCACTGGGTCCCAGCTCCCGGCTGTTAGCCCCATGGGGGTGCCGGGCTTGGC 2033	Qy 3024 TTTCCCACCAGCTCCACAACC
qa		Db 763 yLeuProGlySerPro
οy		RESULT 42 US-09-919-497-56
QQ		Sequence 56, Application US/099196
δλ	2094 GTGGGTAGCTGCACAGCTGGGGGCTGCGCTCCTCTCTCTC	GENERAL INFORMATION: APPLICANT Mutter George 1
QQ	574 1711	; TITLE OF INVENTION: PROGNOSTIC CI
Qy	2154 CTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAA 2213	CURRENT APPLICATION NUMBER: US/OS CURRENT FILING DATE: 2001-07-31
qa		PRIOR APPLICATION NUMBER: US 60/2; PRIOR FILING DATE: 2000-07-31
Qy	2214 GGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGT	; NUMBER OF SEQ ID NOS: 100 ; SOFTWARE: PatentIn version 3.0
qq	613 GlyLeuProGlySerProGlyAlaProGlyThrProGlyProGln 627	; SEQ ID NO 56 ; LENGTH: 1806
Qy	2250 GGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAA 2306	
qa	628 GlyLeuPro	; FEATURE; NAME/KEY: UNSURE
Qy	GCTGAATAAACTC	
qa	643 GlyLeuProGlySerProGlyAlaProGlyThr-ProGlypr 656	Z m
Qy	2367 ¡GCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATG 2426	CTHER INFORMATION: Xaa = any ami US-09-919-497-56
QQ	656 oglnGly 658	nment Scores:
Qy	2427 GGATTTGAACATATGACTTATTTGTAGGGAAGGTCCTGAGGGGCAACACACAC	
Dp	659	Percent Similarity: 31.078 Best Local Similarity: 26.038
Οy	2487 AGGTCCCTCAGCCCACAGCACTGTTTTTGCTGATCCACCCCCTTTACCTTTTATC 2546	
qq	666 oGlyThrProGlyProGlnGly	US-09-759-143-110 (1-3410) x US-09-9
Oy	2547 AGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGACACACGCCATTTAAATATTA 2606	Oy 3101 ACAAAGGCTTGGGAAACCGCAC

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GAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTA 2666
                                                           TCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGG 2726
                                                                                                                                                                                                                                     TGGGCCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTC 2906
                                                                                                                    CTTCTCCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAG 2786
                                                                                                                                                                           CCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGG 2846
                                                                                                                                                                                                                                                                                            CAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCCAAC 3023
                                                                              uProGlySerProGlyAlaProGlyThrPro----- 714
                                                                                                                                                -----GlnGlyLeuProGlySerProGlyAlaProGl 697
                                                                                                                                                                                                                                                                                                                                                                              CCTGTTTGGAGCT-----ACTGCAGGACCAGAA 3072
|||||||
|------GlyAlaProGlyThrProGlyProGln 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LASSIFICATION OF ENDOMETRIAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 1806
Matches: 315
Conservative: 61
Mismatches: 413
Indels: 71
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	2162 G		736 1	2102 G	756 1	2042 A	924	2003 G	796 1	1984 -	816 y	1926 P	830 1	1874 -	838 1	1819 (850	1760	861 1	1730	881	1678 (668	1618 (918	1558 (934	1498	948	1438	964	1378	716	1318	984
qa	oy G	3 &	qa a	٥y	QQ	QY	qa	Qy	qq	Qy	qq	Qy	qa	Ολ	DÞ	ΟŊ	QQ	ΟŊ	qq	ΟŊ	qq	QY	qq	Qy	qq	Qy	qa	Qy	qq	Qy	qa	QY	Db	QY	qa
	TGGTGGGGAAAGTTGGGGGGT 3015	429 GlyGluProAlaValValGluProGlyMetLeuValGluGlyPro 443	AGGGGAAAGTTGGGGGAAATTTTGGGCAGTGCCTTCATCAGCCCAGTCCTAGAG 2955	ProGlyproAlaGlyProAlaGly11eMetGlyProFroGlyLeuGin 459		C10C ***CEMPCC***COO***C	2894 GGGAAGCCGTTGAGACCTGAAGCCCCACCCTCTACCTTCAA 2850 111:::	CATOLOGY DECEMBER OF A THE CONTRACT DECEMBER OF THE CONTRACT O	CACCULARCOLISGOSTRACAGOSTILIGORALITATORISTICATORISTICOGRAPHICONTILICOGRAPHICATORISTICOGRAPH	GTCCAGGGTAGGCATTTTGGGGGGGCCAGACCCCAGGAGAAGG 2745		ATTICHERCAATGACCCAATGACCAACTATCTCAGGGGACCTGAT		methiggigaticicicacicraatattagacacaacacagaaaagctagcaa 2640	LeuThr-GlyAraProGlyProValGlyGlyProGlySerSerClyAlaLysGlyGluSe 555	0.555 TRITICARAMENTA DA MARA DE LA DESENTA DA DE LA CARTE DE DE LA COMPACIONE DE LA COMPACI		05.00	<u> </u>		TAAGAGGGGGTGGATCAGCAAAAAGACTGTGGGGTG 2490	GlyGlyArgGlyMetProGlyGluProGlyAlaLysGlyAspArgGlyFneAspGlyLeu 5U5	AGGGGACCTGGTTCTTGTGTGTTGCCCCTCAGGACTCTTCCCCTACAAATAAGTCAT 2439	ProGlyLeuProGlyAsp b11	ATGTTCAAATCCCATGGAGGAGTGTTTCATCCTAGAAACTCCCATGCA 2391	CON ACCURATION OF THE CONTROL OF THE		AspGlyMetArgGlyGluAspGlyGluIleGlyProArgGlyLeuProGlyGluAlaGly 649	2366 GGTTAAGGGGCTTAGAAGTGGGAAACCAGGTGACTTTATTCAGCTCCCAA 2313	-proArgGlyLeuLeuGlyProArgGlyTnrProGlyAlaProGl	AAACCCTTCTCTAGGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGGCTGGG	4 yGlnProGlyMetAlaGlyValAspGlyProProGly	2255 TAAT		
qa	Qy 3				y 4		0 م										, E		γ Ā					a a									, ,		Š

	697	-GlyProGlnGlyLeuProGlyPro-GlnGlyProIleGlyProProGlyGluLysGlyP 716
	2162	GTCAG
	716	 roGlnGlyLysProGlyLeuAlaGlyLeuProGlyAlaAspGlyProProGlyHisProG 736
	2148	GAGACTGGGGAGAGAGAGAGGGACGCCCCAGCCCCCAGCTGTGCA 2103
	736	11
	2102	GCTACGCACCTCAGCACAGCACGGGGGGGGGGGGGGGCCACATTACTTTGGCAGCAACAG 2043
	756	leGly***ProGlyProArgGlyValLySGlyAlaAspGlyValArgGlyLeuLySGlyS 776
	2042	AAACTGGCGGCCAGCCCGGCAGCCCC
	116	uLysG 796
	2003	GAGC
	1984	TGGCC
	816	
	1926	AAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGAC 1875
_	830	 InAlaGlyGluLysGlyLysLeuG 838
	1874	CCAGGCCTGCGGCAGACACATATAGGCAGTGACAGACTGGCTGAGCTGGACAAT 1820
•	838	lyValProGlyLeuProGlyTyrProGlyArgGln
	1819	AGGGATGGGGCCACCTGGGACAGCAGGAAGGCA
	850	
	1760	
•	861	roGlyAlaAsnGlyGluLysGlyAlaArgGlyValAlaGlyLysProGlyProArgGlyG 881
	1730	CCACCCTGGCCTCGGTGGGCTCACCCACCACACGTACGGAGACATCACA 1679
0	881	InArgGlyProThrGlyProArgGlySerArgGlyAlaArgGlyProThrGlyLy 899
ζ.	1678	GGCAGAGGCCCGCAGAGCGGGGGGGGGGGGGGCGACTGCCTCCAGCACCCAC 1619
0	899	sProGlyProLysGlyThrSerGlyGlyAspGlyProProGlyProProGlyGluAr 918
.	1618	TGGTCATCAGG
0	918	
_	1558	GICCICACIGCIAGCACCICCAGIGICCCCICGGIATITGGGCAGGAACACCIGCITCIC 1499
0	934	GlyProProGlyProPro-GlyArgMetGlyCysProGlyHisP 948
<u>_</u>	1498	CCGGTGGTAGAGGAGGCCAGTGTGGTAGGCAGGATCTGCAGGGCTGAGAAGGTGAAACCC 1439
0	948	roglyglnArgGlyGluThrGly-PheGlnGlyLysThrGlyProPro 9
,	1438	GGTGAGGGCGGCTGAAGCTGTCACCAC
0	964	
>-	1378	AGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCT
۵	977	
>-	1318	CAGCCGGTCCATGACCAGAGAAGACCAGGGAGATGGCGCACTGCAGGAACAGCC 1263
۵	984	

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277 -----GluargGlyGluLysGlyGlualaGlyProProGlyAlaAlaGlyProProGly 1294
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295 AlaLySGlyProProGlyAspAspGlyProLysGlyAsnProGly-ProValGlyPhePr 1314
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329 pGlyValGlyGlyAspLysGlyGluAspGlyAspProGlyGlnProGlyProglyPr 1349
244 ACTCCAGAACTGCTTCGTCTCGGCTCTGCT---CCAGAAGCTGCGGCCTCTCCTTGC 188
                                                                                                                                                                                                                                                      187 TGCCGC-------CAACTGCCTAGGAATCAGCCAGGCGCCCATTTCT---- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147. -GCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGCTGCTGTGGG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JICANT: FOUY TETESA
JICANT: FOUY TETESA
JICANT: FOUY TETESA
JICANT: FOUTET: Gary R.
JICANT: PANCHANDE, Gary R.
JICANT: Manchanabe, Yoshihiro
JICANT: Manchanabe, Yoshihiro
JICANT: Macapher, Madeleine Joy
JICANT: JOH
JICANTON NUMBER: US/10/012,896
JICANTON NUMBER: US/10/012,896
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Matches:
Conservative:
Mismatches:
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Wang, Aljun
Skelky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
MONelll, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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CANT: Xu, Jiangchun
CANT: Dillon, Davin C.
CANT: Mitcham, Jennifer L.
CANT: Harlocker, Susan L.
CANT: Harlocker, Susan L.
CANT: Kalos, Michael D.
CANT: Ralos, Michael D.
CANT: Stolk, John A.
CANT: Day, Craig H.
CANT: Carter, Marc W.
CANT: Carter, Marc W.
CANT: Carter, Carter, Canter, Cante
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196-547
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Similarity:
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Job time : 249 secs
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1 LeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1052 CIICCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCCGGCTC 1105
                                                                                                                                  APPLICANT: Fanger, Gary R. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.534C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-759-143-110 (1-3410) x US-09-895-793-547 (1-58)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 547
LENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Henderson, Robert A.
Hural, John
McNolll, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                                                                                     Sequence 547, Application US/09895793
Publication No. US20020192763A1
                                                                                                                                                                                                                                                                   APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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US-09-895-793-547
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Best Local Similarity:
Query Match:
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992 TTGTCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCCTG 1051
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REPERENCE: 210121.427266
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 547
LENGTH: 58
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Vinals de Bassols, Carlota
                                Sequence 547, Application US/09895814; Publication No. US20020193296A1; GENERAL INFORMATION:
                                                                                      APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Kalos, Mitchael D. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A.
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Hepler, William T.
Henderson, Robert A.
Hural, John
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Vedvick, Thomas S.
Carter, Darrick
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US-09-895-814-547
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Best Local Similarity:
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RESULT 45
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Published_Applications_NA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
7	3409.6	100.0	3410	. 6	US-09-232-880-110	Sequence 110, App
7	3409.6	100.0		6	US-10-012-896-110	Sequence 110, App
6	3409.6	100.0		σ	US-09-895-793-110	Sequence 110, App
4	3409.6	100.0		6	US-09-895-814-110	Seguence 110, App
'n	3409.6	100.0		6	US-10-010-940-110	Seguence 110, App
9	3409.6	100.0		10	US-09-745-288-100	Sequence 100, App
7	3409.6	100.0		10	US-09-759-143-110	Sequence 110, App
- α	3409.6	100.0		10	US-09-780-669-110	Sequence 110, App
o	3409.6	100.0		10	US-09-030-606-110	Sequence 110, App
10	3409.6	100.0		10	US-09-822-827-110	Sequence 110, App
11	3409.6	100.0		10	US-09-115-453-110	Sequence 110, App
12	3292.4	96.6		10	US-09-838-785-1	Sequence 1, Appli
13	2585.4	75.8	4034	σ	US-10-012-896-704	Sequence 704, App
14	2585.4	75.8	4034	6	US-09-895-793-704	Sequence 704, App
15	2585.4	75.8	4034	σ	US-09-895-814-704	Sequence 704, App
16	2585.4	75.8	4034	10	US-09-759-143-704	Sequence 704, App
17	2585.4	75.8	4034	10	US-09-780-669-704	704,
18	2585.4	75.8	4034	10	US-09-822-827-704	Sequence 704, App
19	2196.4	64.4	2904	σ	US-10-012-896-703	Sequence 703, App

03, 03, 703,	Sequence 703, App Sequence 702, App Sequence 702, App Sequence 702, App	702, 702, 05,	05,	Sequence 851, App Sequence 851, App Sequence 851, App Sequence 851, App Sequence 851, App	APP
9 US-09-895-793-703 9 US-09-895-814-703 10 US-09-759-143-703	10 US-09-822-827-703 9 US-10-012-896-702 9 US-09-895-793-702 9 US-09-895-814-702 10 US-09-759-143-702	10 US-09-780-669-702 10 US-09-822-827-702 9 US-10-012-896-705 9 US-09-895-793-705	9 US-09-895-814-705 10 US-09-759-143-705 10 US-09-780-669-705 10 US-09-822-827-705 9 US-10-012-896-851	9 US-09-895-793-851 9 US-09-895-814-851 10 US-09-759-143-851 10 US-09-780-669-851 10 US-09-780-689-851	9 US-09-232-880-10 9 US-10-012-896-10 9 US-09-895-793-10
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ALIGNMENTS

Db 1321 GCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGC 1380	CCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGGGACAG 1 111111111111111111111111111111111	1 GGGTCCTGGAGGCAGTGGCTGCTCCACCTCCACCTCGCGGGCCTCTGCGGGGCCTCTGCGCGGGCCTCTGCCGGGGCCTCTGCCGGGGCCTCTGCCGGGGCCTCTGCCGGGCCTCTGCCGCGCTCTGCGGGGCCTCTGCCGGGCCTCTGCCGGGCCTCTGCCGGGCCTCTGCCGGGCCTCTGCGGGCCTCTGCGGGCCTCTGCGGGCCTCTGCGGGCCTCTGCGGGCCCTGGTGG	1 1 1 1 1 1 1 1 1 1	1861 TGCCGCAGGCCTGGGTCTGGTTGCTTTGCTACACAGGTACTATTGACAAGAG 19	1921 CGACTTGGCCAAATACTCAGCATAGAAACTTCCAGCACATGGGGTGGAGGCCCTGCT 1980	20 20 21 21	2101 GCTGCACAGGCGGCGCGTGGGGCGTCCTCTCTCTCCCCCAGTTTTTAGGGCTGCTTTTTTTT	QY 2221 ATGCACTGGAACTCTGCAGGTGCATTACCCAGGCTCAGGGTTAACAGCTAGC 2280 Db 111111111111111111111111111111111111	OY 2341 GTTTCCCATCTCTAAGCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGGG 2400
	GGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGCTGCTCTGGTGCTGCTGGAAGT 42 GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGCATTGGTCCAGTGCTGGCTG	41 GCCTTCATCTGGCACCTCTGGCATCCTGGCGTGGACGCTATGGCCGCGCGCG	CCTGGGCGTGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGGTCAT 6 CCTGGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTCACTCCACTGGAGCCCT 7 [CATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCTCCTGCCTAGCTTATG [11111111111111111111111111111111111	# ## ## ## ## ## ## ## ## ## ## ## ## #	CGGGC 10 CGGGC 10	1021 CCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTGCAGCTGTGCCG 1080 1081 CATGCCCGCACCCTGCGCGGCTCTTCGTGGCTGAGTGCAGCTGGATGGCACTAT 1140	CCCAG 12 CCCAG 12 CCCAG 12 AGCCT 12 AGCCT 12	3CTGGT 132

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                                        GATCCACCCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA 2580
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 GTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTTGCT
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Sequence 110, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
                                                                                                         APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.
                    us-10-012-896-110
RESULT
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GTGATGAGACGTCCCCCACTGAGGTGCCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG 120 GETGAGCCGCCTGCTGCGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTT 181 GGCGGCAGCAAGGAGGAGGAGGCCGCAGCTTCTGGAGCCAGAGCCGAGACGAAGCAGTTCTG 241 GAGTGCCTGAACGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG 241 GAGTGCCTGAACGGCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG GGTGAGCCGCCTGCGGCACCGGAAAGCCCCAGCTCTTGCTGGTCAACCTGCTAACCTT TGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGCAGAGT GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT 1 | GGBACCAGCCTGCACGCCTCCGGGTGACAGCCGCGCGCCTCGGCCAGGATCTGA 61 GIGAIGAGACGIGICCCCACIGAGGIGCCCCACAGCAGCAGGIGITGAGCAIGGGCTGAG AAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTT TGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT 1 GGGAACCAGCCTGCACGCGCTGGCTCCGGGTGACAGCCGCGCGCCTCGGCCAGGATCTGA Gaps DB 9; Length 3410; .; 0 APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCED 0; Indels ION: DIAGNOSIS OF PROSTATE CANCER 210121.427C27 100.0%; Score 3409.6; 100.0%; Pred. No. 0; iive 0; Mismatches CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001.12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: PASKED for Windows Version 3.0 Carlota Skeiky, Yasir A.W. Hepler, William T. Henderson, Robert A. Hural, John McNeill, Patricia D. Houghton, Raymond L. Vinals de Bassols, C Foy, Teresa Harlocker, Susan L. Jiang, Yuqiu Mitcham, Jennifer Kalos, Michael D. Retter, Marc W. Stolk, John A. Day, Craig H. Vedvick, Thomas Carter, Darrick Best Local Similarity 100. Matches 3410; Conservative Samuel X. ORGANISM: Homo sapiens Wang, Aijun REFERENCE: US-10-012-896-110 SEC ID NO 110 61 121 301 301 361 361 421 421 481 DNA Query Match APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:
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đ		qa	GTGCTGGAGGCAGTGGCCT
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3 8	COMPAGNA CONSTRUCTION ROUND TO THE CONTRACT OF	Qy	CCTGTTTATGGGCTCCATTGTCCAGCTCAGC
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Οy	CTTCGTGGCTGAGCTGTGCAGCTGGATGGCA	δ i	2161 ACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACT
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ογ	GGCGAGGGGCT	λo i	2221 ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTA
QQ	GGATTTCGTG	g (221 ATGCACTGGAATGCGGGGACTCTGCAGGTGGATT
δλ	1201 AGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT 1260	oy i	2 (
QQ	1201 AGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCGCCCT 1260	gr ë	Z81 CTCCTAGTTGAGACACACCTAGAGAAGGGTTT
Qy	1261 GGGGCTGTTCCTGCAGTGCGCCATCTCCTGGTCTTCTCTGGTCATGGACCGGCTGGT 1320	r to	2341 GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTC 2341 GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTC 2341 GTTTCCCATCTTAACCTGAACCTGAACCTGAACACTACTAACACTGAACACTACTAACACTACTAACAAC
qq	GGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGG	3 8	OFI GILLCCCALCLCIANGCCCCCTIANCCTGCACTT
cy G		qa	2401 TTTCTAGGATGAACACTCCTCCATGGGATTTGAACACTCTCCCATGGGATTTGAACACTCCTCCATGGGATTTGAACACTCCTCCATGGGATTTGAA
ò	381 CGGTGCCACGTGCCCACAGGTGTGGCCGTGGTGACATTCAGCGCTGCTGCTCACTTTCCCTGGTGGCTGCTGCTGCTCACTGCTGCTGCTGCTGCTGCTGGTGGTGGTGGTGGTGGTGG	ογ	CCTGAGGGGCAACACACAAGAACCAGGT
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ολ	GTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC	Qy	CAGGA
ପୁପ		qa	2521 GATCCACCCCCTCTTACCTTTATCAGGATGTGG
Qy	SACAG 156	ΟŻ	58
^අ ට	1501 GAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAG 1560	qo :	581 CAGAGACAGGCATTTAAATATTTAACTT
δō í	561 CCTGATGACCAGCTTCCTGCCAGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 162	ζζ	2041 TGCTAGCTTTTCTGTGTTGCTGTCTCTAATATTTGGG 2041 TGCTAGCTTTTTCTGTGTTTTTTTTTTTGTGTGTTTTTGTGTGTTTTAATATTTGTGTGTTTTTAATATTTTGTGTGTTTTTAATATTTTGTGTGTTTTTAATATTTTTGTGTGTTTTTAATATTTTTGTGTGTTGT
ď	. 1561 CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 1620		

ζŅ	1621	GGTGCTGGAGGCAGTGGCTCCAACTCCACCGGGGCTCTGCGGGGCCTCTGCCT
qq	1621	GGGTGCTGGAGGCGCTGCTCCCACCCGCGCTCTGCGGGGGCCTCTGCCTG 1680
οy	1681	CCACCGAGGCCAGGGTGGTTCCGGGGCC
qq	1681	GATGTCTCCGTACGTGGTGGTGGGTGAGCCCACC
Qy	74	GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGTGGCCCC 1800
Db	1741	GGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTTCCCAGGTGGCCC
Qy	1801	TCCCTGTTTATGGCCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTAT
Db	1801	CCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCT
Οy	1861	CAAG
Db	1861	GCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGA
٥y	1921	SCCTGO
qa	1921	GACTTGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGCC
Οy	1981	TCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAG
QQ	1981	ACTGGGTCCCAGCTCCCGGTCCTGTTAGCCCCATGGGGCTGCCGGGGTGGCCGCGCAGT
οy	2041	CACCCTGTGCTGCTGAGGTGCGT
qq	2041	TCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGG
οy	2101	CTCCCCAGTCTCTAGGGCTGCCT
qo	2101	CTGCACAGCTGGGGGCTGGGGGCTCCTCTCTCTCTCCCCCAGTCTCTAGGGCTGC
ρy	2161	SGACTTATACAGGGAGGCCAGAAGGGCTC
qo	2161	CTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACT
ργ	2221	CCAGGCTCAGGGTTAACAGCTAGC 228
qo	2221	TGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGC 228
λ	2281	GAGCTGAATAAACTCAGTCACCT
qq	2281	TCCTAGTTGAGACACCCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTG 234
٥y	2341	TTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGG 240
qc	2341	TTCCCATCTTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGA
Ka	2401	TTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGAA
qc	2401	CTAGGATGAACACTCCTCATGGGATTTGAACATAT
27	2461	3AACCAGGTCCCCTCAGCCCACAGCAGTGTCTTTTTGC
q	2461	CCTGAGGGGC
λy	2521	STGGCCTGTTGGTCCTTCTGTTGCCATC
q	2521	ATCCACCCCCTCTTACCTTTTATCAGGATG
λy	2581	GAGACACAGGCATTTAAATATTTAACTTATTTAACAAAGTAGAAGGGAATCC
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2y 0b	2641	TGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCA 2700
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       GGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCCAGAATCTTCTTCTCTCTGGGGT
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Publication No. US20020192763A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
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Houghton, Raymond L.
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McNeill, Patricia
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Vedvick, Thomas S.
Carter, Darrick
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APPLICANT: Vinals de Bassols, Carlota
APPLICANT: FOY, Teressa
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
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iive 0; Mismatches
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                                                     61 GTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG
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APPLICANT: Ralos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Horderson, Robert A.
APPLICANT: Hordis, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Fanger, Gars
APPLICANT: Fanger, Gars
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427026
CURRENT FALING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 3409.6; Best Local Similarity 100.0%; Pred. No. 0; Matches 3410; Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 110, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: John A.
APPLICANT: Vedvick, John A.
APPLICANT: Vedvick, Thomas S.
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90 Ay	OY OY Ob	Qy Dp	o oy	Qy	oy ob	y y y	Oy Db	Qy Qy Db	do oy
3241 TAGCGGGGTGAATATTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACA 3300 3301 AAATTAAAGGCTTTCTTATATGTTTAAAAAAAAAAAAAA	RESULT 5 US-10-010-940-110 Sequence 110, Application US/10010940 Sequence 110, Application No. US20030088062A1 SEPERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L.	APPLICANT: Harlocker, Susan Louise APPLICANT: Jiang Yuqui APPLICANT: Reed, Steven G. APPLICANT: Ralos, Michael APPLICANT: Fanger, Gary APPLICANT: Reter, Mark APPLICANT: Solk, John	APPLICANT: DBY, CTA149 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.42703 CURRENT APPLICATION NUMBER: US,10/010,940 CURRENT FILING DATE: 2001-12-05 NUMBER OF SEQ ID NOS: 575 OFFWARPF: FASTSED for Windows Version 3.0	SEQ ID NO 110 LENGTH: 3410 TYPE: DNA ORGANISM: Homo sapien S-10-010-940-110	Query Match 100.0%; Score 3409.6; DB 9; Length 3410; Best Local Similarity 100.0%; Pred. No. 0; Matches 3410; Conservative 0; Mismatches 0; Indeis 0; Gaps 0; 1 GGGAACCAGCGCTGGCTCCGGGTGACAGCCGCGCCCCGGCCAGGATCTGA 60	TCTGA CTGAG 	121 AAGCTGGACCACCAAAGGCTGGCAGAATGGGCGCCTGGCTGG		

CCTGATAGGCAGGCCAAATACCGAGGGCACACTGGAGGTGCTACCATGGGCACG CCTGATGACCACTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACCC CCTGATGACACTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACCC CCTGATGACAACTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACCCC CCTGATGACAACTTCCTGCCAGCTCCACCCTCCACCCGGCCCCTTCCCTGCCGGCCCTTCCCTCCTCCTC TGATGTCTCCCTACGTGTGCTGCTGCTCCCCCCCCCC

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                                    CTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAAT
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ING DATE: 2000-12-19
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Xu, Jiangchun
Dillon, Davin C.
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Oy Dp	1 1	OY GGGAACCAGCCTGCAGCGTGACAGCGCGCGCGCCTCGGCCAGGATCTGA 60 DD HILLHILLHILLHILLHILLHILLHILLHILLHILLHIL
Qy Dp	61 G + 61 G	QY GTGATGAGACGTGCCCACTGAGCAGCAGCAGTGTTGAGCATGGCTGAG 120 PILITITITITITITITITITITITITITITITITITITI
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oy Oy	241 G 241 G 241 G	GAGTGCCTGAACGCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG 300
Oy Dp	301 G 1 301 G	GTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTT 360
Oy Pp	361 T 361 T	GGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCTCTGCTGCTGGAAGT 420
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Qy Db	481 C	CTGTGTCCCCGCTCCTAGGCTCAGTGACCACTGGCGTGGACGCTATGGCCGCCCG 540
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Qy	721 6	GCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCTACTCTGTCTATGCCTT 780
Qy	781 (CATGATCATCATGAGGGCTGCCTGGGCTACTTCTGCCTGC
Qy Dp	841. 1	TGCCCTGGCCCCCTACCTGGGCACCCAGAGGAGTGCCTCTTTGGCCTGCTCACCCTCAT 900
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	1201	CCGGAGACACTATGATGAAGCGTTCGGATGGGCAGCCT 12	
	1261	ATTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGF 13	
	1321 1321	ATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGC 138	
	1381 1381	TGTGGCCGTGGTGACAGCTTCAGGCGCCCTCACCGG 14	0 0
	1441	TCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGA 150	
	1501	igttcctgcccaataccgagggacactggaggtgctaggaggggggacac 156 	0 0
	1561	CAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 162. 	0 0
	1621	CAGTGGCCTGCTCCACCTCCACCCGCGCTCTGGGGGCCTCTGCCTG 168	0 0
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· · ·	1801	TGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 186	0 0
~ 0	1861	GGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGA 192. 	0 0
~ 0	1921	CCAAATACTCAGCĞTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT 1981 	0 0
<i>.</i> c	1981	GGGTCCCAGCTCCCGCTCCTGTTAGCCCCATGGGCTGCCGGGCTGGCCGCCAGT 204	0 0
5 ~ 0	2041	GCAAAGTAATGTGGCTCTGTGCTGCCCTGTGCTGCTGAGGTGCGTA 210	0 0

G 2160 Db 7 3181 GAGGTCTTATC1 C 2220 QY 3241 TAGCGGGGTGAA C 2220 QY 3301 AAATTAAAGGCT C 2280 QY 3301 AAATTAAAGGCT C 2280 QY 3301 AAAATAAAGGCT Db 3301 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2400 2400 2460 2460 2460 2460 2460 2460	93180 QY 181 GGGGGAGCAAGG 3180 Db 181 GGGGCAGCAAGG 3240 QY 241 GAGTGCCTGAACG
	2341 GTTTCCCATCTAGCCCCTTAACCTGCAGCTTTAATGTAGCTTTCATGGGGGGGG	3121 ATATCTGTGCTTGGGAAATCTCACACAGAAACTCAGGAGCACCCCTGCCTG
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	241 GAGTGCCTGAACGCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG 300		361 TGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGCAGAGT 420		481 CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTATGGCCGCCGCGCG 540	541 GCCCTTCATCTGGGCACTGTCTGGGCATCCTGCTGGCCTCTTTCTCATCCCAGGGC 600	601 CGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCCT 660	661 CCTGGGCGTGGGGCTGCTGGGCTTCTGTGGCGGGTGTGCTTCACTCCACTGGAGGCCCT 720	721 GCTCTCTGACCTCTTCCGGGACCCGGACCACTGCGCCAGGCCTACTCTGTCTATGCCTT 780 111111111111111111111111111111111111	781 CATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG	841 TGCCCTGGCCCCTACGGCACCCAGAGGAGTGCCTCTTTGGCCTGCTCACCTAT 900	901 CTTCCTCACCTGCGTAGCACACTGCTGGTGGCTGAGGAGGCAGCCTGGGCCCCAC 960 	961 CGAGCCAGCAGAGGGCTGTCGGCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGC 1020			1141 GACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCCTGTACCAGGGCGTGCCCAG 1200 			1321 GCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGC 1380
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Qy	1381	GTECCACATECTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGG 14	4
qq	1381	sccacareccierccacacieresceresisacacercaccecceceres 14	40
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δÿ	26	CTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 16:	0 0
qq	1561	TGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 16:	~
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Db	1621	GIGCIGGAGGCAGIGGCCIGCICCCACCICCACCGCGCTCIGCGGGGCCICIGCTG 16	œ
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Dp	1681	GATGTCTCCGTACGTGGTGGTGGGTGAGCCCACGGAGGCCAGGGTGGTTCCGGGCCG 17	4
Qy	1741	GGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 18	008
Dp	1741	GCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 18	000
QY	1801	CCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 18	Ū.
Dβ	1801	TCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 18	960
٥y	1861	CAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 19	920
qa	1861	CCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 19	920
Qy	1921	GACTIGGCCAAAIACTCAGGGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT	980
οp	1921	TGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT	ā
Qy	1981	ACTGGGTCCCAGCTCCCGGTCCTGTTAGCCCCATGGGGGTGCCGGGCTGGCCGCCAGT 20	4
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Qy	2041	GTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCG	10
Db	2041	ctettecteccaaataateteectetectecaecetetectectectecte	100
Oy	2101	CTGCACACAGGGGGCTGGGGCGTCCCTCTCTCTCCCCAGTCTCTAGGGCTGCCTG 2	16
Dp	2101	TGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCCCCAGTCTCTAGGGCTGCCTG 2	16
Qy	2161	CTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCC 2	22
Dp	2161	GAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCC 2	220
ΟŊ	2221	ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGGTCAGGGTTAACAGCTAGG 2	280
qq	2221	SCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGC 2	280
Qy	2281	CTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTG 2	34
QQ	2281	CTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACTG 2	34
Qγ	2341	GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGGG 2	40
qq	2341	GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAG 2	40
Qy	2401	TITCIAGGATGAAACACICCICCAIGGGAITIGAACAIAIGACITAITIGIAGGGGAAGA 2	460
qq	2401	TTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTGTAGGGAAGA 2	460

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GTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCT 2520
          GATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA 2580
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Sequence 110, Application US/09780669 Patent No. US20020051977a1 GENERAL INFORMATION: APPLICANT: Xu, Jiangchun
                                                                                       Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
RESULT 8
US-09-780-669-110
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                                                                                                                                                                 APPLICANT: ADDAM APPLICANT: Hural, John APPLICANT: Hural, John APPLICANT: Houghton, Raymond L. APPLICANT: Houghton, Raymond L. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TITLE OF INVENTION: 114002/180,669
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
  Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
                                                                               Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                    Skeiky, Yasir A.W.
Hepler, William
                                          Fanger, Gary R.
Retter, Marc W.
                                                                    Stolk, John A.
                                                                                                                                      Wang, Aljun
                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapien
                                                                                                                           Li, Samuel
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SEQ ID NO 110
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GTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG 120
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                                                                                                                                                                       100.0%; Score 3409.6;
100.0%; Pred. No. 0;
iive 0; Mismatches
                TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
      TELECOMMUNICATION INFORMATION
                                                             LENGTH: 3410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                   Best Local Similarity 100. Matches 3410; Conservative
                                                                                                             MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                   linear
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Patent No. US2002001580A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C,
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
3060
                                                                                                                                                                                                                                                                         3241 TAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACA 3300
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                                                                                                                                           1941 CICCCCTCIACICICTCTCTAGGACIGGGCTGAIGAAGGCACIGCCCAAAAITTCCCCIACC
                                                                                                                                                                                         GCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGT
                                                                                                                                                                             CCCAACTITCCCCTACCCCCAACTITCCCCACCAGCTCCACAACCCTGTTTGGAGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: WARL, DAVIG J.
ROSISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: WA
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	2101 GCTGCACAGCTGGGGGCTGCGCCTCTCCTCTCTCCCCAGTCTCAGGCTGCCTG 2160 [2221 ATGCACTGGAATGCGGGACTCTGCAGGTTACCCAGGGTCAGGGTTAACAGCTAGC 2280 11111111111111111111111111111111111	4.1 GTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAG 240	TTCTAGGATGAAACACTCCTCCATGGGATT TCCTGAGGGCAACACACAAGAACCAGGTC 	S21 GATCCACCCCCTTACCTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA 258	2581 CAGAGACACAGGCATTAAATATTAACTTATTAACAAAGTAGAAGGGAATCCAT 2640 2641 TGCTAGCTTTTCTGTGTGTGTCTAATATTGGGTAGGTGGGGGGATCCCCAACAACA 2700 2641 TGCTAGCTTTTCTGTGTTGTGTTAATATTGGGTAGGGTGGGGGGATCCCCAACAATA 2700 2641 TGCTAGCTTTTCTGTGTTGGTGTCTAATATTGGGTAGGGTGGGGGGGATCCCCAACAATCA 2700	CTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAAT [2761 CTGGCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAAT 2820 2821 TCCAAATGCTGTTACCCAAGGTTAGGGTGTTGGAAGGTAGAGGTGGGGCCTTCAGGT 2880 2821 TCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGG	81 CTCAA 81 CTCAA	2941 CTCCCTCTACTCTTTAGGATGGGCTGATGATGGAGGATGCCAAAATTCCCCTACC 3000 2941 CTCCCCTCTACTCTCTCTGGGCTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACC 3000 3001 CCCAACTTCCCCTACCCCCAACTTTCCCCACCAGGCTCCAACCTTTGGAGCTACT 3060
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GTCGGCCCCTCCTTGTCGCCCACTGCTCTCCATGCCGGGC 1020
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	2521	Qy 2581 CAGAGACACA 	Qy 2641 TGCTAGCTTT			2701	Db 2761 CTGGCCCCC		Db 2821 TCCAAATGCT		Qy 2941 CTCCCTCTA	Db 2941 CTCCCTCTA	OY 3001 CCCAACTITO	3061			3121	QY 3181 GAGGTCTTAI 	3241	3241 T	Qy 3301 AAATTAAAGO	3301	3361 AAAAAAAK 		RESULT 11 US-09-115-453-110	; Patent No. US200200903	APPLICANT: Xu, Jiango; APPLICANT: Dillon, De		
1441 GITCACCITCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGA 1500			GAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAG	1561 CCTGATGACCAGCTTCCTGCCAGGCCTTAACCTGGAGCTCCCTTCCCTAATGGACACGT 1620 1561 CCTGATGACCAGCTTCCTGCCAGGCCCTAAAGCTGGAGCTCCCTTTCCCTAATGGACACGT 1620	GGGTGCTGGAGGCAGTGGCCTCCCACCTCCACCGCGCTCTGCGGGGCCTCTGCCTG 1	1621 GGGTGCTGGAGGCCAGCTGCTCCCACCCGCGCTCTGCGGGGCCTCTGCCTG 1680	1681 TGATGTCTCCGTACGTGTGGTGGTGGTGGGCCCACCGAGGCCAGGGTGGTTCCGGGCCG 1740	GGGGATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGCTCCTGGGCCCC 18		ATCCCTGTTTATGGGGTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 1	1801 AFCCCIGTTIATGGGCTCCATTGTCCAGCTCAGTCTGTCACTGCCCTATATGGTGTC 1850	*GCCGCAGGCCTGGGTCTGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG TGCCGCAGGCCTGGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG	1921 CGACTIGGCCAAATACTCAGGGTAGAAAACTICCAGCACATIGGGGTGGAGGGCCTGCCT 1980	1921 GGACTIGGCCAAATACTCAGGGTAGAAAACTTCCAGCACATIGGGGTGGAGGGCCTGCCT 1980	1981 CACTGGGTCCCAGCTCCCGGTCCTTAGCCCCATGGGGCTGCCGGGCTGCCCCGCCAGT 2040 1981 CACTGGGTCCCAGCTCCCGGTCGTTAGCCCCATGGGGCTGCCGGGCTGCCGGCCAGT 2040	TTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCCCTGTGCTGCTGCTGCGTTA	2041 TTCTGTTGCTGCCAAGTAATGTGGCTCTGCTGCCACCCTGTGCTGAGGTGCGTA 2100	2101 GCTGCACAGCTGGGGGCGTCCCTCTCTCTCCCCAGTCTCTAGGCTGCCTG 2160	2101 GCTGCACAGCTGGGGGGTGGGCGTCCTCTCTCCCCAGTCTCTAGGGCTGCCTG 2160	2161 ACTGGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCC 2220			2281 CTCCTAGTTGAGACACCTAGAGAGAGTTTTGGGAGCTGAATAAACTCAGTCACCTG 2340	2281 CICCIAGIIGAGACACACCIAGAGAAGGGIITIIGGGAGCIGAAIAAACICAGICACCIG 2340	2341 GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAAATGTAGCTCTTGCATGGGAG 2400	7 6	TITCTAGGATGAAACACICCICCATGGGATTIGAACATAGACITIIOINTIGOAGGAAAA 24 TITCTAGGATGAAACACICCICCATGGGATTIGAACATATGACTTATTIGTAGGGGAAGA 24	2461 GTCCTGAGGGGAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTTTTGGT 2520	2461 GTCCTGAGGGGCAACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTTTTTGCT 2520
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                                                                                            'ACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACC
CCCTCTTACCTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA
                    CCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA
                                        AGGCATTTAAATATTTAACTTATTTAACAAAGTAGAAGGGAATCCAT
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gchun

Davin C. COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE 1121.427C4

CURRENT APPLICATION NUMBER: US/09/115,453B CURRENT FILING DATE: 1998-07-14

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                                                                                                          Gaps
                                                                                      Length 3410;
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Pred. No. 0;
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NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                   Query Match 100.0%; S. Best Local Similarity 100.0%; P. Matches 3410; Conservative 0;
                                                    ; ORGANISM: Homo sapien
US-09-115-453-110
                    SEQ ID NO 110
LENGTH: 3410
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δy	1081	3CCCCCCACACTCCCCCCCCCCCCTCTTCGTGGCTGAGCTGTGCAGCTGGAGCTGCATGGCAGTCAT 114
qq	1081	ATECCCCCCCACCTGCGCCGCCTCTTCGTGGCTGAGCTGTGCTGGATGGCACTCAT 1
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3 ,	* *	CCLICACGCIGITITACACGGAITICGIGGGCGAGGGGCTGTACCAGGGCGTGCCCAG
QY	1201	ACCTGAGCGGGGCACGCCGGAGACACTAGATGAAGGCGTTCGGATGGGAAGCCT 1260 ACCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGATGAGCGGTTCGGATGGGCAACCCT 1260 ACCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGATGAAGGCGTTCGGATGGCAACGCAACTATGATGATGAAGCCGTTCGGATGGCAACGCAACACCT 1260
Οy	1261	
qq	1261	GGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTG
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QQ	1321	CAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTG
Qy	38	CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGG 1440
QQ	1381	GGTCCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACGTTCAGCCGCCCTCACCGG 14
QY	4 4	0
QQ	44	TTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC
δλ	0	GAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGGTGCTAGCAGTGAGACAG 1560
QQ	1501	SCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAG 1
ζŏ	56	CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 1620
qq	1561	CTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGGTCCCTTCCCTAATGGACACGT 16
ΟŊ	1621	GGGTGCTGGAGGCCTGCTGCTCCCACCTCCCGCGCTCTGCGGGGCCTCTGCCTG 1680
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Qy	1741	GGTG
qq	1741	GGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTTCCCAGGTGGCC
Qy	1801	ATCCCTGTTTATGGCCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 1860
qa	1801	CCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCTATATGGTGTC 186
Qy	9	CATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 192
qq	1861	GCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 192
Qy	CI	GAAAACTTCCAGCACATTG
q	92	ACTTGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT
Qy	1981	CACTGGGTCCCAGCTCCCCGCTCTTAGCCCCCATGGGCTGCCGGGCTGGCCGCCATCTTAGCCCCCATGGCTGCCCGCCC

2040 2100 2100 2160 2160 2220 2220 2280 2280 2340	2400 RESULT 12 2400 ; Sequence 2460 ; Patent N 2460 ; APPLICA 2460 ; APPLICA 2520 ; APPLICA 2580 ; TILE E 2580 ; TILE E	2640 2640 2700 2700 2760 2820 2820	2980 QY 2940 Db 2940 QY 3000 Dr 3060 QY 3120 Dt 3120 QY
1981 CACTGGGTCCCAGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGGTA 2041 TTCTGTTGCTGCCAAAGTAATGTGGCTCTTCTGCTGCTGCGGGCTGCCGGGCTGGCGGTA 2041 TTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCCCCCTGTGCTGAGGTGCGTA 2041 TTCTGTTGCTGCCAAAGTAATGTGGCTCTCTTCTGCTGCTGCTGGTGGTGCGTA 2041 TTCTGTTGCTGCCAAAGTAATGTGGCTCTCTTCTCCCCCTGTGCTGGTGGTGCGTA 2041 TTCTGTTGCTGCCAAAGTAATGTGGCTCTCTCTCCCCTGTGCTGGTGGTGCGTA 2041 TTCTGTTGCTGCGGGCTGGGGCTCCTCTCTCCCCCGGTGCTGGTGG	2341 GTTTCCCAFCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGAGG [CAGAGACACAA	2821 TCCAAATGCTGTTACCCAAGGTTAGGGGAAGGTAGGGTGGGGCTTCAGGT 2821 TCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGTGGGGCTTCAGGT 2821 TCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGG
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1321 AGCGATTCGGCACTCGAGCAGTCTATTT 1383 GTGCCACATGCCTGTCCCACAGTGTGGC	Qy 1503 AGCAGGTGTTCCTGCCCAAATACCGAGG Db	Qy 1683 ATGTCTCCGTACGTGGGGGGGGGGGGGGGGGGGGGGGGG	1923 1921 1983 1981 2043 2103 2103	0y 2163 TGGAGGCTTCCAAGGGGTTTCAGTCTT DD 2161 TGGAGGCTTCCAAGGGGGTTTCAGTCTT DD 2121 TGGAGGCTTCCAAGGGGGTTTCAGTCTT OY 2223 GCACTGGAATGCGGGGACTCTGCAGTGG OY 2283 CCTAGTTGAGACACCCTAGAGAAGGGTT DD 2281 CCTAGTTGAGACACACCTAGAGAAGGGTT DD 2281 CCTAGTTGAGACACCCTAGAGAAGGGTT DD 2343 TTCCCATCTCTAAGCCCCTTAACCTGCAC OY 2343 TTCCCATCTCTAAGCCCCTTAACCTGCAC OY 2403 TCTAGGATGAACACTCCTAAGCTGCAT DD 2401 TCTAGGATGAACACTCCTCCATGGGATT DD 2401 TCTAGGATGAAACACTCCTCCATGGGATT DD 2401 TCTAGGATGAAACACTCCTCCCATGGGATT DD 2401 TCTAGGATGAACACTCCTCCCATGGGATT DD 2401 TCTAGGATGAACACTCCTCCCATGGGATT DD 2401 TCTAGGATTAACTCTCCTCCATGGGATT DD 2401 TCTAGGATTAACTCTCCTCCCATGGGATT DD 2401 TCTAGGATTAACTCTCCTCCCTCCCATGGGATT DD 2401 TCTAGGATTAACTCTCCTCCCTCCCTCCATGGGATT DD 2401 TCTAGGATTAACTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC
	GGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGGCCTGGTCTGTGTGTG	GCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCTGGAGCTGGCACTGCTATCC 66		1083 TGCCCGCACCCTGCGCCGGCTCTTCGTGGCTGTGCAGCTGGATGGCACTCATGA 1142 11081 TGCCCGCACCCTGCGCCGGCTCTTCGTGGCTGTGCAGCTGGATGGCACTCATGA 1142 11081 TGCCCGGCACCCTGCGCCGGCTGTTCGTGGCTGTGCAGCTGCTGCATGA 1140 1143 CCTTCACGCTGTTTTACACGGGTTTCGTGGCGGGGCTGTACCAGGGCGTGCCCAGGG 1202 111111111111111111111111111111111
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1383	TTCAGCCGCCCTCACCGG
1381	TGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGGTGTTTCAGCCGCCTCACCGGGT
1443 T 1441 T	TCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC
1503 p	AAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCC 1567
1563 T 1561 T	SACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGG 162:
1623 G	CACCGGGGTTTGGGGGGCGTCTGCCTGTG 168
.1683 A 1681 A	ATGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAGGCAGGGTGGTTCCGGGCCGGG 1742
1743 G 1741 G	GCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTGCCCGAGTGGCCCCAT 1802
1803 C 1 1801 C	CCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTG 1862
 1863 C 1 1861 C	TTACTTTGCTACACAGGTAGTATTTGACAAGAGG 192
1923 A 1921 A	CTTGGCCAAATACTCAGGGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT
1983 C	TIGGTCCCAGCTCCCGGTCCTGTTAGCCCCATGGGGCTGCCGGCTGGCCGCCAGTTT 2042
2043 C 2041 C	CTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCCCTGTGCTGCTGAGGTGCGTAGC 2102
2103 T 2101 T	GCACAGACTGGGGGCTGGGGCGTCCCTCTCCTCCCCAGTCTCTAGGGCTGCCTGAC 2162
2163 T 2161 T	PGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGGAGCCAGAAGGGCTCCAT 2222
2223 G 2221 G	CACTGGAATGCGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCT 2282
2283 C 2281 C	CTAGTTGAGACACACCTAGAGAGGTTTTGGGAGCTGAATAAACTCAGTCACCTGGT 2342
2343 T	TICCGATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTT 2402
2403 T	CTAGGATGAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA 2460

THE THERAPY AND

APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Hanger, Ge Bassols, Carlota
APPLICANT: Fanger, Gary R.
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27

Skeiky, Yasir A.W. Hepler, William T.

APPLICANT: APPLICANT:

Li, Samuel X. Wang, Aijun

Retter, Marc W. Stolk, John A. Day, Craig H. Vedvick, Thomas S Carter, Darrick

APPLICANT: APPLICANT:

APPLICANT APPLICANT APPLICANT CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: PASLSEQ FOR WINDOWS Version 3.0

ORGANISM: Homo sapiens

4034

TYPE: DNA

SEQ ID NO 704

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                   DB 9; Length 4034;
                 75.8%; Score 2585.4;
82.4%; Pred. No. 0;
ative 0; Mismatches
                             Best Local Similarity 82.4
Matches 3325; Conservative
US-10-012-896-704
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Sequence 704, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.

RESULT 13 US-10-012-896-704

qq	541 CTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGG 600		•
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Qy Dp	7 7	δδ Q	1398 CCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCC 1457 [111111111111111111111111111111111111
Qy	TCATGAC 114	Qy Dp	1458 TGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCACGGGAGAAGCAGGTGTTCCTGC 1517
Q.y Db	CCAGAGC 12	Qy Dp	1518 CCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCC 1577
Q7 Dp	1204 TGAGCCGGGCACCGAGACCCGGAGACACTATGATGA	Oy Op	1578 IGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTG 1637
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qq	1261 AGGCTGGTGTGGGAGCCGCCCACCAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCC 1320	g :	41 GCCTGCTCCCACCTCCACCGGCGCTCTGCGGGGGCCTCTGCCTGTGATGTCTCCGTACGTG 24
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Qy	1240 1239	Vo	818 CCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGCCTGGGTC 18
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TITATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACAAAATTAAAGGCTTTC 4019
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AGGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTATTAGCGGGGTGAATAT
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.53462
CURRENT APPLICATION NUMBER: US/09/895,793
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82.4%; Pred. No. 0;
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NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                     Sequence 704, Application US/09895793 Publication No. US20020192763A1
                                                                                                                                                                                                                                                                                                                                                                                 Harlocker, Susan L.
Jiang, Yudiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hural, John
McNeill, Patricia D.
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Vinals de Bassols,
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Hepler, William T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 82.4
Matches 3325; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Foy, Teresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-895-793-704
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qq		qa	1261 AGGCTGGTGTGGG
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qq		qq	1321 TCTCCATCCTGGCC
οy	GAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGG 3	δλ	1240
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3 8	CCIONASSICIATITICACCACAGCATCACCIAIOTACCACCICACCICACACAGAGAGA 42	δλ	1240
S 8	424 GGIARGARGARAITATARGANCAIGGIACIGGIACIAGAGATICAGIACIGGGCTIGGTCTG 483 [qq	1501 AGTCTAGAGGGAG
ò	TGTCCCGCTCCTAGGCTCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCC	δλ	1240
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ολ	CTCATCCCAAGGGCCG	Qy	0
qq	541 CTTCATCTGGGCACTGTCGTTGGGCATCCTGCTGAGCCTCTTTCTCATCCAAGGCCCGG 600	qa	1621 CGTCCTAGAAGCG1
ογ	CTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCGT 6	δ da	1240
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8 8	664 GGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGCTTCACTCCACTGGAGGCCCTGCT 723	qa	1741 GGCGTTGCCCACAT
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දු දු	/24 CTCTGACCTCTTCCGGGACCCGGACCACGCCTACGCTACTCTGTCTATGCCTTCAT 783 	qa	1801 GAAAGGGGAAGGGI
^0	GATCAGTCTTGGGGGCTGCCTGGGGTACCTCTGCCTGCCATTGAGTGGGACACCAGTGC	δλ	1240
: 음	781 GATCAGTCTTGGGGGCTGCCTGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGC 840	qa	1861 CTGTGGTTCCGCCT
δλ	CCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCTT 90	Qy	1240
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QQ		qq	1981 GGGCCATCTCCCTG
δλ	GCCAGCAGAAAGGGCTGTCGGCCCCTTGTCGCCCCACTGCTGCTCCATGCCGGGCCCG	. Оу	1338 GAGCAGTCTATTTG
qq		qq	2041 GAGCAGTCTATTTG
Qy	CTIGGCTTICGGAACCIGGGGGCCCTGCTTCCCCGGCTGCCACCAGCTGTGCTGCCGCAT 1	QY	1398 CCCACAGTGTGGCC
QQ		qq	CCCACAGI
δy		Qy	1458 TGCAGATCCTGCCC
ДD		qa	- F.
٥y	CTTCACGCTGTTTTACACGGATTTCGTGGGCGGGGGGTGTACCAGGGCGTGCCCAGAGC 12	δδ	1518 CCAAATACCGAGGG
qq		qa	2221 CCAAATACCGAGGG
οy	1204 TGAGCCGGGCACCGAGGCCCGGAGACACTATGATGA	ολ	1578 TGCCAGGCCCTAAG
qq		qa .	2281 TGCCAGGCCCTAAG
Qy	1240 1239	δy	1638 GCCTGCTCCCACCT
`		qq	2341 GCCTGCTCCCACCT

2400	GCCTGCTCCCACCTCCACCTCCGCGCTCTGCGGGCCTCTGCCTGTGATGTCTCCGTACGTG	2341	qq
1697	-	1638	οy
1637	TGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGGAG	1578	oy Ob
1577 2280	CCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACGAGCCTGATGACCAGCTTCC 	1518	oy Op
2220		2161	qq
1517	TGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTT	1458	٥y
o		2101	qq
1457		1398	οy
2100		2041	QQ
1397		1338	δy
2040	GCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACC	. 1981	Dp
1337	2525	1278	οy
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	301 GAAAGGGGAAGGGTGCTGGGGAGCAGGGCTGGTCCACAGCAGCTCTCGTGCAGGTAC 186		QQ
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1800	. GGCGTTGCCCACATTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTA	1741	QQ
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1740	. GTCCTCACAGGTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGG	1681	QQ
1239		1240	Οy
1680	. CGTCCTAGAAGCGTCTTGAAGCCTATGGCCAAGCTGTCTTGTGTTCCCTCTCACCGGCT	1621	QQ
1239		1240	οy
1620	TGTGCCCTCTGCTCCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCCAGGTCAGG	1561	Dp
1239		1240	οy
1560	. AGTCTAGAGGGAGTGGAGGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAG	1501	qq
1239		1240	δy
1500	. TAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAA	1441	QQ
1239		1240	ΟY
1440	. CGGCTTCTCATGGGTGTGGAACATCTCTGCTTGCGGTTTTCAGGAAGGCCTCTGGCTGCTC	1381	pp
1239	0	1240	οy
1380	CATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGGATGGACCCCATCT	1321	qq
1239	0	1240	٥y
1320	1 AGGCTGGTGTGGGAGCCGCCCACCAGAGACGACACTCGGGGCTGTGTGTG	1261	Ωp

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Qy 2776 GCCTAA 	2836 3540	3 600	2956 3660	3720	Oy 3076 CAAAGI Db 3780 CAAAGI	3840	3900	3256 3960 3316	OY 5310 ITALE. Db 4020 TTATE.	RESULT 15 US-09-895-814-704 ; Sequence 704, App.	GENERAL INFOR APPLICANT: X APPLICANT:	# APPLICANT: MICO # APPLICANT: HICO # APPLICANT: Jian # APPLICANT: Kaloo # APPLICANT: RAIO	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: APPLICANT: APPLICANT: APPLICANT:		; TILLE OF INVENTI ; FILE REFERENCE: ; CURRENT APPLICAT ; CURRENT FILING D
1698 TGGTGGTGGTGACCCACCGAGGCCAGGGTGGTTCCGGGCCGGGCATCTGCCTGGACC 1757	1758 TCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCT 1817	1818 CCATTGTCCAGCTCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTC 1877 	1878 IGGICGCCATTTACTITGCIACACAGGIAGIATTTGACAAGAGCGACTIGGCCAAATACT 1937 	1938 CAGCGTAGAAAACTTCCAGCACATTGGGTGGAGGGCCTGCCT	1998 CGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGCCCCAGTTTCTGTTGCTGCCCAAAG 2057	2058 TAATGTGGCTCTCTGCTGCCACCCTGTGCTGAGGTGCGTAGCTGCACAGCTGGGGGC 2117	2118 TGGGGCGTCCCTCTCTCCCCAGTCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAG 2177	2178 GGGGTTTCAGTCTGGACTTATACAGGGGCCCAGAAGGGCTCCATGCACTGGAATGCGGG 2237 	2238 GACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCT	2298 CCTAGAGAGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGC 2357 	2358 CCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACAC 2417 	2418 TCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGACCCTGAGGGCAAC 2475 	2476 ACACAAGAACCAGGTCCCTCAGCCCACAGCACTGTCTTTTTGCTGATCCACCCCCTCT 2535	2536 TACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGACACAGGCAT 2595 	2596 ITAAATATTTAACTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGT 2655 	2656 GTTGGTGTCTAATATTTGGGTAGGGTGGGGATCCCCAACAACAGGTCCCCTGAGATAG 2715 	2716 CTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTGGGGTCTGGCCCCCCAAAAT 2775
Qy Dp	Oy Db	Q7 Db	o P	QY Db	Qy Dp	ζο Op	Qy Db	Q Pp	Oy Db	දු පු	O. D.	ζο G	QY DP	. да	Qy Db	Qy Db	QV Db

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DAACTITCCCCACAGGTCCACAACCTGTTGGAGCTACTGCAGGACCAGAAGCA 3075
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AACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTAC 2835
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                                                           GITAGGGTGTTGAAGGAAGGTAGAGGTGGGGCTTCAGGTCTCAACGGCTTCCCT
                                                                          iger, Gary R.

TON: COMPOSITIONS AND METHODS FOR THE THERAPY AND TION: DIAGNOSIS OF PROSTATE CANCER 210121.427026

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tcham, Jennifer L.
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	NUMBER OF SEQ ID NOS: 990 SOFTWARE: FastSEQ for Windows Version 3.0	QQ	
	SEQ 1D NO 704 TYPE: DNA ORGANIEM: Homo sapiens	. Qy	964 GCCAGCAGAAGGGCTGTCGGCCCCCTCCTT
)	Ouery Match Ouery Match Best Local Similarity 82.48; Pred. No. 0; Matches 3325; Conservative 0; Mismatches 1; Indels 709; Gaps 3;	Qy DD	1024 CTTGGCTTTCCGGAACCTGGGCGCCCTGCT
y g	TIGGCTCCGGGTGACAGCCGCGCGCCTCGGCCAGGATCTCAGTG 63	Qy	1084 GCCCGCACCCTGCGCCGGCTCTTCGTGCC HILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
δλ Pa	ATGAGACGTCTCCCCACTGAGGTGCCCCACAGCAGGTGTTGAGCATGGGCTGAGGAGTGTTTTAGCCATGGGCTGAGAAGTGTTTTAGCCATGGGCTGAGAAGTGTTTTAGCCATGGGCTGAGAAGTGGCTGAGAAGTGGCCCCACAGCAGCAGGGGTTGAGCATGGGCTGAGAGAGTGGCCCCACAGCAGCAGCAGGAGTTGGGCTGAGAGAGA	Qy Dp	1144 CTTCACGCTGTTTTACACGGATTTCGTGGG
cy ep	366CTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTGGC 18	oy. Db	1204 TGAGCCGGCACCGAGGCCCGGAGACACTA
λο qα	24	Qy Dp	1240
y d	TGCCTGAACGGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGGTTTTGGCGCGCTGAACGGCCCCCTGAGCCTGTGGGGTTTTTGCTGGCCTGAACGGCCCTGAGCGCTGTGGGGTTTTTTTT	Qy	1240
\ \delta \.	GAGCCCCTGCTGCGCACCCGAAAGCCCAGCCCCATGCTGCTCCAACCTTTGG	Qy Db	1240
7. V da		Qy Dp	1240
Qy Db		Qy	12401501 AGTCTAGAGGAGGAGGAGGAGGAGGTTAAGGCTG
Qy Dp		ογ Db	1240
γο	544 CTTCATCTGGGCACTGTCGTTGGCATCCTGCTGAGCCTCTTCTCATCCCAAGGCCGG 603	QY Db	1240
Qy	604 CTGGCTAGCAGGCTGCTGTGCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCT 663	Qy	· e
Oy Db	664 GGGCGTGGGGCTGCACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCT 723 	Qy	1240
<i>ò</i> ₽	724 CTCTGACCTCTTCGGGACCGGACCACTGTCGCCAGGCCTACTCTGTTATGCCTTCAT 783	Qy Db	1240
O _Y	784 GATCAGTCTTGGGGCTGCCTGGGCTACCTCCTGCCATTGACTGGGACACCAGTGC 843 	Qy	
o,	844 CCTGGCCCCTACCTGGGCACCCAGGAGGACTGCCTCTTTGGCCTGCTCACCTT 903	Oy Dp	1240AGGCGTTCC
àà	CCTCACCTGCGTAGCACCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCCACCGA	Οy	1278 GCGCCATCTCCCTGGTCTTCTCTCTGGTCA

qq	901	
0y	964	CAGCAGAAGGGCTGTCGCCCCCCTTGTCGCCCCCACTGCTGCTATGCCGGGCCC
Db	961	GCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCCACTGTTGTTGTCGGGGCCCG 1020
Oy	Ñ	CTTGGCTTTCGGGAACCTGGGCGCCCTGCTTCCCGGCTGCACCAGCTGTGCTGCGCGAT 1083
QQ	1021	TGGCTTTCCGGAACCTGGCCGCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCG
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qq	1081	CCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGCAGCTGGATGGCACTCAT
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qq	1141	TTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAG
Qγ	1204	GAGCCGGGCACCGAGGCCCGGAGACACTATG
QQ	1201	AGCCGGCCACCGAGCCCGGAGACACTATGATG
γo	1240	1239
Db	1261	AGGCTGGTGTGGGAGCCGCCCACCAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCC 1320
QY	1240	1239
Db	1321	TCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAGTGGGGATGGACCCCATCTGCATACA 1380
٥y	1240	1239
Db	1381	CGGCTTCTCATGGGTGTGGAACATCTCTGCGTTTCAGGAAGGCCTCTGGCTGCTC 1440
Qy	1240	1239
qq	1441	TAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAAGGAAAGGCGGAGCTTATTCAA 1500
Qy	1240	1239
Dp	1501	AGTCTAGAGGGAGTGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAG 1560
QY	1240	1239
qa	1561	TGTGCCCTCTGCTCCCCCAACGACTTTCCAAATATCTCACCAGCGCCTTCCAGCTCAGG 1620
δ	1240	1239
Dβ	1621	CGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCCGCCT 1680
Qy	1240	1239
qq	1681	GTCCTCACAGGTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGG 1740
QY	1240	1239
Db	1741	GGCGTTGCCCACATTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTA 1800
٥y	1240	1239
Db	1801	GAAAGGGGAAGGGTGCTGGGGAGCAGGGCTGGTCCACAGCAGGTCTCGTGCAGCAGGTAC 1860
Οy	1240	1239
qq	1861	CTGTGGTTCCGCCTTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCC
Qy	1240	3GCGTTCGGATGGGCAGCCTGGGGCTGTTCCT
qq	1921	GCGTTCGGATGCCCAGCCTGGGCTGTTCCTG
٥y	1278	GGGCCATCTCCCTGGTCTTCTCTGTGATGACCGGCTGGTGCAGCGATTCGGCACTC 1337

GGGCATCTCCCTGGTCTCTCTGGTCATGGACCGGTGGTGCTGCGGCGTTTCGGCATTCGGCATTCGGCATTCGGCATTCGGCATTCGGCATTCGGCATTCGGCATTCGGCATTCGGCATTCGGCATTCGGCCAGTGTGGCTGTTTCCCTGTGGCTGCCGGTGCCACTTTCTGTTTTGGCCAGTGTGGCAGTTTCCCTGTGGCTGCGGGTTCACCTTCTCAGCCCTGTTTTTGTGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCCCTGTTTTTTTT
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TGGGGCGTCCCTCTCCTCCCCAGTCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAG
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SGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTA PCCCCACCAGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCA SGACCTTGGAAATTCTACTCATCCCAAATGATATTCCAAATGCTGTTAC FTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGG ATATTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAG SGCTGATCATTGCCAGAATCTTCTTCTTCTGGGGTCTGGCCCCCCAAAAT ATTTGAACATATG - - ACTTATTTGTAGGGGAAGAGTCCTGAGGGGCAAC AGGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCTCT AAAAA 3330 AAAAA 4034

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                                                                                                                                                  AND METHODS FOR THE THERAPY AND PROSTATE CANCER
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Pred. No. 0;
                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHON; TITLE OF INVENTION: COMPOSITIONS AND METHON; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE C; FILE REFERENCE: 210121,427C23; CURRENT APPLICATION NUMBER: US/09/759,143; CURRENT FILING DATE: 2001-01-12; SOFTWARE: FRAFFCE.
                                                                                                                                                                                                                                                                                               0; Mismatches
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                            Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
 Mitcham, Jennifer L.
           Susan L.
                                                                  Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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82.4%;
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                    Jiang, Yuqui
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         Harlocker,
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211. 282 217 217 223	298 CCTAGAGAGGGTTTTGGGAGCTGAATAACTCAGTCACCTGGTTCCCATCTGAGGC 23 298 CCTAGAGAGGGTTTTGGGAGCTGAATAACTCAGTCACCTGGTTTCCCATCTCTAAGC 23 11111111111111111111111111111111111	2418 3121 2476 3181		QY 2656 GTTGGTGTCTAATATTGGGTAGGGGGGATCCCCAACAATCAGGTCCCTGAGATAG 2715 D 111111111111111111111111111111111111	QY 2776 GCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTAC 2835 Db 3480 GCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTAC 3539 QY 2836 CCAAGGTTAGGGTGTTGAAGGAAGGTAGGGGGCTTCAGGTCTCAACGGCTTCCCT 2895 Db 3540 CCAAGGTTAGGGTGTTGAAGGTAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCT 3599	QY 2896 AACCACCCTTTCTTTGGCCCAGCTGGTTCCCCCACTTCCACTTCCTTACTCTC 2955 111111111111111111111111111111111111	A 307 A 377 5 313 5 383	OY 3136 GAATCTCACACAGAACTCAGGAGCACCCCTGCCTGAGCTAAGGGAGGTCTTATCTCTC 3195 1111111111111111111111111111111111
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GCCTGAACGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGC AGCCGCCTGCTGCGCACGGCAAAGCCCACTTGCTGGTCAACTGCTG		64 GGGCGTGGGGCTGCACTTCTGTGGCCAGGTGTCTTCACTCCACTGGAGGCCCTGCT 7 [111111111111111111111111111111111111	4 CCTGG 1 CCTGA 4 CCTCA 7 CTCA 1 CCTCA 4 GCCAG 1 GCCAG	1024 CTTGGCTTTCCGGAACCTGGCCCCGGCTGCCGGCTGCCGCGCTT 1083	1204 TGAGCCGGGCCCGGAGACACTATGATGA
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QY 3196 AGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT	RESULT 17 US-09-780-669-704 Sequence 704, Application US/09780669 Patent No. US20020051977A1 GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Mitcham, Jennifer L. APPLICANT: Hitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Henderson, Robert A. APPLICANT: Henderson, Robert A. APPLICANT: Kalos, Mitchael D. APPLICANT: Fanger, Gary R.	Retter, Marc W. Stolk, John A. Stolk, John A. Day, Craig H. Vedvick, Thomas S. Carter, Darrick Li, Samuel Wang, Aljun Skeiky, Yasir A.W. Hepler, William Hural, John McNeill, Patricia D. MUNDWICH, CANDESTRICK AND MENURAL	TILLE OF INVENTION: COMPOSITIONS AND METHOUS FOR THE THERAPY AND FILE REFERENCE: 210121.427C24 FILE REFERENCE: 210121.427C24 CURRENT APPLICATION NUMBER: US/09/780,669 NUMBER OF SEQ ID NOS: 943 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 704 TYPE: DNA TYPE: DNA OSCANISM: Homo sapiens US-09-780-669-704	Query Match 75.8%; Score 2585.4; DB 10; Length 4034; Best Local Similarity 82.4%; Pred. No. 0; 1 Indels 709; Gaps 3; Qy 4 AACCAGCCTGCACGCTCGGCTCGGGTGACAGCCGCGCCTCGGCCAGGATCTGAGTG 63 IllIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	rregc 18 rregc 18 regag 24

Db 181 GGCAGCAAGGAGAGAGGCC Qy 244 TGCCTGAACGGCCCCCTGAC 	Qy 304 GAGCCGCCTGCTGCGGCCCCC 111111111111111111111111111111111111	Oy 424 GGTAGAGGAGAAGTTCATGA 	0y 544 CTTCATCTGGGCACTGTCCT Db 541 CTTCATCTGGGCACTGTCCT Oy 604 CTGGCTAGCAGGGCTGCTGT Db 601 CTGGCTAGCAGGGCTGCTGT	Oy 664 GGGGTGGGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTG	721 784 781 844 841	Oy 904 CCTCACCTGGGTAGCAGCCA 	Qy 1024 CTTGGCTTTCCGGAACCTGG Db 1021 CTTGGCTTTCCGGAACCTGG Qy 1084 GCCCGCACCTGCGCCGGC Qy 11081 GCCCGCACCTGCGCCGCGCGCGCGCGCGCCGCCGCCGCCCGC
Db 3540 CCAAGGTTAGGGTGTTGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGCTTCCCT 3599 Qy 2896 AACCACCCTCTTCTTGGCCCAGCTGGTTCCCCCACTCCACTCTACTCT 2955 Db 3600 AACCACCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTT	2956 TCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTA 301. 1610	3076 CAAAGTGGGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGG 313 11111111111111111111111111111111	3196 AGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAGCGGGGGGGAATAT 325:	AIGGIGACAAAAITAAAGGCITIC 4UI	US-09-822-827-704 ; Sequence 704, Application US/09822827 ; Patent No. US20020081680A1 ; GENERAL INFORMATION: ; APPLICANT: Xu, Janagchun ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER ; FILE REFERENCE: 210121.53407 ; CURRENT APPLICATION NUMBER: US/09/822,827	; CURRENT FILING DATE: 2001-03-28 ; NUMBER OF SEQ ID NOS: 982 ; SOFTWARE FEASTSEQ for Windows Version 3.0 ; SEQ ID NO 704 ; LENGTH: 4034 ; TYPE: DNA ; OSP-08-104. Homo sapiens	Ouery Match Best Local Similarity 82.4%; Pre Best Local Similarity 82.4%; Pre Best Local Similarity 82.4%; Pre Matches 3325; Conservative 0; 4 AACCAGCCTGCAGGCGTGGCTC

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                      AGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGT
                                                                    CGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGG
                                                                                                               GCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGTGGG
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                                                                                                                                                                                                                                      721 TCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTTACCTTCTGTGCC
                                                                                                                                                                                                      Gaps
                                                                                                                                                                 DB 9; Length 2904;
                                                                                                                                                                                                  Indels 343;
                                                                                                                                                                                                    1;
                                                                                                                                                               64.4%; Score 2196.4;
88.2%; Pred. No. 0;
Live 0; Mismatches
RENT FILING DATE: 2001-12-10
BER OF SEQ ID NOS: 1011
WARRE: FastSEQ for Windows Version 3.0
ID NO 703
GCTH: 2904
PE: DNA
                                                                                                                                                                                                    es 2560; Conservative
                                                                                                            ANISM: Homo sapiens
                                                                                                                                                                                  Local Similarity
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1339 INCREMENTATION INCREMENTATION		QY 2467 AGGGCAACACACACAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCA 2526 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 2527 CCCCCTCTTACCTTTATCAGGATGTGCCCTGTTGGTCCTTCTGTTGCCATCAGAGA 2586 111111111111111111111111111111111111	QY 2587 CACAGGCATTAAATATTAACTTATTAACAAAGTAGAAGGGAATCCATTGCTAG 2646	QY 2647 CTTTCTGTGTTGTCTAATATTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCC 2706	QY 2707. CTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTCCTGGGGTCTGGCC 2766	A 2767 CCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAA 2826	OY 2827 TGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGTGGGGCTTCAGGTCTCAAC 2886	AS 2887 GGCTTCCCTAACCACCCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCACTCCCC 2946	AN 2947 TCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCAAC 3006	A 3007 TITCCCTACCCCAACTITCCCCACAACTCTCACAACCTGTTTGGAGCTACTGCAGGA 3066 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	Qy 3067 CCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCT 3126	A 3127 GTGCTTGGGGAATCTCACAGAAACTCAGGAGCACCCCTGCCTG	QY 3187 TTATCTCTCAGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTATTATTAGGGG 3246	Qy 3247 GGTGAATATTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACAAATTA 3306 .	Qy 3307 AAGGCTTTCTTATATGTTTAAAAA 3330 	RESULT 20 US-09-895-793-703 ; Sequence 703, Application US/09895793	; Publication No. US20020192763A1 ; GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun ; APPLICANT: Dillon, Davin C.	; APPLICANT: Mitcham, Jennifer L. ; APPLICANT: Harlocker, Susan L.
	1329 TCGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGAGCAGAGCTTTTCCCTGTGGCTGCCAAAAAAAA	1389 CATGCCTGTCCCACAGTGTGGCGTGACACAGCGTTCAGCCGCCTCACCGGGTTCACCCTTCAGCCGCGTTCACCCTTCAGCCGGGTTCACCCTTCAGCCGGGTTCACCCTTCAGCCGGGTTCACCCTTCAGCGGTTCACCCTTCAGCGGTTCACCCTTCAGCGGTTCACCCTTCAGCGGTTCAGCGTTCAGCGGTTCAACAGAACAGGTTCAACAGGTTCAACAGGTTCAACAGCGGTTCAACAGAACAGGTTCAACAGCGGTTCAACAGAACAGGTTCAACAGCGGTTCAACAGAACAGGTTCAACAGAACAGGTTCAACAGAACAGGTTCAACAGAACAAC	1449 TCTCAGCCCTGCAGATCCTGCCTACACTGCCCTCCTCTACCGGGAGAAGCGGGTCTCTACCGGGAGAAGCGGGGAGAGTCTGCCTCCTCTACCGCGAGAGAGGGGGGTCCTCTACCGGGAGAGCGGGAGAGAGCGGGGAGAGAGCGGCTCCCTTACCGGGAGAGAGA	1509 TGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGA 111111111111111111111111111111111	1569 CCAGCTTCCTGCCAGCCCTAAGCCTGGAGCTCCCTTCCTAATGGACGTGGTGGTGCTG 1111111111111111111111111	1629 GAGGCAGTGGCCTGCTCCACCTCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCT	1689 CCGTACGTGTGGTGAGCCCACCGAGGCAGGGTGCGCCGGGGCCACGTCT	1749 GCCTGGACCTCGCATCCTGGATAGTGCCTTCCTGGTGTCCCAGGTGGCCCCATCCCTGT	1809 TTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACCTATATGGTGTCTCGCGCAG 186	1869 GCCTGGGTCTGGTCACTTTGCTACACAGGTAGTATTGACAAGAGCGACTTGG 1	1929 CCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGCCTGCCT	1989 CCCAGCTCCCGGCTCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTCTGTTG	2049 CTGCCAAAGFAATGTGGCTCTCTGCTGCCACCCTGTGCTGGTGGGTGCGTAGCTGCACAAAAAAAA	2109 GCTGGGGGCTGGGGCCTCCTCTCTCTCCCCAGTCTTAGGGCTGCCTGACTGGAGG	2169 CCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGGCCAGAAGGGCTCCATGCACTG	2229 GAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGT	2289 TGAGACACACCTAGAGAGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA	2349 TCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG	2409 ATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGAGTCCTG

; APPLICANT: Jiang, Yuqiu : APPLICANT: Kalos. Michael D.	qa -	541 GCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTT 600
arc W.	Ž OY	1241
Day, Craig H.	qa	601 CCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTT 660
	Qy	1241
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	Qy	1241
APPLICANT: Hural, John AppliCANT: McMeil) Darricia D	qa	721 TCACCCGCCTGTCCTCACAGCTGCAGAACCCTTCAGACTACCTTCCTCTGCC 780
Houghton, Raymond Vinals de Bassols,	Oy	
Foy, Teresa Fanger, Gary R.	qa ——	TTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGCGTTCGGATGGGCAGCCTGGGGCTGT
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER ; FILE REPERENCE: 210121.534C2	₩ 90 A	1269 TCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGCAGCGGCTGGTGCAGCAT 1328 11
; CURRENT APPLICATION NUMBER: US/09/895,793 ; CURRENT FILING DATE: 2001-06-29 minded of the NOS 100 100 100 100 100 100 100 100 100 10	ζ	1329 TCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCA 1388
SOUNDER OF SEQ ID NOS: 962 SOUNDER: EstSEQ for Windows Version 3.0 SEO ID NO 703	qa	901 TCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCA 960
; LENGTH: 2904 ; TYPE: DNA	٥٨	CATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCACCGCCCCTCACCGGGTTCACCT
; ORGANISM: Homo sapiens US-09-895-793-703	ପ୍ଧ	1 CATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCT
tch 64.4%; Score 2196.4; DB 9; Length 2904; sal Similarity 88.2%; Pred. No. 0;	Oy Dp	1449 TUTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGAGAAGCAGG 1508 1021 - - - - - - - - - - - - - - - - - -
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770 GTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG	7 A	
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61 TGGGACACCACGGGCCCCCTACCTGGGCACCCCGGGAGGAGTGCCTTTGGCCTG 12	qq	cca6ctrccrccagecccraagccr6gagcrccrrccraargaacargagrgcrg 1
CTCACCTCATCTTCCTCACCTGCGTAGCAGCCACCACTGCTGGTGGTGGAGGAGGGGGGGG	Qy Dp	1629 GAGGCAGTGGCTGCTCCACCTCCACCGGCGCTCTGCGGGGCCTCTGCTGTGATGTCT 1688 1201 GAGGCAGTGGCTGCTCCAACTCACCGCGCTTTTTTTTTT
Db 121 CTCACCCTCATCTTCCTCACCTGCGTAGCACCCACTGCTGGTGGCTGAGGAGGCAGCG 180	ò	
Qy 950 CTGGGCCCCACCGAGCCAGCAGAAGGCTGTGCGGCCCCTCCTTGTCGCCCCACTGCTGT 1009 Db 181 CTGGGCCCCACCGAGCAGCAGCAGCAGCGCTGCGGCCCCTCCTTGTCGCCCCACTGCTGT 240	qa ———	261 CCGTACGTCGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGCCATCT
1010 CCATGCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAG	Qy	1749 GCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGCTCCCAGGTGGCCCCATCCCTGT 1808
CTGTGCTGCCGCATGCCCCGCACCTGCGCGCCTTTCCTGGCTGCTGGGCGCCTGGGGGCGCTGGGGGG	Qy	1809 TTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTCGCCTATATGGTGTCTGCCGCAG 1868
	2 8	GCCTGGGTTTTGGTTTTCCCCTTTTTGTTACTTACTTACT
Qy 1130 ATGCCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTGTACCAG 1189	qq	GCCTGGGTCTGGTCGCCATTTACTTTGCTACACGGTAGTATTTGACAAGAGCGACTTGG
1190 GGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAA 1	Qy	1929 CCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT
421 GGCGTGCCCAGAGCTGAGCCGGGCACCGGAGACACTATGATGAAGGAAG	Qy	1989 CCCAGCTCCCGGTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTTCTGTTG 2048
Oy 1241 1240 Dis AB1 CHICAGACACACACACACACACACACACACACACACACACAC	qa	
1241	Oy Db	2049 CTGCCAAAGTAATGTGGCTCTCTGCTGCCCCCTGTGCTGCTGAGGTGCGTAGCTGCAAA 2108

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	TGAGACACCTAGAGAGGTTTTTGGGAGCTGAATAAACTCACTGGTTTCCCA 2348	CCCCCCTTTACCTTTATCAGGATGTGGCCTGTTGGTTGTTGCCATCACAGAG 2586	82 40 46 94	TCTACTCTCTAGGACTGGCTGATGAAGGCACTGCCCAAATTTCCCCTACCCCCAAC 2580 TTTCCCCTACCCCCAACTTCCCCACCACCACCACACACTGCAGGA 3066 TTTCCCCTACCCCCAACTTCCCCACCACCACCACACTGTTGGAGCTACTGCAGGA 3066 TTTCCCCTACCCCCAACTTCCCCACCACCACCACACACTGTTTGGAGCTACTGCAGGA 2640 CCAGAAGCACAAAGTGCGGTTTCCCCACCACCCTGTTTGGAGCTACTGCAGGA 2640 CCAGAAGCACAAAGTGCGGTTTCCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCT 3126 [
2109 1681 2169 1741 2229	2289. 1861 2349 1921 2409 1981 2467	2527 2101 2587 2161 2647 2221 2707	2767 2341 2827 2401 2887 2461	2521 3007 2581 3067 2641 3127 2701

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               1; Indels 343; Gaps
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Raids, Michael D.
APPLICANT: Raids, Michael D.
APPLICANT: Rater, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Ordig H.
APPLICANT: Ordig H.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT APPLICATION NUMBER: US/09/895,814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 2904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.4%; Score 2196.4;
88.2%; Pred. No. 0;
iive 0; Mismatches
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                                                                                                                     3307 AAGGCTTTCTTATATAAAA 3330
                                                                                                                                     2881 AAGGCTTTCTTATATGTTTAAAAA 2904
                                                                                                                                                                                                                        Sequence 703, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                      Harlocker, Susan L.
Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 88.2
Matches 2560; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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ENGTH: 2904
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1021 TCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCC	q a —	_
1449 TCTCAGCCCTGCAGATCCTGCCCTACACACACTGGCCTCC	QY	Query Match 64.4%; Score
961 CATGCCTGTCCCACAGTGTGGGCGCGTGGTGGTTCA	qa	; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens 11S-109-759-143-710
1389 CATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCA	Qy	; SEQ 1D NO 703 ; LENGTH: 2904 : TYPE: DNA
901 TCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCT	ପ୍	; NOMBER OF SEQ ID NOS: 934 ; SOFTWARE: FastSEQ for Windows Version 3.0 . SEO ID NO 703
1329 TCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCT	Qy	; CURRENT APPLICATION NUMBER: US/09/759,143 ; CURRENT FILING DATE: 2001-01-12 · NIMBER OF SEC ID MOS. 934
	୍ଷ	TATE CANCER
1269 TCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTC	Ó	Villiam COMPOSITIONS AND METE
781 TTCAGCAAGGGGGGTTGCCCACATCTCTGAGGGGGGTT	qa	; APPLICANT: Wang, Aijun ; APPLICANT: Skeiky, Yasır A.W.
1241GGCGTT	Qy	; APPLICANT: Carter, Darrick ; APPLICANT: Li, Samuel
721 TCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAAC	qa	APPLICANT: Vedvick, Thomas S.
1241	QY	APPLICANT: Stolk, John A.
661 CCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGG	QQ	, APPLICANT, MAIOS, MICHAEL D.
1241	Qy	APPLICANT: Jiang, Iudul ; APPLICANT: Henderson, Robert A.
601 CCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTC	q ₀	; APPLICANT: MICHAM, Jennier L. ; APPLICANT: Harlocker, Susan L.
1241	Qy	AAPPLICAN: Advantagement APPLICANT Dillon Davin C.
541 GCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTÅAGGC	qa	GALERIC NO. USZUOZZZZABAI GENERAL INFORMATION:
1241	Qy	S-09-139-143-703 Sequence 703. Application US/09759143
481 CTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCA	qa	RESULT 22
1241	QY	DD ZB81 ARGCTTTCTTATATGTTTAAAA 2904
	qa	3307 AAGGCTTTCTTATATGTTTAAAAA
1190 GGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAG	Qy	2821 GGTGAATATTTTATACTGTAAGTGAGCAAT
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	qq	2761 TTATCTCTCAGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT
1070 CIGIGCIGCCGCAIGCCCGCACCCIGCGCCGGCTCTTC	٥٨	DD Z/OI GIGCTIGGGGGATCICACACAGAAACICAGGGGGCACCCCTGGCCIGAGCIAAGGGGGC Z/OO 3187 TTTATCAGGGGGGGGGTTTTTAAGTGCAGGAGGGGGGGGG
241 CCATGCGGGCCGCTTTGGCAAACCTGGGCGG	Z qq	3127 GTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCCTGCCTG
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770 GTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGG		TGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGTGGGGCTTCAGGTCTCAAC 246

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CCCTGCTTCCCGGCTGCACCAG 1069
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GTTCCTGCCCAAATACCGAGG 	GGCAGTGGCCTCCTCCCCA GGCAGTGGCCTGCTCCCC GTACGTGGGGGGGGGG	3-8 4-4 5-6	CAAATACTCAGGGTAGAA 	2AAAGTAATGTGGCTC 2AAAGTAATGTGGCTC 2AAGGTAGTGGCTCCC 11	CCTTCCAAGGGGTTTCAGTCTG	TGAGACACCCTAGAGAAGGGTTT	ATGAACACTCCTCCATGGGATTI 	CCCCCTCTTACTTTATCAGGATU
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RESULT 23
US-09-780.669-703
US-09-780.669-703
Sequence 703, Application US/09780669
Setent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Ni, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Langer, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Samel

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1241	1241	781	DD 841 TCCTGCAGTGCCCATCTCCTGGTG	QY 1329 TCGCCACTCGAGCAGTC	Db 901 TCGGCACTCGAGCAGTCTATTTGGCC	Oy 1389 CATGCCTGTCCCACAGTGTGGCCGTG	1449		. 82	Db 1081	CTG 889 OY 1569 CCAGCTTCCTGCAGGCCTTAAGCTT	120 Qy 1629	949		240 Db 1261	CAG 1069 QY 174.9 GCCTGGACCTCGCCATCCTGGATAGT	300 1321	1129 OY 1		420 Db 1441	Oy 1929 CCAAATACTCAGGTAGAAACTTCC 1240 Db 1501 CCAAATACTCAGGTAGAAAACTTCC Db 1501 CCAAATACTCAGGAAAACTTCC	480 QY 1989	1240		Db 1621	1240 QY	T 660 1681	Oy 2169 CCTTCCARGEGGGTTTCAGTCTGGA 1240	720	OY 2229 GANTECCECEGALTCIECAGGIGGALT 1240	780 1001
. APDLICANT. Henler william	Hural, John	THE COLUMN	בא נו	; CURRENT APPLICATION NUMBER: US/09/780,669 ; CURRENT FILING DATE: 2001-02-09	; NUMBER OF SEQ ID NOS: 943; SOFTWARE: FastSEQ for Windows Version 3.0	; IENGTH: 2904 ; TYPE: DNA ; ORGANISM: Homo sapiens	-703	Query Match Best Local Similarity 88.2%; Pred. No. 0; Matches 2560: Conservative 0: Mismatches 1: Indels 343: Ga	Ov 770 GICIATGCCITCAIGAFCAGICITGGGGGGCTGCCTGGCTACCTCCTGCCTGCCTGCCTGCTACTTGCTGCCTGC	DD 1 GTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGCCTACCTCCTGCCTG	Oy 830 TGGGACACCAGTGCCCTGGCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTG	Db 61 TGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGC	QY 890 CTCACCTCATCTTCCTCACCTGCGTAGCACCACACTGCTGGTGGCTGAGGAGGCAGCG	121		Qy 1010 CCATGCCGGGCCCGCTTGCGGAACCTGGGCGCCCTGCTTCCCGGGTGCACAGG	Db 241 CCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTTCCCCGGCTGCAAC	Qy 1070 CTGTGCTGCCGCATGCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGGTGCAGCTGGTGCAGCTGGTGCTGCAGTGCTGAAGTGCGAAGCTGGTGAAGTTAAGTTGAAGTTAAGTTGAAGTTAAGAAG	1130		Qy 1190 GGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGATGAA	421	0) 1241	1241		1241	Db 601 CCAGCGGAGTGTGCCCTCTGCTCCCCAACGACTTTCCAAATAATCTCACCAGCGCCT	Qy 1241	Db 661 CCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTC	Оу 1241	Db 721 TCACCGGCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCC

306CATCTCCTGGTCTTCTCTGGTTGTTCTTCTGGGTGGGGCACCTGGTTTGGCCAGTGTGGCAGCAGTGTGGCAGCAGCAGTGTGGCAGCAGCAGCGTGGCAGCTGGCAGCTTCTTCTTCTTTTGGCCAGTGTGGCAGCTTCTTTTTTTGGCCAGTGACAGCTTCTTCTTTTTTTT
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GCCCAAATACCGAGGGACACTGGAGGTGC
SCHOOLCCIAAACCIGAACCICCCCCCCCCCCCCCCCCCCCCCCC
316GTGGTGGGTGAGCCCACCGAGGC
TCTGGTCGCCATTTACTTTGCTACACAGG
ACTCAGGGTAGAAACTTCCAGGACATTG
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RESULT 24

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950 CTGGGCCCCACCGAGCCAGCAGAGGCTGTCGGCCCCTCCTTGTCGCCCCACTGCTGT 1009
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                                          GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: LOADSOIL OF PROSTATE CANCER

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C1

CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: RASLSEQ for Windows Version 3.0

SEQ ID NO 703

LENGTH: 2904
                                                                                                                                                                                                                                                                                                    Query Match 64.4%; Score 2196.4; Best Local Similarity 88.2%; Pred. No. 0; Matches 2560; Conservative 0; Mismatches
               Sequence 703, Application US/09822827
Patent No. US20020081680A1
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ORGANISM: Homo sapiens
US-09-822-827-703
US-09-822-827-703
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Qy	2289	TGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACTGGTTTCCCA 2348
qa		AGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA 192
ΟY	2349	TCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG 2408
qa	1921	CTCTAAGCCCCTTAACCTGCGTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG 1
δλ	2409	46
Dp	1981	SAAACACTCCTCCATGGGATTTGAACATATGAAAGTTATTTGTAGGGGAAGAGTCCT
οy	2467	CAGGTCCCCTCAGCCCACAGCACTGTTTTTGCTGATCCA 252
QQ	2041	GGGGCAACACACAGAACCAGGTCCCCTCAGCCCACAGCACTGTTTTTTTT
Qy	2527	CCCCCCTCTTACCTTTTATCAGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGA 2586
qq	2101	CCCCCTTTTTTTTTTTTTTCAGGATGTGGCCTGTTGGTCCTTCTTTTTTTGCTCCATCAGAGA 216
Qy	2587	CACAGGCATTTAAATTTTAACTTATTTAATAACAAAGTAGAAGGGAATCCATTGCTAG 2646
οp	2161	acaggcatttaaatatttaacttatttatttaacaaagtagaaggcaatccattgctag 222
Qy	2647	CTTTTCTGTGTTGTGTGTGTAATATTTGGTAGGGTGGGGGATCCCCAACAATCAGTCCC 2706
qa	2221	TTTTCTGTGTTGTGTCTAATATTTGGGTAGGGTGGGGGGATCCCCAACAATAAGTTCTCT
Qy	2707	IGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGGCC 276
qq	2281	GAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGGCC 234
Qy	2767	CCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAA 2826
qa	2341	CCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAA 240
ογ	2827	TGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGTGGGGCCTTCAGGTCTCAAC 2886
qa	2401	GCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGTGGGGGCTTCAGGTCTCAAC 246
ΟY	2887	reterregeceageergerreececatrecactee 294
QQ	2461	GCTTCCCTAACCACCCTCTTCTTTGGCCCAGCCTGGTTCCCCCCACTTCCACTCCCC 252
ΟY	2947	AAGGCACTG
Dþ	2521	CTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAA
Qy	3007	AGCTCCACAACCCTGTTTGGAGCTACTGCAGGA 306
qq	2581	SCCTACCCCCAACTITCCCCACCACCTCCACAACCTGTTTGGAGCTACTGCAGGA 264
Qy	3067	CCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCT 3126
qq	2641	cadaascacaaaagrecegrifeceaageerrrefecarereageeeeeagrafarer 270
Qy	3127	GIGCTIGGGGAATCICACACAGAACICAGGAGCACCCCCTGCCIGGCIAAGGGAGGIC 3186
qq	2701	TGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCTGCCTG
Qy	3187	CTTATTTATTTAGCGG 324
qa	2761	TATCTCTCTCAGGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT
Qy	3247	GGTGAATATTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACAAAATTA 3306
qq	2821	GTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACAAATT
Οŷ	3307	AAGGCTTTCTATATGTTTAAAAA 3330
qq	2881	SGCTTTCTTATATGTT

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2751 TGCTCCGACCCTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGGCGTTCG 2810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.8%; Score 2142.8;
80.1%; Pred. No. 0;
Live 1; Mismatches
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CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                        Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
                   Sequence 702, Application US/10012896 Publication No. US20020183251A1 GENERAL INFORMATION:
                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carier, Marc W.
APPLICANT: Carier, Thomas S.
APPLICANT: Carter, Darrick
                                                                                                                                                                                                                                                                                                                           Skeiky, Yasır A.W.
Hepler, William T.
Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                   Hural, John
McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.8
Best Local Similarity 80.1
Matches 2872; Conservative
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                                                                                                                                                                                                                                                                                     Li, Samuel X.
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CORGANISM: Homo sapiens
US-10-012-896-702
                                                                                                                                                                                                                                                                                                               Wang, Aijun
US-10-012-896-702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 702
LENGTH: 4894
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QΩ	1731	GCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCACCACTGCTGGTG 1	790
Qγ	935	CCGAGCCAGCAGGGCTGTCGGCCCCCTTG 9	94
Db	1791	CTGAGGAGGCAGCGCTGCTCTCTTTTTTTTTTTTTTTTT	850
٥y	995	TCGCCCCACTGCTGTCCATGCCGGCCCGCTTGCCTTTCCGGAACCTGGGCGCCCTGCTT 10	054
qa	1851	CGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 1	910
Qy	1055	GGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGGCCGGC	14
QQ	1911	CCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCT 1	970
QY	1115	AGCTGTGCAGCTGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGG	74
qa	1971	GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC 20	30
φy	1175	GAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTAT 12	234
qq	2031	3666CTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACGCCCGGAGACACTAT 2	.060
Qy	1235	ATG	33
QQ	2091		50
οy	1240		39
QQ	2151	ACACTCGGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGCCCCGACTTCTCTGTCAGG 22	210
Qy	1240	12	39
qq	2211	AAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCT 22	120
Qy	1240		39
Db	2271	TTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCG	30
Oy	1240		39
Dp	2331	TGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGGTAAAGGCTGG 23	90
Oy	1240	12	39
qq	2391	CAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGC	20
Qy	1240		39
qq	2451	ATAATCTCACCAGGGCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCA 25	10
oy.	1240	12	39
QQ	2511	GCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGACTCCCCAGGAAACCTT 25	70
Qy	1240	12	39
QQ	2571	CAGACTACCTTCCTCTGCCTTCAGCAAGGGGGCGTTGCCCCACATTCTCTGAGGGTCAGTGG 26	30
07	1240	12	39
qq	2631	AAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGTGCTGGGGAGCAGGGCTG 26	90
Qy	1240	12	39
QQ	2691	GTCCACAGCAGGTCTCGTGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCCTGAGAC 27	20
٥y			48
4	27.7.1		(

	2867 2867 4431 2927 4491 2987 4551 3047 4611	Oy 3167 TGCCTGAGCTAAGGAGTTATCTGTGCTTATCTGTGCTTATCTGTGCTTATCTGTGCTAAGGAGGTCTTATCTTATTATCTGTGAGGAGTCTTATCTTATCTTATCTTATCTTATCTTATCTATC
1249 GATGGGCAGCTGGTCCTCCAGTGCGCCATCTCCTTGGTCTTCTCTGGTCAT .1308	3231 GGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGGTGGGTG	1591
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4670 2746 2926 4490 2986 4550 3046 4610 3106 3166 4730 ACACTCCTCCATGGGATTGAACATATG--ACTTA 2446 2506 2566 2626 2686 4250 AAATGCCTAACCCAGGACCTTGGAAATTCTACTCA 2806 2866 ATATTTTATACTGTAAGTGAGCAATCAGAGTATAA 3286 3950 CAACACACAAGAACCAGGTCCCCTCAGCCCACAGC 4070 AGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATC CCCTAACCACCCTCTTCTCTTGGCCCAGCCTGGT TCTCTCTAGGACTGGCTGATGAAGGCACTGCCCA TCTCAGGGGGGTTTAAGTGCCGTTTGCAATAATG CTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGG TTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGG CCCTAACCACCCCTCTTCTTTGGCCCAGCCTGGT CAACACACAGAACCAGGTCCCCTCAGCCCACAGC CTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCC GCATTTAAATATTTAACTTATTTAATTTAACAAAGT CTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGG TTTCTTATATGTTTAAAAA 3330

1791 GCTGAGGAGCCGCCCCCCCCAGCAGAAGGCCTGTCGGCCCCTCCTTG 1850 QY 995 TCGCCCACTGCTGCTGCTGCTTTGCGGAACCTGGGCCCCTCCTTG 1850 QY 111111111111111111111111111111111	1175 2031 1235 2091 1240 1240	1240	2331 TGACAGAAGGAAAGGGGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGATTAAGGCTGG 1240	QY 1240 1239 Db 2571 CAGACTACCTCCTCGCATGCAGGGCGTTGCCCACATTCTCTGAGGGTCAGTGG 2630 QY 1240 1239 Db 2631 AAGAACCTAGATTCCTAGAAGGGGAAGGGTGCTGGGGAGCTGGCTG
	INV INV INV PPL	; CVRENT FILLING DATE: 2001-06-29 ; NUMBER OF SEQ ID NOS: 982 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 702 ; LENGTH: 4894 ; TYPE: DNA ; VRGANISM: Homo sapiens US-09-895-793-702 QUETY MATCH Best Local Similarity 80.1%: Pred No 0.	GGCATTGCTCCAGTGGGGGGCATTGGTCCAGTGCTGGGGGCATTGGTCCAGTGCTGGGCGTGGGCGTATGGCCGGGCGCTATGGCCGCGTATGGCCGCTATGGCCGCTATGGCCGCTATGGCCGCTATGGCCGCTATGGCCGCTATGGCCGCTATGGCCGCTATGGCCGCTATGGCCGCTATGGCCGCTGGGCCGCTATGGCCGCTGGGCCTATGGCCGCTATGGCCGCTGGGCCTATGGCCGCTATGGCCGCTGGGCCGCTATGGCCGCTGGGCCGCTATGGCCGCTATGGCCGCTCTTTCTCATCCCCTCTCCATCCCCTCTATGCCATCCCCTCTATGCCATCCCCTCTATGCTCATCCCATCCCCTCTATGCTCATCCCATCCCCTCTATGCTCATCCCATCCCCTCTATGCTCATCCCATCCCCTCTATGCTCATCCCATCCCATCCCCTCTATGCTCATCCCATCCCCTCTATGCTCATCCCATCCCCTCTATGCTCATCCCATCCCCTCTATGCTCATCCCATCCCCTCTATGCTCATCCCATCCCATCCCCTCTATGCTCATCCCATCCCCTCTATGCTCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCATCCCATCCATCCCATCCCATCCATCCCATCCCATCCCATCCATCCCATCCCATCCATCCCATCCATCCCATCCCATCCATCCCATCCCATCCATCCCATCCCATCCATCCCATCCATCCCATCCATCCATCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCATCCATCCCATCCCATCCATCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCATCCCATCCCATCCCATCCCATCCATCCCATCCCATCCATCCATCCCATCCATCCCATCCATCCATCCCATCAT	0y 635 AGGCCCTGGAGCTGGCCTCTCTCTGGGCGTGGGGCTTCTTGTGGCCAG 694 1491 AGGCCCTGGAGCTGGCTGGGGCGTGGGGCTTCTTGTGGCCAG 1550 0y 695 GTGTGCTTCACTCGACTGCTCTCTTCTGGGCTTCTTGTGGCCACTGT 754 111111111111111111111111111111111111

Oy 2447 T Db 4011 T	QY 2507 A		Qy 2567 T			Qy 2687 A Db 4251 A	Qy 2747 T Db 4311 T		Oy 2867 G Db 4431 G		298 455					Qy 3287 T Db 4851 T	RESULT 27 US-09-895-814-7 ; Sequence 702,	GENERAL INFOF APPLICANT: APPLICANT: APPLICANT:	; APPLICANT: ; APPLICANT: ; APPLICANT: ; APPLICANT:
1369 CCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGC 1428	1 CCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGC 2999	1429 GGCCCTGACGGGTTCACTTGTCAGCAGATCCTGCCTAGACTTGGCTTCGT 1488 19111111111111111111111111111111111	1489 CTACCACCGGGGAGAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAG 1548	3051 CTACCACCGGGAGAAGCAGTGTTCCTGCCCAATACCGAGGGGACACTGGAGGTGCTAG 3110	1549 CAGTGAGGACAGCTGATGACCAGCTTCCTGCCAGGCCTGAAGCCTGGAGCTCCCTTCCC 1608	1609 TAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCGCGCTCTGCGG 1668 1111111111111111111111111111111111	GGCCTCTGCCTGTGTGTCTCCGTACGTGTGGTGGGGTGACCCCACCGAGGCCAGGGT 17	1729 GGTTCCGGGCCGGGGCATCTGCCTGCGCGTCGTGGTGGGTG	1789 CCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGC 1848	1849 CTATATGGTGTCTGCCGCAGGCCTGGGTCTGCTTTACTTTGCTACACAGGTAGT 1908	1909 ATTGACAAGGGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTG 1968 	1969 GAGGGCTGCTCACTGGGTCCCAGCTCCCGGTCTAAGCCCCATGGGGCTGCCGGG 2028 	2029 CTGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCTGCTGTGCTG 2088 .	2089 CTGAGGTGCGTGCACCTGGGGGCTGGGGCGTCCCTCTCTCT	2149 TAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGC 2208 	2209 CAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGG 2268 	2269 TTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAA 2328 	2329 CTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCT 2388	2389 CTTGCATGGGAGTTTCTAGGATGAAACACTCCTCGGGATTTGAACATATGACTTA 2446
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                                                                                                                              TTCTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAATAAGT
                                                                                       AGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGG
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TTTGTAGGGGAAGAGTCCTGAGGGGCAACACACAGAACCAGGTCCCCTCAGCCCACAGC
                                      ACTGTCTTTTTGCTGATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCC
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RESULT 27
US-09-895-814-702
Sequence 702. Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: AFLICANT: Retter, Marc W.
APPLICANT: Retter, Machael D.

	2331 TGACAGAAGGCGGGGCGTTATTCAAAGTCTAGAGGGAGTGGAGGTTAAGGCTGG	Db 2391 ATTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAA 2450 Qy 1240	1240	0 0 0 0 0 0 0 0 0 0
APPLICANT: Stolk, John A. APPLICANT: Bay, Craig H. APPLICANT: Vedvick, Thomas S. APPLICANT: Vedvick, Thomas S. APPLICANT: Vedvick, Thomas S. APPLICANT: Li, Samuel X. APPLICANT: Mang, Aljun A. APPLICANT: Mederson, Robert A. APPLICANT: Hepler, William T. APPLICANT: Hepler, William T. APPLICANT: Houghton, Robert A. APPLICANT: Houghton, Raymond L. APPLICANT: Houghton, Raymond L. APPLICANT: Houghton, Raymond L. APPLICANT: Fanger Gary R. APPLICANT: Fanger Gary R. TILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TITLE OF INVENTION INVERSE: 2010-16-29 NUMBER OF SEQ ID NOS: 990 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 702 LENOTH: 4894 TYPE: DNA ORGANISM: Homo sapiens US-09-895-814-702	Ouery Match Best Local Similarity 80.1%; Pred. No. 0; Matches 2872; Conservative 1; Mismatches 3; Indels 708; Gaps 2; Oy 455 GGGATTGGTCCCAGTGTGGGCTGGTTGTGTCCTAGGTCTAGGCTCAAGCAAC 514	ACCAC TCCTG TCCTG TCCTG TCCTC TCCTC ATCCCC	SCCAG 	0y 815 CTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCAGGAGGAG 874 1671 CTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCAGGAGGAG 1730 Qy 875 TGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGCACCACTGCTGGTG 934 11731 TGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTACCACTGCTGGTG 1790 Qy 935 GGTGAGGAGGCACCTCACCTCATCTTCCTCACCTGCGTACCACCTCTTG 994 1111111111111111111111111111111111

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        CCTACCCCCAACTTTCCCCACCAGCTCCACAACCC 4610
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2626
                                                                     SATAGCTGGTCATTGGGCTGATCATTGCCAGAATCT
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SGCATTTAAATTTAACTTATTTATTTAACAAAGT
                                                                                                                                                                                                                     CTCTCTCTAGGACTGGCTGATGAAGGCACTGCCCA
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APPLICANT: Wang	; APPLICANT: Wang, Aijun ; APPLICANT: Skeiky, Yasir A.W.	qa	2091
TITLE OF INVENTIC	II, WILLIAM NN: COMPOSITIONS AND METHODS FOR THE THERAPY AND NN: DIAGNOSIS OF PROSTATE CANFE	Qy	1240
FILE REFERENCE:	210121.427C23 20 NIMBER - 115.09.759 143	QQ	2151
CURRENT FILING DE	TTE: 2001-01-12 (2001-01-12)	Qy	1240
SOFTWARE: FastSI SECTONO 702	Nos: 534 Of for Windows Version 3.0	qa	2211
; LENGTH: 4894		QY	1240
Homo	sapiens	qq	2271
Ollers	erons.	Qy	1240
Best Local Similarity 80.18 Matches 2872: Conservative	; Core size; of to be so the size of the s	qq	2331
7.	「ザールをひとびかっているのでは、「サールのでは、「サールをできない」というできません。 こうしゅうしょう しょうしゅう しゅうしゅう しゅう	Qy	1240
1311		qq	2391
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1371	HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	qa	2451
		Qy	1240
1431		qa	2511
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1491		qa	2571
		Qy	1240
1551	GTGTGCTTCACTCCACTGGAGGCCTGCTCTTCGGGACCCGGACCACTGT 1610	qa	2631
Qy 755 CGCCAC		Qy	1240
1611		qa	2691
Qy 815 CTGCC1		Qy	1240
1671		QC	2751
		Qy	1249
1731	THE THIRD THE TH	qa	2811
9, 0		QY	1309
1791		qa	2871
566		Qy	1369
1851		qa	2931
1055	111	QY	1429
1911	CCCCGGCTGCACCACGTGCTGCCGCATGCCCGCACGCTGCGCCGGCTTTCGTGGCT 1970	qa	2991
Qy 1115 GAGCTC		Qy	1489
1971		qq	3051
Qy 1175 GAGGG		0y	1549
Db 2031 GAGGGC		qa	3111
Qy 1235 GATGA-	1239	ογ	1609

qq	2091	GATGAAGGTAAGGCCTTGGCAGCCAGCAGAGGCTGGTGTGGGAGCCGCCCACCAGAGACG 2150
ογ	1240	1239
QQ	2151	ACACTCGGGGCTGTGTGTGGGGGTGCCTCTCCATCCTGGCCCCGACTTCTCTGTCAGG 2210
Qy	1240	1239
QQ	2211	AAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCT 2270
٥y	1240	1239
QQ	2271	TGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTT 2330
Qy	1240	1239
QQ	2331	TGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGTTAAGGCTGG 2390
Qy	1240	1239
QQ	2391	ATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAA 2450
δy	1240	1239
Db	2451	ATAATCTCACCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCA 2510
Οÿ	1240	1239
Db	2511	GCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGACTCCCCAGGAAACCTT 2570
Qy	1240	1239
QQ	2571	CAGACTACCTTCCTCTGCCTTCAGCAAGGGGGGTTGCCCCACATTCTCTGAGGGTCAGTGG 2630
Qy	1240	1239
ОР	2631	AAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGGTGCTGGGGAGCAGGGCTG 2690
Qγ	1240	1239
qq	2691	GTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCCTGAGAC 2750
δλ	1240	SCGTTC
q 0	2751	TGCTCCGACCCTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCCTCTGCAGGCGTTCG 2810
οy	1249	GATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCAT 1308
QQ	2811	ATGGGCAGCCTGGGGGTGTTCCTGCAGGGCCATCTCCCTGGTCTTCTCTCTGGTC
Qy	1309	GGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTT 1368
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QY	1429	CGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCT 1488
qq	2991	CCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCC
Qy	1489	CTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAG 1548
qq	3051	ACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTA
λο i	54	AGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGGTCCCTTCCC 160
an an	7 :	JAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCC 317
ολ	1609	TAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCCGCTCTGCGG 1668

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3	ı innissacacsissisi	2747 FOFFERENCE VO
λο da	1669 GGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGGTGAGCCCACCGAGGCCAGGGT 1728 1	43
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		Qy 2867 GTGGGGCTTCAGGTCTCAACGGCTTCCTAA
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	49 CTATATGGTGTGTGGCGGCAGGCCTGAGTCTGGTCGCCATTTATATATA	Qy 2927 TCCCCCACTTCCACTCCCCTCTACTCTCTC
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qa	3471 ATTTGACAAGGGGACTTGGCCAAATACTCAGGGGTAGAAAACTTCCAGCACATTGGGGTG 3530	4551
yo qq	0 4	UY 3047 TGTTTGGAGCTACTGCAGGACCAGAAGCACA,
δλ	029 CTGGCCGCCAGTTTCTGT	Oy 3107 TCAGCCCCCAGAGTATATCTGTGCTTGGGGA
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රු සි	2149 TAGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGC 2208	
δλ	CAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTAACCAAGGTCAAGGG	Qy 3287 TGTTTATGGTGAAAATTAAAGGCTTTCTT
q	11	Db 4851 TGTTTATGGTGACAAAATTAAAGGCTTTCTT
ογ	. 2269 TTAACAGCTAGCCTCCTAGTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAA 2328	RESULT 29
q	3831 TTAACAGCTAGCCTCCTAGTTGAGACACCTAGAGAGGGTTTTTGGGAGCTGAATAAA 3890	US-09-780-669-702 ; Sequence 702, Application US/09780669
ò t	329 CTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGGT	Fatent No. (GENERAL INF(APPLICANT:
αn ·		APPLICANT:
oy O	2389 CTTCCATGGGAGTTTCTAGGATGAACACTCCTCCATGGGATTTGAACATATGACTTA 2446 11111111111111111111111111111111111	APPLICANT: Harlocker, Susan APPLICANT: Jiang, Yuqui
Qy	IGAGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGC	APPLICANT: APPLICANT: APPLICANT:
qa		APPLICANT:
Qy	2507 ACTGTCTTTTGCTGATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCC 2566	APPLICANT: APPLICANT:
qq	4071 ACTGTCTTTTTGCTGATCCACCCCCTCTTACCTTTATCAGGATGTGGCCTGTTGGTCC 4130	APPLICANT: APPLICANT:
Qy Db	2567 TTCTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAATTTAACAAAGT 2626 4131 TTCTGTTGCCATCACAGACACACACACATTAAATATTTAACTTATTTAACAAAAGT 2626 4131 TTCTGTTGCCATCACACACACACACACATTAAAATAATTAAT	APPLICANT: Wang, Aljun APPLICANT: Skelky, Yasir A.W.
Qy	AGAAGGGAATCCATTGCTAGCTTTTCTGTGTGTCTAATATTTGGGTAGGTGGGGG	
qa	4191 AGAAGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTAAATATTTGGTAGGTGGGGG 4250	TITLE OF INVENTION: COMPOSITIONS AND METHO ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
Qy	9	
QQ O	4251 ATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCT 4310	

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TTCCACTCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCA 2986
                                                                                                                                                                                                                                                                                                                                               CTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATC 3106
                                                                                                                                                                                                                                                            AGAGTATATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCC 3166
                                                                                                                                                                                                                                                                      TAAGGGAGGTCTTATCTCTCAGGGGGGGTTTAAGTGCCGTTTGCAATAATG 3226
                                          GGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCA
                                                                                                                                                                       CTACCCCCAACTTTCCCCTACCCCCAACTTTCCCCACCAGCTCCACAACCC
                                                                                                                                                                                                                                                                                                                                                                                           TGACAAAATTAAAGGCTTTCTTATATGTTTAAAAA 3330
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, Raymond L. COMPOSITIONS AND METHODS FOR THE THERAPY AND TAGNOSIS OF PROSTATE CANCER 121.427C24 tion US/09780669 ngchun Davin C. , Jennifer L. er, Susan L. Yuqui n, Robert A. ichael D. Patricia D. ohn A. ig H. Thomas S. Yasir A.W. William Gary R. Marc W. Darrick

	OPTWARE: FastSEO for Windows Version 3.0 .	qa	2211 AAAGTGGG
S:		Qy	1240
	TYPE: DNA ORGANISM: Homo sapiens	qa	2271 TGCGGTTT
60-S0	20/-699-107	Qy	1240
5 ŭ :	COFE 2142.8; UB 10; Length 4894;	qa	2331 TGACAGA
Ĕ	28/2; Conservative I; Mismatches 3; Inders /U8; Gaps	δλ	1240
δ d	455 GCATTGGTCCAGTGCTGGGCTGGTCTGTGTCCCCGCTCCTAGGCCTCACCCAGTGACCAC 5.14	qa	2391 ATTTCAG
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y 4		qa	2511 GCTGTCTI
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; a		qq	2571 CAGACTAC
ìè	GIGHGCHTCACHCCACHGGAGGCCCHGCHCTCHGACCHCTTCCGGGGACCCGGACCACHGT 7	Qy	1240
7 E	GTGTGCTTC ACTCCACTGCAGCCCTGCTCTTCAGACCCGGGACCGGGACCACTGT	qa	2631 AAGAACCI
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q		δy	1369 CCCTGTG
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Oy.	GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGCC	qa	3051 CTACCAC
QQ	GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGGC 2	Qy	1549 CAGTGAGG
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an d	GATGAAGGTAAGGCCTTGGGCAGCCAGGAGGCTGGTGTGGGGAGCCGCCCCACCAGAGGCG	٥٧	1669 GGCCTCT
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Q	2211	AAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCT 2270
>-	1240	1239
۵	2271	CGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTG
>-	1240	
Ω	2331	GACAGAAGGAAGGCGGAGCTTATTCAAAGTCT
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д	2391	TTCAGATCTGCCTGGTTCCAGCCGCAGTGTGC
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Ф	2451	ATAATCTCACCAGGGCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCA 2510
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Ω	2511	TTCCCTCTCACCCGCCTGTCCTCACA
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Q	2571	AGCAAGGGGCGTTGCCCACATTCTCTGAGGGTCAGT
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Y	1240	AGGCGTTCG 1248
۾	275 į	CCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGGCG
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>-	1309	CCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTT
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Q	2991	GCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCT 305
λ	1489	54
ð	3051	TACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCT
Δi	1549	CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCCAGGCCCTAAGCCTGGAGCTCCCTTCCC 1608
ą	3111	AGTGAGGACAGCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTC
λi	1609	TAATGGACACGCGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCTCCGCGCTCTGCGG 1668
ą	3171	SACACGTGGGTGYTGGAGGCAGTGGCCTGCTCCCACCTCCACCTGCGCTCTGCG
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ζį, Q	1729	GGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTC 1788

DD 1491 AGGCCCCTGGGGCTGCCACTGGA(4371 TCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGTTCAAGGAAGG	Dp
635	TCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAG	Qy
-	2747 TCTTCTCTGGGGCTCTGGCCCCCAAATGCCTAACCAGGACCTTGGAAATTCTACTCA 2806 	Oy Op
Qy 575 CTGAGCCTCTTTCTCATCCC	ATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCT 431	q Q
137	ATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCT 274	ð á
	4191 AGAAGGAATCCATTGCTAGCTTTCTGTTGGTGTCTAATATTTGGGTAGGGTGGGG 4250	qa
Db 1311 GCATTGGTCAGTGGG	2627 AGAAGGGAATCCATTGCTAGCTTTTCTGTGTGTGTGTGTAATATTTGGGTAGGGTGGGG 2686	δλ
	4131 TICTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAACAAAGT 4190	qq
Query Match 62.8%; 8 Best Local Similarity 80.1%; 1 Matches 2872; Conservative 1:	TTCTGTTGCCATCACAGACACAGGCATTTAAATATTTAACTTATTTAT	QY
ORGANISM: Homo sapiens S-09-822-827-702	2507 ACTGTCTTTTGCTGATCCACCCCCTCTTACCTTTATCAGGATGTGGCCTGTTGGTCC 2566	Qy Dp
; LENGTH: 4894 ; TYPE: DNA	TTTGTAGGGGAAGAGTCCTGAGGGGCAACACACAAAACCAGGTCCCCTCAGCCCACAGC 407	qq
SEO ID NO 702	2447 ITTGTAGGGAAGAGTCCTGAGGGCAACACAAGAACCAGGTCCCCTCAGCCCACAGC 2506	Qy
; FILE REFERENCE: 210121.534C1 ; CURRENT APPLICATION NUMBER: US/C ; CURRENT FILING DATE: 2001-03-28	2389 CTTGCATGGGAGTTTCTAGGATGAAACACTCCTGGGATTTGAACATATGACTTA 2446 	Oy Dp
; GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun ; TITLE OF INVENTION: COMPOSITION: · TITLE OF INVENTION: DIAGNOSIS (2329 CICAGICACCIGGITICCCAICTCIAAGCCCCTTAACCIGCAGCITCGITTAAIGIAGCI 2388 	<u> </u>
Sequence 702, Application US/0982	3831 TTAACAGCTAGCTCCTAGTTGAGACACCTAGAGAGGGTTTTTGGGAGCTGAATAAA 3890	3 8
DD 4851 TGTTTAIGGTGACAAAATTA	CAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGG 383	qq
C1 0	CGGAGGCTCCATGCACTGGAATGCGGGACTCTGCAGGTGGATTACCCAGGCTCGGG	δλ
	2149 TAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGAGGC 2208 11111111111111111111111111111111111	yo da
4731	2089 CTGAGGTGCGTAGCTGCACAGCTGGGGGCGTCCCTCTCTCT	Qy Dp
4671	2029 CIGGCCGCCAGITICIGIIGCCCAAAGIAAIGIGGCICTCIGCIGCCACCCTGIGCIG 2088 	Qy Dp
4611 T	1969 GAGGGCTGCCTCACTGGTCCCAGCTCCCCGCTCCTGTTAGCCCCATGGGCTGCCGGG 2028	Qy
	1909 ATTGACAAGGGGACTTGGCCAAATACTCAGGGTGAGAAAACTTCCAGCACTTGGGGTG 1968 	oy Db
4491	1849 CTATATGGTGTCTGCCGCAGGCCTGGGTCTGCTCCCATTACTTTGCTACACAGGTAGT 1908 	Dp
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                                                                                                                                                                                                   TGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCC 3166
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                                                              UTITICCCTACCCCCAACTITICCCCACCAGCTCCACAACCC 3046
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                                                                                                                                                  GCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCAC
                                                  TCTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCCA
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                                                                                                                                                                                                                                                                                                                                                          AAAGGCTTTCTTATATGTTTAAAAA 3330
                                                                                                                                                                                                                                                                                                                                                                         AAAGGCTTCTTATATGTTTAAAAA 4894
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version 3.0
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Db 2631 AAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAG	Dp 2691 GTCCACAGGTCTCGTGCAGCAGGTACTTGTAGTTTCCC	1340	2751	0 – 0	Qy 1309 GGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTAT	Qy 1369 CCCTGTGCGGCTGCCGCAATGCCTGTCCCACAGTGTG 111111111111111111111111111111111	Qy 1429 CGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTG	Qy 1489 CTACCACGGGAGAAGCAGGTGTTCCTGCCCAAATACCGA	Qy 1549 CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCTT	1609	ه ب	323	17	3291	Dy 1789 CCAGGTGGCCCATCCTGTTTATGGGTCCATTGTCAGG	1849	Db 3411 CTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCAFT	Oy 1909 ATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAA.	1969	א ניס	TCCC	3591	2089	302	2149	3711
1551 GFGFGCTTCACTCCACTGGAGGCCCTGCTCTCACCTGTTCCGGGACCCGGACCACTGT 1610	CGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTC 814	CATGATCAGTCTTGGGGGCTGCCTGGGCT	815 CTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAG 874	875 TGCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCACCACACTGCTGGTG 934	AGCAGAAGGGCTGTCGGCCCCCTCCTTG 99	TCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGGCCCCTCTT 105	rrcgreecr 111.	rrrcgregec 117	GAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTAT 1	2031 GAGGGGTGTACCAGGGGGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTAT 2090 1235 GATGA	GATGAAGGTAAGGCCTTGGCAGCCAGGAGGCTGGTGTGGGAGCCGCCCACCAGAGACG 2	1240 1239 2151 ACACTGGGGGGTGTGTGTGGGGTGGTGGTGCTGGGCTGG	123	2211 AAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCT 2270		T 233	TGACAGAAGGAAAGGCGGAGCTTATTCA		2391 ATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAA 2450	1	2451 ATAATCTCACCAGCGCTTCCAGCTCCAGGGGTCTTGAAGCCTATGGCCA 2510		2511 GCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTT 2570		2571 CAGACTACCTTCCTCTGCCTTCAGCGAGGGGCGTTGCCCACATTCTCTGAGGGTCAGTGG 2630	1240 1239
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2751	CTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGGCGTTC	-
1249	GATGGCAGCCTGGGGCTGTTCTGCAGTGCGCCATCTCCCTGGTCTTCTTCTGGTCAT :	
30	SACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCTAGTTTT	36
2871		9
36	CAGCTTCAGC	42
n d	UNITED STATEMENT OF THE CONTRACT OF THE CONTRA	66
2991	GECCETCACCESSITEACETFCTCASCCETGCAGATCCTGCCCTACACACTGGCCTCCTTTTTTTTTT	1488
1489	CTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGGTGCTAG	1548
54	AGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGGTCCCTTCCC	9
11	CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCC	17
1609	TAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGCTTCTGCGG	1668
. 99	SCOTCTGCCTGTGATGTCCGTACGTGATGGTGGTGAGCCCACCCA	3 5
23	GCCTCTGCCTGTGTGTGTCTCCGTACGTGTGTGGTGGTGGTGTGTGT	29 4
1729	GGTTCCGGCCCGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTC	1788
1789	CAGGTGGCCCCATCCTGTTATGGGCTCCATTGTCCAGGCTCAGCCAGTCTGTCACTGC	84
3351		3410
3411	CTATATGGTGTCTGCCGCAGGCCTGGGTCTGGCGCATTTACTTTGCTACACAGGTAGT 1	1908
90	ATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTG	96
4	ITGACAAGAGGTTGGCCAAATACTCAGGGTAGAAAAGTTGCAGGACATTGGGGGTG	53
1969	GAGGGCCTGCCTCACTGGGTCCCAGCTCCCCGCTCCTGTTAGCCCCATGGGGCTGCGGG 2	2028 3590
2029	CTGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCCTCTCTGCTGCCACCCTGTGCTG	98
,	166CCGCCAGIIICIGIIGCIGCCAAAGIAAIGIGGCICICIGCIGCCACCTGIGCIG	0
3651	CTGAGGTGCGTAGCTGCACAGCTGGGGCCTGGGGCGTCCCTCTCCTCTCCCCAGTCTC 2	2148 3710
2149	TAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGC	2208
+	AGGGCIGCCIGACIGGAGGCCIICCAAGGGGGTIICAGICIGGACIIAIACAGGGAGGC	

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                                                 TTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAA
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                                                                                                                 CTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCT
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COMPOSITIONS AND METHODS FOR 1
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Pred. No. 0;
0; Mismatches
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APPLICANT: Wantanabe, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CA
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CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
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Vinals de Bassols, Carlota
                                                                                                          Sequence 705, Application US/10012896 Publication No. US20020183251A1 GENERAL INFORMATION:
                                                                                                                                                         APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Hepler, William T.
Henderson, Robert A.
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Jiang, Yuqiu
Kalos, Michael D.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Best Local Similarity 98.7%;
Matches 1841; Conservative
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CCTGGGTCTGGTCGC 	CAAATACTCAGCGTA 	STCCCAGCTCCCCGCTCCT 	SCCAAAGTAATGTGG 	SCACAGCTGGGGGCTGGGGCGTTTTTTTTTTTTTTTTTTT	CCAAGGGGGTTT 	CGGGGACTCTG	CCAGGCTCAGGGTTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGC 	TTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGC 	ICTAGGATGAAACACTCCTCCATGGG 	3TCCTGAGGGGAACACACAGAACCA 	SATCCACCCCCTCTTACCTTTTATCA	AGAGACACAGGCATTTAAATATTTAA 	CITAITITATITAACAAAGTAGAAGGAATCCAITGCTAGCTITITCTGTGTTGGTGTGTGTAAA 	GTCCCCTGAGATAGCTGGTCATTC 	TGGCCCCCCAAAATGCCTAACCCAG 	CATCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGG 	HOHOOOO KOOK KHOOOHHOOOOK KOHOHOOOKOH
GTCACTGCCTATATGGTGTCTG	CACAGGTAGTATTGACAAGAGCGACTTGGC 	TTGGGGTGGAGGCCTGCCTCACTGG 	CTGCCGGGCTGGCCACTTTCTGTTGTCTCT 	CTGTGCTGCTGAGGTGCGTAGCTG 	CTCCTCTCTCCCCAGTCTCTAGGCTGCTGACTGGAGGCTTT 	TGGACTTATACAGGGGGGGGCAGAAGGCTCCATGCACTGGAATG 	SCTCAGGGTTAACAGCTAGCCT 	GAATAAACTCAGTCACCTGGT 	TGTAGCTCTTGCATGGGAGTTT 	AACATATGACTTATTTGTAGGGGAAGAGTC(AACATATGAAAGTTATTTGTAGGGGAAGAGTC	CCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCT(GTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGACACAGCAT" 	ACAAAGTAGAAGGGAATCCAT7 	GGGTAGGGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTV 	GATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGGCCC 	CTACTCATCCCAAATGATAATT 	GAAGGAAGGTAGAGGGTGGGGCTTCAGGTC
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CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SECTION NOS: 982
LENGTH: 6976
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Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Carick, Michael S.
APPLICANT: Carick, Thomas S.
APPLICANT: Carick, Thomas S.
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Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
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; ORGANISM: Homo sapiens
US-09-895-793-705
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Sequence 705, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION:
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Harlocker, Susan L.
Jiang, Yuqiu
Kalos, Michael D.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer I
APPLICANT: Harlocker, Susan L
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marce W.
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                                                 APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 705
                                                                                                                                                                                                                                                                                                                        Length 6976;
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        Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
Li, Samuel X.
Wang, Aljun
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GAAACTCAGGAGCACCCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGTTTA
                     AGTGCCGTTTGCAATAATGTCGTCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAA
                               DB 10; Length 6976;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
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Pred. No. 0;
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan·L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Vedvick, Thomas
Carter, Darrick
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; ORGANISM: Homo sapiens
US-09-759-143-705
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Matches 1841; Conserv
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                                                                                         CTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCAACTTTC
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APPLICANT: Houghton, Patricia D.
APPLICANT: Houghton, RAPMond L.
TITLE OF INVENTION: CORPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 3.0
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CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.6
SEQ ID NO 705
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 705, Application US/09780669 Patent No. US20020051977A1 GENERAL INFORMATION:
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Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
Wang, Aljun
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Dillon, Davin C.
Mitcham, Jennifer L.
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Jiang, Yuqui
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Hepler, William
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ORGANISM: Homo sapiens
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Score 1815.8;
Pred. No. 0;
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Query Match 53.2
Best Local Similarity 98.7
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APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.53421
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
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Patent No. US20020081680A1
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Best Local Similarity 98.7%;
Matches 1841; Conservative
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SEQ ID NO
FastSEQ 1
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         SOFTWARE: FastS
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oy Db	2488 GGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCCTCTTACCTTTATCA 2547	
δy Db	2548 GGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGACACAGGCATTTAAATATTAA 2607 	
Qy Db	2608 CTTATTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGGTCTAA 2667 	
Qy Db	2668 TATTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGG 2727 	<u>. </u>
Qy Db	2728 CTGATCATTGCCAGAATCTTCTCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGG 2787	
Qy Dp	2788 ACCTIGGAAATICTACTCATCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGG 2847 	, <u>-</u>
Qy Db	2848 IGTIGAAGGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCT 2907 	0
Qy Db	2908 TCTCTTGGCCCAGCCTGGTTCCCCCCACTCCACTCCCTCTACTCTCTAGGACTGG 2967	
Qy Db	2968 CTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCAACTTTCCCCTACCCCCAACTTTC 3027 	
Qy Db	3028 CCCACCAGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTT 3087 	
Qy Db	3088 TCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACA 3147	
oy Oy	3148 GAAACTCAGGAGCACCCCTGCCTGAGGAGGTCTTATCTCTCAGGGGGGGTTTA 3207 	
Oy Dp	3208 AGTGCCGTTTGCAATAATGTCGTCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAA 3267 	
Qy Db	3268 GIGAGCAATCAGAGTATAATGTTTATGGTGACAAAATTAAAGGCTTTCTTATATGTTTAA 3327 	
م م	3328 AAAAA 3332 6972 aaaaa 6976	
3	160 AAAAA 0316	

Sequence 851, Application US/10012896 Publication No. US20020183251A1 GENERAL INFORMATION:

US-10-012-896-851

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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Mandaleline Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION UNBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                             Houghton, Raymond L.
Vinals de Bassols, Carlota
: Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqiu
Kaloo, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Patricia D.
                                                                                                                                          Li, Samuel X.
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: LENGTH: 1203
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-012-896-851
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
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Hepler, William T.
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Vedvick, Thomas S
Carter, Darrick
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Pred. No. 4.5e-142;
0; Mismatches 4; Indels 0;
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CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ 1D ATE: 2001-06-29
SOFTWARE: FASTSED 6-
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Publication No. US20020192763A1
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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Wang, Aljun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Patricia D.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY, TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER FILE REPRENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FASTSEQ for Windows Version 3.0
LENGTH: 1203
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                       23.3%; Score 794.6; DB 9; 99.5%; Pred. No. 4.5e-142; ive 0; Mismatches 4;
                                      Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
Fanger, Gary R.
            Hural, John
McNeill, Patricia D.
Henderson, Robert A.
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Best Local Similarity 99.5'
Matches 797; Conservative
                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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                        APPLICANT:
APPLICANT:
APPLICANT:
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Jecant: Skeiky, Yasin

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C23

CURRENT APPLICATION NUMBER: US/09/759,143

CURRENT FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSEQ for """

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                                                   1159 CACGGATTTCGTGGGCGAGGG 1179
                                                                     ; Sequence 851, Application US/09759143; Patent No. US20020022248A1; GENERAL INFORMATION:
                                                                                                                                                                                                                             Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
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Retter, Marc W.
Stolk, John A.
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Matches 797; Conservative
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US-09-759-143-851
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US-09-759-143-851
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942 AGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCAGCAGCAGGGGT
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                GGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGGAAGTGGGGGGTAGAGAAGTT
                                                               CATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGG
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                                                                                                                                                                                           Sequence 851, Application US/09822827

Patent No. US/20020081680A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1

CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT APPLICATION DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-822-827-851.
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     762 GGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGG 821
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                                    CTGCCTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTACCT
                                                     859 GGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCTTCCTCACCTGCGTAGC
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APPLICANT: HILCHARM, CHILLEL D.
APPLICANT: Harlocker, Saban L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Hepler, William
APPLICANT: Houghten, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND APPLICANT: HOUGHTEN, RANGONGSIS OF PROSTATE CANCER
FILE OF INVENTION: LIAGNOSIS OF PROSTATE CANCER
FILE OF INVENTION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
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Pred. No. 4.5e-142;
); Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 851, Application US/09780669; Patent No. US20020051977al; GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.; APPLICANT: Harlocker, Senafer L.; APPLICANT: Harlocker, Susan L.; APPLICANT: Jiang, Yuqui
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
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99.5%;
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Matches 797; Conservative
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US-09-780-669-851
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                                                               GTCGGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAA 1061
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                                                 Gaps
                              DB 10; Length 1203;
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                                                Indels
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
                          Score 794.6; DB 10
Pred. No. 4.5e-142;
0; Mismatches 4;
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                           Query Match 23.3%;
Best Local Similarity 99.5%;
Matches 797; Conservative
ORGANISM: Homo saptens
; ORGANISM: noun
US-09-822-827-851
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TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR UFFILE REFERENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232,880
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SEGTWARE: PASLESQ FOR WINDOWS VERSION 3.0
LENGTH: 789
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94.2%; Pred. No. 4.8e-119;
vative 0; Mismatches 40;
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                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C
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                                                                                                                                                                                 ORGANISM: Homo sapien FEATURE:
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Best Local Simi
Matches 745;
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                                       1641 IGCICCCACCICCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGGG 1700
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
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Vinals de Bassols, Carlota
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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Hepler, William T.
Henderson, Robert A.
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McNeill, Patricia D.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Kalos, Michael D.
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Li, Samuel X.
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LOCATION: 9, 380, 451, 565, 582, 716, 718, 758, 762, 765, 768, 771,
LOCATION: 779, 778, 779, 779
OTHER INFORMATION: n = A,T,C or G
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.7%; Score 673.4; DB 9; Length 789; 94.2%; Pred. No. 4.8e-119; tive 0; Mismatches 40; Indels 6
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CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
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Vinals de Bassols, Carlota
                                                                                                                           Sequence 10, Application US/10012896
Publication No. US20020183251A1
                                                                                                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Jiang, Yudiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
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Hural, John
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Hepler, William T.
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        778 TNGGGNGTTCC 788
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ORGANISM: Homo sapiens
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                                                   : NAME/KEY: misc_feature
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US-09-895-793-10
                                                                                                      Query Match
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Matches 745; Conservative
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                    TYPE: DNA
ORGANISM: Homo sapien
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Search completed: June 9, 2003, 22:23:03 to time: 609 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                OM nucleic - protein search, using frame_plus_n2p model
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(without alignments) 10628.880 Million cell updates/sec 9, 2003, 19:43:44; Search time 85.5 Seconds US-09-759-143-110 June Perfect score: Run on: Title:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table: Sequence:

908470 segs, 133250620 residues Searched:

1816940 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Match 100% Post-processing: Minimum Match 0% Maximum

Command line parameters:

-MODEL=frame+ n2p.model -DEV*xlp -Q=/cgn2_1/USPTO_spool/US09759143/runat_05062003_111318_23032/app_query.fasta_1.3591 -Q=/cgn2_1/USPTO_spool/US09759143/runat_05062003_111318_23032/app_query.fasta_1.3591 -DB=A_Geneseq_101002 -OFMT=fastan -SUFFIX=rag -WINMATCH=0.1 -LOOPCL=0 -LIST=45 -DOOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MI=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -USFR=US09759413_GCN_1_119_grunat_05062003_111318_23032 -NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES—0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPOP=6

Database :

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986 DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:* /gcgdata/geneseq/geneseqp-embl/AA1989.DAT: DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT /SIDS2/gcgdata/geneseq/genesegqp-emb1/AA1983.DAT: /SIDS2/gcgdata/geneseq/genesegqp-emb1/AA1984.DAT: IDS2/gcgdata/geneseg/genesegp-emb1/AA1990. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000. /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2001. /gcgdata/geneseg/genesegp-emb1/AA1991 /gcgdata/geneseg/genesegp-embl/AA1996 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997 /gcgdata/geneseq/genesegp-embl/AA1999 /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1993 /gcgdata/geneseg/genesegp-emb1/AA1995 /gcgdata/geneseq/geneseqp-embl/AA1992 /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1981. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982 A_Geneseq_101002:* /SIDS2 /SIDS2 /SIDS2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AAW71869 standard; Protein; 553 AA (first entry) 06-JAN-1999 AAW71869; RESULT 1 AAW71869

ALIGNMENTS

Prostate; cancer; tumour; vaccine; immunogen; clone Amino acid encoded by prostate tumour clone L1-12.

Homo sapiens.

409837093-A2

27-AUG-1998

98WO-US03492. 25-FEB-1998;

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The present sequence is an immunogenic portion of a prostate tumour protein. The immunogen, or the DNA encoding it, can be used as a vaccine for the treatment of prostate cancer. The immunogen was isolated from a prostate tumour cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.
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                                                                                                                                                                                                                                                                                                                                                                        This sequence is encoded by a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting approstate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as this protein sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat proceate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragments - useful
                                                                                                                Prostate tumour specific gene; human; prostate cancer; detection;
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                                                                                             Prostate tumour specific gene clone L1-12 protein.
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                                      AAW69385 standard; Protein; 553 AA.
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Best Local Similarity:
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Pred. No.:
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             61 ProvalLeuGlyLeuValCysValProLeuElySerAlaSerAspHisTrpArgGly
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Seguence

421 AlaSerSerGluAspSerLeumethHrSarPheLeuProGlyProLysProGlyAlable 421 AlaSerSerGluAspSerLeumethHrSarPheLeuProGlyProLysProGlyAlable 434 PheProAssGlyHisYalGlyAlaGlySerGlyProLysProGlyProLysProGlyAlable 441 PheProAssGlyHisYalGlyAlaGlySerGlyLeuLauProProProProAlable 464 TocoGGGCCTTCCCGCCCTCCCTCCTCCTCCTCCTCCTCCTCCT
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321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu
                                                      304 GTCATGGACCGCCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA
                                                                                     GCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT
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                                                                                                                                                          Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
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                                                                                                                                                                                                                                                                                                                                                                           GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
                                                                                                                                                                                                                                                                                                                                                                                    protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunogenic; cytostatic; vaccine.
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immunogenic portion of a prostate tumour profein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polypeptides can be used as probe or to modulate the expression of the polypeptides. AAA06241 to AAA06391 and AAV82000 to AAX82020 represent sequences used in the exemplification of
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                                                                                                                                                                                           New polypeptide useful for treating and diagnosing prostate cancer comprises an immunogenic portion of prostate tumor protein \,
                                                                                                                                                                                                                                                                      The present invention describes isolated polypeptides, comprising
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                                                                                                                                    Yuqin J,
98US-0116134.
98US-0159812.
98US-0159822.
99US-0232149.
99US-0232880.
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                                                                                                                                   Dillon DC, Harlocker
                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
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Best Local Similarity:
14-JUL-1998;
23-SEP-1998;
23-SEP-1998;
15-JAN-1999;
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544 GAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCCAGGTGTGCTTC

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prostate cancer -
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ck TS, Carter D;
on RA;
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	1361 AlaPheProvalAlaGlyAlaThrCysLeuSerHisServalAlaValThrIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400 Qy 1484 TCCTCTACCACGGGAGAGAGAGAGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGT 1543 L	1544 GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 160	1604 TTCCCTAATGAACACGTGGTGGTGGAGCCAGTGGCCTCCTCCACCTCCACCTCCGGCTC 166	1664 TGCGGGCCTCTGCCTGTGATGTTCCCTACGTGGTGGGTGAGCCCACCGAGGCC 172 	OY 1724 AGGGGGGCGGGGGATCTGCCTGGACCTCGCCATCTGGATAGTGCCTTCTG 1783	1784 CTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 184	1844 ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCA		30L 304	AAU04961; 24-OCT-2001 (first entry)	Human prost Human; pros	HOM US6	17-JUL-2001. 25-FEB-1998; 98US	B-1997; G-1997; B-1998;	PA (CORI-) CORIXA CORP. XX
Score: 2861.00 Matches: 553 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 44.58% Indels: 0 DB: 22 Gaps: 0 US-09-759-143-110 (1-3410) x AAU69763 (1-553)	284 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGAAAGCCCAGCTCTTGCTG 343	21 ValAsnLeuthrPheGlyLeuGluValCysLeuAlaAlaGlyleThrTyrValPro 40 4 CCTCTGCTGGAAGTGGGGGTAGAGAGTTCATGACCATGGTGGCTGGGCATTGGT 463 41 ProfesionGlyValGl	CCAGTGCTGGGCCTGGTCTGCCCCCTCCTAGGCTCAGCCAGTGACCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	524 CGCTATGGCCGCGCGCCCTTCATCTGGCACTGTCCTTGGGCATCCTGCTGAGCCTC 583	584 TITCICAICCCAAGGCCGGCTGGCTACAGGGCTGCTGCTGCCGGATCCCAGGCCCTG 643	644 GAGCTGGCACTGCTCATCCTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGTGCTTC 703 111111111111111111111111111111111111	ACTCCACTGGAGGCCTGCTCTCACCTCTTCCGGGACCCGGACCACTGTCGCCGGCCCTGTTTTTTTT	764 TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGTGCCTGGGCTACCTGCCTG	824 ATTGACTGGGACACCAGGCCCTGGCCCTGGGCACCCAGGAGGAGTGCCTCTT 883	884 GGCCTGCTCACCCTCATCTTCCTCACCIGCGTAGCACCACCACTGCTGGTGGCTGAGGAG 943	944 GCAGCGCTGGGCCCCACCAGCAGCAGAGAGGGCTGTCGGCCCCTCCTTGTCGCCCCAC 1003 1111111111111111111111111111111111	1004 TGCTGTCCATGCCGGCCCGCTTGCCGGAACCTGGGCGCCCTGCTTGCCGGGTG 1063	1064 CACCAGCTGTGCTGCCGCATGCCCGCCCCGCGCTCTTGTGGGCTGAGCTGTGC 1123	1124 AGCTGGATGGCACTCATGACGTTTTACACGGATTTCGTGGCGAGGGCTG 1183	1184 TACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGC 1243 	1244 GTTCGGATGGGCAGCCTGGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTCTCTTCTTCTCTG 1303

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                                                                               s sequence is a partial prostate tumour protein, encoded by a mour specific cDNa. The DNa is useful for inhibiting the devel prostate cancer or for treating prostate cancer in a patient.
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Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                            New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and
                                                                                                                                                                                                                                                                      Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW;
                                            prostate cancer; prostate-specific; diagnosis; vaccine;
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              Human prostate-specific amino acid sequence L1-12
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                                                          cytostatic; gene therapy; metastasis
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Kalos MD, Fanger GR, Day CH,
Wang A, Meagher MJ;
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                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
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chromosome 11p13; zinc finger transcription factor.
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                                          GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA
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Polypeptide comprising part of the Wilm's Tumour gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WTI \,
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                                                                                                                                                                                                                                     and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a polypeptide described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 AIGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTG
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AAB74800 standard; Protein; 553 AA

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                                                                                                                                                                                                                                                                     CACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGC 1123
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                                                                                                                944 GCAGCGCTGGGCCCCACCAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCAC 1.003
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                                                        181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 AlaSerSerGluAspSerLeuMetThr:SerPheLeuProGlyProLysProGlyAlaPro
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                                                                                                                                                                                             TGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG
                                                                                                                                                                                                                                   241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. AANU02422 to AAN12872, AAB74798 to AAN74821 and AAN14830 are sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer \boldsymbol{\cdot}
                                                                                            Human; prostate tumour antigen; prostate tumour; therapy; diagnosis; prostate cancer; immunogenic; cytostatic; vaccine.
                                                            Prostate tumour antigen predicted amino acid sequence for L1-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 157-158; 276pp; English.
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                                                                                                                                                                                                                                              04-OCT-2000; 2000WO-US27464.
                               14-JUN-2001 (first entry)
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N-PSDB; AAH02530.
                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP
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                                                                                                                                                                               WO200125272-A2.
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                                                                                                                                                  Homo sapiens.
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AAB74800;
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CTGGTCTGTGTC 	CGCCGCCCTTC	ProPh	11111 G1yTr	CTGGG	CCCTGCTCTCT	lllllllll	CCTTCATGATC	CCAGTGCCCTG		TCATCTTCCTC	eullepheLeu	GCCCACCAGCAGCAGAA	roThrGluPro	11111	rgAlaArgLeu	GCCGCATGCCC	ysArgMetPro	TCATGACCTTC	euMetThrPhe	CCAGAGCTGAG	roArgAlaGlu	SCCTGGGGCTG!	erLeuGlyLeu	rGGTGCAGCGA'	euValGlnArg	GGCTGCCGGTGCCACATGCC	laAlaGlyAla	CGGGTTCACC	ırGlyPheThri	3GGAGAAGCAG(
CAGTGCTGGGCC 	TATGGCCGC	TCCCA		AGCTGGCACTGCTCATC	CACI	ThrProLeuGluAla	TACTCTGTCTATGC	CIC	ASPT	GGCCTGCTCACCC	- 遺	GCAGCGCTGGGCC	la Le uG	GCTGTCCATGCCGC	sCysProCysA	() —	isGlnLeuCysC	CTGGATGGCAC	erTrpWetAlaLeuWetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLe	PACCAGGGGGTGC	31n	TTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCAT	lArgMetGlyS	GTCATGGACCGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGG	lMetAspargL	CTTTCCCTGTGG	Prova	CAGCCGCCTCACCGG	галамдарешт	CCCTCTACCACC(
464 CC P1	524 CGC	81 AJ 584 TJ	01	644 GP	04 A	-	764 TF	24	8	884 GG	201 G1	44	21	T 7	241 Cy	064 CA	261 ні	124 AG	281 Se	84 T	01 I	44 G –	21	04	41	64	61 A	24 2		84 T 01 S
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                                           1604 TTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGGGGTC 1663
                                                                                        1784 CTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
1544 GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
                                                                                                                                                                                                                             1844 ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903
                                                                      460
            Human; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity
                                                        1724 AGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG
                                                                                                                                                                                            Human mast cell related splice variant protein MC14 SEQ ID NO 13.
                                                                                                                                                                                                                                                                         1904 GTAGTATTTGACAAGAGGGACTTGGCCAAATACTCAGCG 1942
                                                                                                                                                                                                                                                                                     541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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                                                                                                                                                                                                                                                                                                                                          ABB77575 standard; Protein; 553 AA.
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14-MAR-2001; 2001US-275479P.
28-MAR-2001; 2001US-279115P.
02-APR-2001; 2001US-280143P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-2001; 2001WO-US46180
                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-2002 (first entry)
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The invention relates to isolated nucleic acid (ABNB1319-ABNB1324), corresponding to genes differentially expressed in mast cells following activation or in patients with allergic hypersensitivity disease, (I) that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of (II) if at least 6 amino acids. (II) is useful for identifying binding

partities. (1) to (1) is useful to unaquesting of tracturing actimus. (2) cate (e.g. allergic hypersensitivity, acasonal thinitis, asthma, urticaria or atopic dermatitis or mastocytosis) in a subject which involves determining the level of expression of (1) or (11). A computer system, comprising a database containing information identifying the expression level in a tissue or at least one mast cell of (1), is useful for presenting information to identify the relative expression level of (1). (11) is used as a marker to dentify the relative expression level of (1). (11) is used as a marker to defect of alleques or it and allergic response in a patient. The protein can also serve as a target that modulate gene expression or activity and as an antigen to raise polyclonal or monoclonal antibodies. (11) is useful for identifying agents that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as agents beloageal activity and function of (11) and thus are useful for for alleviating disease conditions such as allergic hypersensitivity, seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis. treating a disease (II) is useful for diagnosing or 8888888888888888888

553 AA;

GGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG GAGCTGGCACTGCTCATCCTGGGCGTGCTGCTGGACTTCTGTGGCCAGGTGTGCTTC ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCGGCACCGGAAAGCCCCAGCTCTTGCTG 344 GICAACCIGCIAACCITIGGCCIGGAGGIGIGIIIIGGCCGCAGGCAICACCIAIGIGCCG CCTCTGCTGCTGCAAGTGGGGGTAGAGGAGATTCATGACCATGGTGCTGGGCATTGGT CCAGTGCTGGGCCTGGTCTGTGTCCCGCTCTAGGCTCAGCCAGTGACCACTGGCGTGGA ProvalLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly CGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTC TTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTG ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC ATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT 553 00 00 00 Matches: Conservative: Mismatches: Length: Indels: Gaps: (1-553)US-09-759-143-110 (1-3410) x ABB77575 2.89e-208 2861.00 100.008 100.008 Similarity: Percent Similarity: Alignment Scores: 21 104 81 644 704 141 764 161 284 41 464 61 524 584 101 884 201 Query Match: Best Local Score: q g QC q à δ Q ò ò ò à ò g ò QQ ò Db ŏ Dp ò g

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1483 1723 1843 1123 1243 1303 1363 1423 1543 AGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1783 ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903 AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTG 1183 GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603 440 TICCCIAATGGACACGIGGTGCIGGAGGCAGTGGCCTGCICCCACCTCCACCCCCCCCCTC 1663 480 500 GCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTTGTCGCCCCAC 1003 380 420 400 460 ThralaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540 300 320 340 360 260 CTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC TACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGC GTTCGGATGGGCAGCCTGGTGCTGTTCCTGCAGTGCGCCATCTCCCTGGTTCTCTCTG GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA GCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT TCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1484 TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTT AlaserSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro TGCGGGGCCTCTGCGTGATGTCTCCGTACGTGGTGGTGGTGGCTGACCCACCGAGGCC TGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG CACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCGGCTCTTCGTGGCTGAGCTGTGC GTAGTATTTGACAAGAGGGACTTGGCCAAATACTCAGCG 1942 553 ABG61900 standard; Protein; 553 1724 481 1784 521 421 1664 1844 501 541 1544 1604 944 221 1004 241 1064 261 1124 281 1184 301 1244 321 1304 1364 1424 381 RESULT 12 ABG61900 QQ qq q δλ qq ολ q ò q δ q QQ QQ qq g δ à Ω δ δ ò Ω ò qq 염 οy q ò g QΥ qq οy ò

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The present invention relates to methods of detecting a prostate
cancer-associated transcript in a cell from a patient. The method
comprises contacting a blological sample from the patient with
comprises contacting a blological sample from the patient with
prostate cancer-associated polynucleotides (designated PC genes) that
co them. The prostate cancer-associated polynucleotide sequences
to them. The prostate cancer-associated polynucleotide sequences
corporate cancer and are derived from the tissues of various
prostate cancer and are derived from the tissues of various
organisms such as humans or other mammals (e.g. mice, sheep and dogs).
The methods of the invention are useful for diagnosing and treating
prostate cancer in mammals. The prostate cancer associated genes are
useful for diagnosing or treating prostate cancer, as well as for
identifying modulators of prostate cancer or agents that inhibit
prostate cancer. The nucleic acid sequences are particularly useful
constate cancer. The nucleic acid sequences are particularly useful
constate cancer associated proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue
                                                                                     Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mack DH, Wilson KE, Afar D, Hevezi P;
                                                    Prostate cancer-associated protein #101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; Page 386; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                2000US-0687576.
2000US-0733288.
2000US-0733742.
2001US-263957P.
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2001US-281922P.
                                                                                                                                                                                                                                                                                                                                                                                     24-APR-2001; 2001US-286214P.
30-APR-2001; 2001US-0847046.
04-MAY-2001; 2001US-288589P.
                                                                                                                                                                                                                             12-OCT-2001; 2001WO-US32045
                                                                                                                                                                                                                                                                                                                                     2001US-276791P
                15-AUG-2002 (first entry)
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N-PSDB; ABK92217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 553 AA;
                                                                                                                                                          WO200230268-A2.
                                                                                                                                                                                                                                                                                                                                                                      06-APR-2001;
                                                                                                                                                                                                                                                                                                                                     16-MAR-2001:
                                                                                                                                                                                                                                                                                                                                                    16-MAR-2001;
                                                                                                                                                                                                                                                              13-OCT-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                    24-JAN-2001;
                                                                                                                                                                                                                                                                                                 08-DEC-2000;
                                                                                                                                                                                               18-APR-2002
                                                                                                                        Mammalia.
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US-09-759-143-110 (1-3410) x ABG61900 (1-553)

Qy Db	344	GTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCGGGGCATCACCTATGTGCCG 403
Qy	404	CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGTTCATGACCATGGTGCTGGCATTGGT
Dp	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 6
Oy Db	464	CCAGTGCTGGGCCTGGTCT
δλ δ		CGCTATGCCCGCCGCCGCCCTTCATCTGGCCACTGTCGTTGGGCATCCTGCTGAGCCTC 58
20 '	ρi.	ArgıyrulyargargargProPhellefrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 1
oy Db	584	TTTCTCATCCCAAGGCCGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTG 643
Qy Db	644	CCTGGGCGTGGGGCTG
oy Jb	704	FGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC 76
3 8		rronementaleureureuserAspieurheargaspiroasphisCysArgGlnAla 16
qa	اف ا	Articlarication and the state of the state o
Qy	824	TTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCCAGGAGGAGTGCCTCTTF 88
DP	181	
oy d	ထဲ င	TAGCAGCCACACTGCTGGTGGCTGAGGAG
an	0	yLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 22
Qy Db	944	GCAGCGCTGGGCCCCACCGAGCCAGCAGAGAGGCTGTCGCCCCCTCTTGTCGCCCCAC 1003
Οy	1004	GCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGGTG 10
QQ	241	9
, o _y	1064	GGCATGCCCGCACCCTGCGCCGCTCTTCGTGGCCTGAGCTGTG
Db	261	isGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 28
QV DP	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGGCGAGGGCTG 1183
QY	1184	PAGGGCGTGCCCAGAGCTGAGCCGGGCACCAGAGACACTATGATGAAGGC 12
qq	301	20
Οy	1244	16GGCAGCCTGGGGCTGTTCTGCAGTGCGCCATCTCCCTGGTCTTCTCTG 13
qq	321	alArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 3
Qy	Õ	IGGTGCAGCATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA
qq		alMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 36
Qy Dp	1364	"ACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT
Qy	Ñ	CAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 14

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(HEPL/) H
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                                                                                                                                                                                 1784 CTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
                                                                                                                                                                                                              1844 ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903
                                                                                     TTCCCTAATGGACACGTGGTGCTGGACGCAGTGGCCTGCTCCCACCTCCACCGCGCTC 1663
                                                                                                                   1664 receesescretecergrearstreceraceraresesses and 1723
                                                                                                                                                  1724 AGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1783
                                                      GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC:1603
                                                                                                                                                                                                                              540
                      TCCCTCTACCACCGGGGAGAGCAGGTGTTCCTGCCCAAATACCGGGGGGACACTGGGGGT 1543
                                                                                              421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                                                                                                                                                              1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
                                                                                                                                                                                                                                                     ABB95222 standard; Protein; 553 AA.
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20000S-0570737.
20000S-0593793.
20000S-0605783.
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98US-0020956.
98US-0030607.
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2000US-0536857.
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98US-0159812.
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13-JUN-2000;
27-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                  gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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18-NOV-1999;
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CCAGTGCTGGGCCTGGTCTGTGCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGG 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlylleThrTyrValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGT
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, SR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; SEQ ID NO 113; 87pp; English.
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2861.00
100.00%
100.00%
44.58%
10-AUG-2000; 2000US-0636215.
29-AUG-2000; 2000US-0651236.
06-SEP-2000; 2000US-0657279.
02-OCT-2000; 2000US-0693426.
10-OCT-2000; 2000US-0685166.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
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                                                                                                                                                              MITCHAM J L.
HARLOCKER S
                                                                                                                                           DILLON D C.
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Best Local Similarity:
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GCAGCGCTGGGCCCCACCGAGCCAGCAGGGCTGTCGGCCCCCTCCTTGTCGCCCCAC 1003 1004 recreteccargecegecegerreceraacergegececergerrecegeerg 1063 CACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGC 1123 GTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTG 1303 AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTG 1183 TACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGC 1243 GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCA 1363 1543 1603 1364 GCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT 1423 TCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483 TTCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGGGGGTC 1663 1664 TGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAGGCC 1723 703 763 823 180 883 200 94.3 360 400 460 380 TTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGTGCCCGGATCCCAAGGCCCCTG 884 GGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG GAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCCAGGTGTGCTTC ATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCCAGGAGGAGTGCCTTTT ACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGT 1544 GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 584 644 704 764 201 944 221 1124 1184 1244 321 1304 1424 1484 1604 824 261 281 301 361 381 401 421 δ g ò g ò q g οy ð g ò g g 8 g ò ò ò ò g ò Q ò g ò g δ οp ò q g ŏ δy g ò g

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The invention relates to an isolated PROST 03 polypeptide (I) and to the polynuclectide (II) encoding PROST 03. Fragments of (I) were used to generate antibodies (III) to PROST 03. (III) is useful for selectively destroying a cell expressing (I), and for treating a disease-state associated with expression of PROST 03 in a human patient. (III) is useful for diagnosing metastasis associated with (I), in a subject. (I) is also useful for diagnosing metastasis associated with (I), in a subject. (I) is also useful for diagnosing and treating diseases of cell proliferation such as prostate cancers. (I) is also useful for generating antibodies to PROST 03. (III) is useful in detecting the levels of PROST 03 containing cells. (II) is useful in diagnostic response to PROST 03 containing cells. (II) is useful in diagnostic assays for detecting the levels of polynucleotides encoding PROST 03 in cells and tissues. (II) is useful as DNA probes, as targets for antisense and ribozyme therapy, and as templates for the production of antisense polynucleotides. (I) and (II) are useful in research, biological,
                                                                                                                           1843
                                                                                                                                                                                          1903
                                                                                                                                                                                                                         540
                      480
                                                                                                                                                                                                        Novel PROST 03 polypeptides and polynucleotides useful in research, diagnosis and therapeutic applications, particularly for use in cancer
                                                                    metastasis; prostate cancer; tumour; immune response;
                                                  1724 AGGGTGGTTCCGGGCCGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG
                                                                                                                                       1844 ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG
                     CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla
                                                                                                                    1784 CTGTCCCAGGTGGCCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC
Steinbrecher R;
                                                                                                                                                                                                                                                      1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-2001; 2001WO-US13323.
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20-APR-2001; 2001US-0200065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkes D,
                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; vaccine
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                                                                                                                                                                                                                                                                                                                    ATTGACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTTTT
                                                                                                                                                284 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTG
                                                                                                                                                           GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCG
                                                                                                                                                                                                                             CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGT
                                                                                                                                                                                                                                                                   CCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGA
                                                                                                                                                                                                                                                                              CGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTC
                                                                                                                                                                                                                                                                                                                                                TTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                      GAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence represents 03.
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Mismatches:
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Matches:
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                                                                                                                              (1-553)
                                                                                                           Gaps:
  clinical and therapeutic purposes. The the amino acid sequence of human PROST
                                                                                                                               US-09-759-143-110 (1-3410) x AAU10324
                                                          2.89e-208
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                                                                                                          GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA 1363
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                                                                GITCGGATGGGCAGCCTGGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTG 1303
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SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
                                           TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
                                                                           1364 GCTTTCCCTGTGGCTGCCGGTGCCATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT
                                                                                                                                                                  TCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC
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                                                                                                                        Human; breast tumour polypeptide; breast cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
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The invention relates to polynucleotides encoding breast tumour polypeptides. The sequences are useful for treating cancer, preferably breast cancer, in a patient or for stimulating an immune response. The polynucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that binds to a breast tumour polypeptide, detecting in the sample an amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient. Sequences AAU82641-AAU82655 represent human breast tumour polypeptides of the invention.
                                                                                                                                                                                                                                                              Polynucleotides encoding breast tumour polypeptides, useful for treating breast cancer or stimulating an immune response -
                                                                                                                                                          Reed SG, Xu J, Dillon DC, Retter MW, Harlocker SL;
                                                                                                                                                                                                                                                                                                                       Claim 2; Page 144-145; 150pp; English.
                                      22-JUN-2000; 2000US-0602877.
12-OCT-2000; 2000US-0687507.
06-FEB-2001; 2001US-0778381.
12-JUN-2001; 2001WO-US19032
                                                                                                                                                                                                WPI; 2002-147792/19.
N-PSDB; ABK29012.
                                                                                                                        (CORI-) CORIXA CORP.
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553 AA; Sequence

0 8 8 7 0	943 220 1003 240	1063 260 1123 280	1183 300 1243	320 1303 340	1363 360	1423	1483	1543	1603	1663 460	1723 480	1783 500	1843
AlaLeuLeuSerAspLeuPheArgAspProAspHisCysAr. SCCTTCATGATCAGGGCTGCCTGGGCTACCTCCT	GGCCTGCTCACCTCATCTTCCTCACCTAGCAGCCACCACTGCTGGTGGCTGAGGAG [TGCTGTCCATGCCGGGCCCGCTTGCCGGAACCTGGCCCCTGCTTCCCCGGCTG	AGCTGGATGCACTCATGACCTTCACGCTGTTTTACAC	Tyrclindlyvalprofighteriordlyprodiation of the control of the cont	GTCATGGACCGGCTGCTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAATTIIIIIIIIII	CCĜGTGCCACATGCCTGTCCCACAGTGTCGC 	4 TCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC	1 TCCCTCTACCACCGGGAGAAQCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT 	4 GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC	4 TTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCACCCGCCGCGCTC	4 TGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGGTG	AGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCTG	CTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC
141 764 161 824 181	884 201 944 221	1004 241 1064 261		301 1244 321	1304	1364	1424	1484	1544	1604	1664	1724	1784
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ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903
           The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or lis variant. (I) have extostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendrittc cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. AMH02422 to AAH2872, AAB74798 to AAN174821 and AAB74830 are sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer \cdot
                                                                                                                                                                                                               prostate tumour antigen; prostate tumour; therapy; diagnosis;
                                                                                                                                                                                        Prostate tumour antigen amino acid sequence for a fusion protein
                                              GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
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                                                                                                                                                                                                                            prostate cancer; immunogenic; cytostatic; vaccine.
                                                             ValValPheAspLysSerAspLeuAlaLysTyrSerAla
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Mismatches:
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Matches:
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Best Local Similarity:
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Tue Jun 10 11:28:19 2003

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CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 1006
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                                                              GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
                                                                                                 TICCCTAATGGACACGIGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGCTC 1663
                                                                                                                                    ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903
TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT
                                    Thioredoxin; ubiquitin; P501S; prostate; tumour; antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                          Thioredoxin-ubiquitin-P501S(aa55-553)-His triple fusion protein.
                                                                                                                                                                                                                                                                                  GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
                                                                                                                                                                                                                                                                                            /label= UBP1_cleavage_site
203..702
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/label= Histidine_tail
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1.109
/label- Thioredoxin
110.125
/label- Linker
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/label= Ubiquitin
201..202
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703.710
                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                          - Homo sapiens
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30-OCT-2000;
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                                                                                                                                                                                                                The present sequence is that of a triple fusion protein comprising, from the N terminal end, Escherichia coli thioredoxin, human ubiquitin and amino acids 55-530 of human prostate antigen P501S, followed by a histidine affainity tail. The triple fusion protein was produced in E. coli G1724 host cells transformed by an expression vector comprising DNA (see ABA91283) encoding the fusion. This is an example of the production of triple fusion proteins of the invention that comprise ubiquitin fused between thioredoxin and a protein of interest, in this case P901S(aa55-553). A claimed method of producing a recombinant protein of interest involves: culturing a host cell (preferably E. coll) under conditions which endoporotease (especially UBP1 from Saccharomyces cerevisiae); and recovering the recombinant protein directly from the bacterial cells after it has been subjected to the action of the ubiquitin-specific endoprotease in vivo. In the present case, the product is a P501-like protein of 509 amino acids. The recombinant protein of 509 amino acids. The
                                                                                                                 Novel DNA sequence encoding triple fusion protein comprising ubiquitin fused between thioredoxin and polypeptide of interest, useful for producing recombinant polypeptide of interest suitable for medicinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 ATGACCATGGTGCTGGCCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGC
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              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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                                           Delisse AEF;
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                                        Cabezon Silva TEV,
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. (I) and the antibodies are also used in vaccines. The antibodies or prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to inprove diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH99337 to AAH99944 and AAM01115 to exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCATCACCTATGTGCCGCCTCTGCTGCTGGAGTGGGGGTAGAGGAGAAGTTCATGACC 445
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YAW;
                                                                                                                                                                                              cancer; prostate-specific; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                        SL, Jiang Y, Reed
, Stolk JA, Skeiky
                                                                                                                                                                  prepro-P501S recombinant protein amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide encoding a prostate-specific protein, diagnosing, monitoring and treating prostate cancer in a for use in vaccines -
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Mismatches:
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                                                                                                                                                                                                              cytostatic; gene therapy; metastasis
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                                                                                   AAM01318 standard; Protein; 595
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GR, Day CH,
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Wang A, Meagher MJ;
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                            ACCTICACGCIGITITACACGGATITCGIGGGCGAGGGGCTGIACCAGGGCGIGCCCAGA 1201
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441 LysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSer 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "translation of the DNA sequence of Figure 12a (ABA91284) places a Val residue between Met-202 and Gln-203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thioredoxin; ubiquitin; P501S; prostate; tumour; antigen; cancer; vaccine; therapy; human.
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by the DNA sequence of
(ABA91284)"
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/label= Ubiquitin
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- Escherichia coli.
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/label= L
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/label= UF
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Nocka K, Pirozzi G,
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02-APR-2001;
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vasotropic;
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                                                                                                                                                                                                   The present sequence is that of a triple fusion protein comprising, from the N-terminal end, Escherichia coli thioredoxin, human ubquittin and amino acids 1-320 of human prostate antigen P501S, followed by a histidine affinity tail. The triple fusion protein was produced in E. coli G1724 host cells transformed by an expression vector comprising DNA (see ABA01284) encoding the fusion. This is an example of the production of triple fusion proteins of the invention that comprise ubjquitin fused between thioredoxin and a protein of interest, in this case F501S(aa55-553). A claimed method of producing a recombinant protein of interest involves: culturing a host cell (preferably E. coli) under conditions which callow co-expression of the triple fusion and a ubjquitin-specific allow co-expression of the triple fusion and a ubiquitin-specific and recovering the recombinant protein directly from the bacterial cells after it has been subjected to the action of the
                                                                                                                        Novel DNA sequence encoding triple fusion protein comprising ubiquitin fused between thioredoxin and polypeptide of interest, useful for producing recombinant polypeptide of interest suitable for medicinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCCAGAGGCTGTGG----GTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTG
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                                                                                                                                                                                                                                                                                                                                                                            ubiquitin specific endoprotease in vivo. In the present case, expression was controlled by addition of tryptophan. The recombinant protein can used as a vaccine for cancer therapy.
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                                           (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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                                                                   Delisse AEF;
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1677.50
99.69%
99.38%
         26-JUN-2000; 2000GB-0015619.
30-OCT-2000; 2000GB-0026484.
                                                                                        2002-147888/19.
                                                                  Cabezon Silva TEV,
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                                                                                                    N-PSDB; ABA91284
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1064 CACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGC 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  884 GGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG
                                                                                                                                                                                                                                                                                                                    824 ATTGACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT
                                                                           ACTICCACTGGAGGCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTGGCCAGGCC
                                                                                                                                                  Human mast cell related protein MC14-2 SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB77571 standard; Protein; 326 AA.
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2001US-275479P.
2001US-279115P.
2001US-280143P.
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Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity

Claim 31; Page 103-104; 119pp; English.

corresponding to genes differentially expressed in mast cells following activation or in patients with allergic hypersensitivity disease, (1) that encodes protein (ABD7759, (11) or a protein fragment of (11) if at least 6 amino acids. (11) is useful for identifying binding partners. (1) or (11) is useful for diagnosing or treating a disease strines. (1) or (11) is useful for diagnosing or treating a disease strines (e.g. allergic hypersensitivity, seasonal rhinitis, asthma, urticaria or atopic dermatitis or mastocytosis) in a subject which involves determining the level of expression of (1) or (11). A computer system, comprising a database containing information identifying the cypression level in a tissue or at least one mast cell of (1), is useful for presenting information to identify the relative expression level of (1). (11) is used as a marker to detect, diagnose or identify an allergic response in a patient. The protein can also serve as a target that modulate gene expression artitledies. (11) is useful for identifying polyclonal antibodies. (11) is useful for identifying agents that modulate expression of the protein or agents, such as agonists or antagonists. The agonists or antagonists are useful for modulating biological activity and function of (II) and thus are useful for alleviating disease conditions such as allergic hypersensitivity, seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis. invention relates to isolated nucleic acid (ABN81319-ABN81324),

Sequence 326 AA;

ProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyr 135 347 AACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCT 406 GTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGC 526 CCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTAC :::|||:::
SerLeuValProLeuProLeuAlaLeuTyrLeuSerGlnProLeuThrHisThrThrSer TATGGCCGCCGCCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTT CTCATCCCAAGGGCCGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAG CTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGTTCACT TCTGTCTATGCCTTCATGATCAGTCTTSGGGGCTGCCTGGGCTACCTCCTGCCTGCCATT CTGCTGCTGGAAGTGGGGGTAGAGGAGAAAGTTCATGACCATGGTGCTGGGCATTGGTCCA Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-759-143-110 (1-3410) x ABB77571 (1-326) Gaps: 6.64e-107 1522.50 58.85% 57.69% 23.72% Best Local Similarity: Percent Similarity: Alignment Scores: 29 36 527 26 647 96 116 σ 467 587 16 167 407 707 Query Match: DB: .. 02 δ q qq ò В ö 셤 οy qq ογ g ò ŏ g ŏ

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466

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992

Οy	827 G	ACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGG
Db	156 A	
Οy	887 C	CTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCA 946
QQ	176 L	LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluA
Qy	47	Ō
qq	196 A	aLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCy
. Оу	1007 T	STCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCC
Db	216 ¢	ysproc
Qy	1067 C	AGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGC 1126
qq	218 -	218
Οy	1127 T	GGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGGGGGGTGTAC 1186
qq	218 -	218
Qy	1187 C	AGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTT 1246
QQ	218 -	218
οy	1247 C	GGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTC 1306
qq	218 -	218
Qy	1307 A	ATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGTGGCAGCT 1366
qq	218 -	
δy	1367 T	TCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCA 1426
qq	218 -	218
Oy	1427 G	GCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCC 1486
qa	218 -	218
Qy	1487 C	TCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCT 1546
qq	218 -	218
δλ	1547 A	CCAGCTTCCTGCCA
QQ	219 -	Gln-AlaLeuSerLeuGluLeuProS
QY	1607 0	CCTAATGGACACGTGGGTGCTGGAGCAGTGGCCTCCCACCCA
QQ	227 r	IMETASPThrTrpValLeuGluAlaValAlaCysSerHisLeuHisProArgSerA
Qy	1667 G	GGGCCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGGTG
qq	247 a	3]yProLeuProValMetSerProTyrValTrpTrpTrpValSerProProArgProG
QY	1727 G	GIGGIICCGGGCCGGGCCATCTGCCTGGACCTCGCATCCTGGATAGTGCCTTCCTGCTG 1786
qq	267 y	rpPheArgAlaGlyAlaSerAlaTrpThrSerProSerTrpIleValProSerCysC
Qy	1787 T	CCCAGGEGCCCCATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACT 1846
DP	287 \$	ProArgT
ÓΣ	1847 G	GCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGG 1904
QQ	307 u	rolleTrpCysLeuProGlnAlaTrpValTrpSerProPheThrLeuLeuHi

136

qq

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04-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides for antigenic epitopes derived from them, and antigen-presenting cells expressing the polypeptides from them, and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer. Sepecially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The present sequence is a prostate specific for the content of the content 
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|SerLeuValProLeuProLeuAlaLeuTyrLeuSerGlnProLeuThrHisThrThrSer 28
                                                                                                                                                                     Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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                        AA.
                      AAU69875 standard; Protein; 371
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2000US-0636215.
2000US-0651236.
2000US-0657279.
2000US-0657279.
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2000US-0570737
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N-PSDB; AAS64038.
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Best Local Similarity:
                                                                                                                                                                                                                                          WO200173032-A2.
                                                                                                                                                                                                          Homo sapiens
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10-AUG-2000;
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02-OCT-2000;
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947 GCGCTGGGCCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCCACTGC 1006
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                                                                                                                                                            GTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGC
                                                                                       TATGGCCGCCGCCGCCCTTCATCTGGGCACTGCTTGGGCATCCTGCTGAGCCTCTTT
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29 LeuLeu------
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1187 CAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACTATGATGAAGGCGTT 1246
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296 AlaLeu-AlaAlaSerArgGlyTrpCysGlySerArgProProGluThrThrLeuGlyAl
  CTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                         CIGGCACTGCTCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACT
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SerLeuValProLeuProLeuAlaLeuTyrLeuSerGlnProLeuThrHisThrThrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -
                                                                                                                                                                                                                                                                                                                                              Reed SG;
Skeiky YAW;
                                   Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis.
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                                                                                                                                                                                                                                                                                                                                              SL, Jiang ', Stolk JA,
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splice variant P553S-14 amino acid #2.
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Retter MW,
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3R, Day CH,
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                                                                                                                                                                                                                                                                                                                                                                                                                         Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New prostate-specific polynucleotides for diagnosing and treating
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A, Day CH, Vedvick TS,
epler WT, Henderson RA;
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Matches:
Conservative:
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Indels:
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Wang A, Skeiky YAW, Hepler WT,
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                                                                                                  14 -JAN-2000; 2000US-0483672.
27 -MAR-2000; 2000US-0536857.
09 -MAY-2000; 2000US-0568100.
12 -MAY-2000; 2000US-0570737.
13 -UN-2000; 2000US-0570737.
27 -JUN-2000; 2000US-0565125.
28 -AUG-2000; 2000US-0551236.
06 -SEP-2000; 2000US-0657279.
       9805-0020956
9805-0030607
9805-0115453
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HEPLER W T.
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                                                                                                                                                                                                                                                                                              FANGER G R. RETTER M W.
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DILLON D C.
                                                                                                                                                                                                                                                                                                                  STOLK J A.
DAY C H.
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KALOS M D.
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13-JUL-1999;
12-NOV-1999;
                                                                                           .8-NOV-1999;
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Pred. No.:
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                                                   S-JAN-1999
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988

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Human gene 11 encoded secreted protein HWBAR14, SEQ ID NO:84.

(first entry)

18-JUL-2001

AAE01362

347 AACCIGCTAACCTTTGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCGCCT 406

õ g

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SerLeuValProLeuProLeuAlaLeuTyrLeuSerGlnProLeuThrHisThrThrSer

present sequence represents a human secreted protein of

foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; denerosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; anglogenic disorder; kindney disorder; disorder; allergy; pregnancy related disorder; endocrine disorder; allergy; pregnancy related disorder; endocrine disorder; allergy; call culture; chemotaxis; vulnerary; binding partner identification; protein; proliferative disorder; cancer; tumour; therapy Human; foetal gene

Homo sapiens

49..371 /label= Mature_human_secreted_protein 1..48 /label= Signal_peptide Location/Qualifiers Peptide Protein

/label= Unknown /note= "Encoded by TNC" Misc-difference

WO200134629-A1

17-MAY-2001

08-NOV-2000; 2000WO-US30654.

99US-0164835 27-JUL-2000; 2000US-0221142 12-NOV-1999;

(HUMA-) HUMAN GENOME SCI INC

Baker KP; Ruben SM, Komatsoulis GA, Wei P, Fiscella M,

2001-308779/32. N-PSDB; AAD05230

or New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autoimmune disease and cancer, and used as a food additive o preservative

Claim 11; Page 438-440; 490pp; English.

AAD05220-AAD05282 represent cDNAs corresponding to 21 human secreted protein genes, and AAE01352-AAE01413 represent the protein sthey encode. AAE01415-AAE01431 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 21 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, feetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune disorders, cancer, tumours, feetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune disorders, schizophrenia, asthma, skin disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders, pregnancy-related disorders, atherosclerosis, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proteins can also be used to aid wound healing and epithelial cell proteins transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding process. preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., raddoimmunoassay or enzyme linked immunosorbent assay (ELISA).

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Mismatches:
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Query Match:
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307 gProProGluThrThrLeuGlyAlaValSerGly 318

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therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndicme, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzhahmer's, parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG65318 represent albumin fusion proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to albumin fusion proteins comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein \,
                                                                                                                                                                     Albumin fusion protein; therapeutic protein X; human albumin; HA;
                                                                                                                                                                                 human serum albumin, HSA; cancer; reproductive disorder; digestive disorder: immune disorder; endocrine disorder; hadmatopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinfammatory; antiinleer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371
269
9
13
1
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1018-1019; 2102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                              ABG64105 standard; Protein; 371 AA
                                                                                                                                 Human albumin fusion protein #780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2000, 2000US-229358P.
25-APR-2000, 2000US-199384P.
21-DEC-2000, 2000US-256931P.
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1419.00
95.218
92.128
22.118
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                                                                                                                                                                                                                                                                                       osteopathic; antiarthritic.
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA, Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-010886/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                      WO200177137-A1
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                                                                                                 27-AUG-2002
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                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                               ABG64105;
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9
RESULT 25
               ABG64105
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GCCCCCTCCTTGTCGCCCCACTGCTGCATGCCGGGCCCGCTTGCCTTTCCGGAACCTG 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1223 CGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGGCTGTTCCTGCAGTGCGCC 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1102
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                                    562
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                                                                                                                                                       107
                                                                                                                                                                                                                                                                                                                                                                       ACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCG 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 ArgArgHisTyrAspGluGlyLysAlaLeu-AlaAlaSerArgGlyTrpCysGlySerAr 307
SerLeuLeuAlaGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySer 47
                                                          29
                                                                                                       87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate protein/M. tuberculosis Ral2 fusion protein RA12-P501S-E2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate cancer; cytostatic; immunostimulant; tumour; immunogen; protein.
                                               TTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGAC
                                                                                                                                                                                                                                                                                                                         ACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                    1043 GGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCC
                                                                                                                                                                                                                            743 CCGGACCACTGTCGCCAGGCCTACTCTGTTTTGCCTTCATGATCAGTCTTGGGGGGTGC
                                                                                                                                                                                                                                                                            CTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU69907 standard; Protein; 400 AA.
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                                   503
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Chimeric - Homo sapiens

US-09-759-143-110 (1-3410) x ABG64105 (1-371)

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1076 TGCCGCATGCCCCGCACCCTGCGCCGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGCA 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr
                                                                                                                                                                               ACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACC
                                                                                                                                                                                                                                              CCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCTTGTCGCCCCCACTGCTGTCCATGC
                                                                                                                                                                                                                                                                                                                                                                                          1016 CGGGCCCGCTTGGCTTTCCGGAACCTGGCCCCTGCTTCCCCCGGCTGCACCAGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                     347 ArgalaargLeualaPheArgAsnLeuGlyalaLeuLeuProArgLeuHisGlnLeuCys
187 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro
                                                                           CTCATCCTGGGCGTGGGGCTGCTGGTGTGTGCCCAGGTGTGCTTCACTCCACTGGAG
                                                                                                                              GCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCCAGGCCTACTCTGTCTAT
                                                                                                                                                                                                                                                                                    CTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCCTGGGC
                        AGGGCCGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTG
                                      SL, Jiang Y, Reed SG;
, Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate cancer; prostate-specific; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1136 CTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAG 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 LeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlu 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ral2-P501S-E2 construct amino acid sequence.
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Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; gene therapy; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
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Kalos MD, Fanger GR, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JAN-2001; 2001WO-US01574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-2000; 2000US-0483672.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-425873/45
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                        969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the of cancer and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is fusion protein comprising a prostate specific polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCA 595
                                                                                                                                                                                                                                                                                                                                                                 human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                       Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400
267
0
2
5
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Matches:
Conservative:
Mismatches:
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 Chimeric - Microbacterium tuberculosis.
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                                                                                                                                                     20000S-0605783
20000S-0636215
20000S-0651236
20000S-0657279
20000S-0679426
20000S-0685166
                                                                                                                 2000US-0568100.
2000US-0570737.
2000US-0593793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.39e-98
1403.50
97.45%
97.45%
21.87%
                                                                            27-MAR-2001; 2001WO-US09919
                                                                                                                                                                                                                                                                                                                           2001-639232/73.
                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS64153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                          WO200173032-A2
                                                                                                                                                      27-JUN-2000;
10-AUG-2000;
29-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aliqnment Scores:
                                                                                                                                                                                             06-SEP-2000;
                                                                                                                                                                                                                        10-ocT-2000;
                                                                                                     27-MAR-2000;
                                                                                                                   -MAY - 2000;
                                                                                                                              12-MAY-2000;
                                                                                                                                             JUN-2000;
                                                                                                                                                                                                                                                                                       Fanger GR,
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DB:
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266 835 286 895 306 955

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226 655

1075

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New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines.

Claim 8; Page 504-506; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, antibodies to (II), fusion proteins comprising (II), and isolated and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. (I) and the antibodies for monitoring the progression of cancer in a patient. (I) can be used for improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AH1931357 to AH1931944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
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Alignment Scores: 7.39e-98 Length: 400
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 1187% Gaps: 1
DB: 22.87% Gaps: 1

400 AA;

Seguence

US-09-759-143-110 (1-3410) x AAM01262 (1-400)

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CCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCTCCTTGTCGCCCCACTGCTGTCCATGC 1015
                              1016 CGGCCCGCTTGGCTTTCCGGAACCTGGCCCCTGCTTCCCCGGCTGCACCAGCTGTGC 1075
                                                               1076 TGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCA 1135
         cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                CTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAG 1177
                                                                                                         Ral2-P501S-E2 construct SEQ ID NO 852.
                                                                                                                                                                                                                                         Chimeric - Mycobacterium tuberculosis
                                                                                                                                                 AA.
                                                                                                                                                ABB95367 standard; Protein; 400
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2000US-0636215.
2000US-0651236.
2000US-0657279.
2000US-0679426.
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98US-0020956.
98US-0030607.
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98US-0159812.
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2000US-0568100.
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MITCHAM J L.
HARLOCKER S L.
JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
VEDVICK T S.
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09-APR-1999;
13-JUL-1999;
12-NOV-1999;
18-NOV-1999;
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10-AUG-2000;
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(JIAN/)
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(FANG/)
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(CART/)
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(DAYC/)
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                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                     The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                CGCCGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCA
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                                                  Kalos M
Carter
                                                                                                  New prostate-specific polynucleotides for diagnosing and trediseases, in particular prostate cancer, and as markers for progression of cancer
                                                 Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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267
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Mismatches:
Indels:
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Matches:
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1403.50
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LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
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                                                                                   WPI; 2002-255649/30
                                                                                                                                                                                                 400 AA;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as benign prostatic hyperplasia (BPH), prostatitis, prostatic intraepithelial neoplasia (PIN) and cancer. In particular the products can be used in drug screening and gene therapy.
                                                                                                                                                                                                                                                                              307 LeuilePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGly
                                                                          CGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; prostate disease; benign prostatic hyperplasia; BPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostatitis; prostatic intraepithelial neoplasia; PIN; cancer; drug screening; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAG 1177
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Gordon J, Granados EN, Hodges SC, Klass MR, Kratoch
Roberts-Rapp L, Russell JC, Stroupe SD;
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V, Klass MR, Roberts-Rapp L, S
Russell JC, Hodges SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                 Kratochvil JD,
                                                                                                            02-MAY-1997;
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The sequence represents the amino acid sequence of prostate-specific PS108 #1, encoded by PS108 expressed sequence tag (EST) consensus sequence. The sequence was produced from overlapping PS108 ESTs sequences to produce a full length consensus sequence. This sequence was then used to produce the PS108 polypeptide which is useful in assays for detecting antibodies to prostate tissue, and as an immunogen to produce antibodies. The polypeptide is useful for screening compounds which specifically bind to the polypeptide and for screening for drugs, compounds, or any other agent which can be used to treat diseases associated with PS108. The antibody is useful to detect, or for image localisation of, PS108 antigen
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GlualaArqValValProGlyArqGlyIIICHSSEASpLeuAspLeuAlaIIELeuAspSerAla
                                                                                                                                                                           Prostate; PS108; immunogen; drug screening; image localisation; diagnostic; therapeutic; prostate tissue disease; cancer; metastasis; expressed sequence tag; EST.
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Klass MR, Kratochvil JD, Roberts-Rapp L;
Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful in assays for detecting antibodies {\tt immunogens} to produce {\tt PS108} antibodies -
                                                                                                                                                                                                                                                                            ACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
                                                                                                                                                                                                                                                                                            Prostate-specific PS108 polypeptide #1
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97US-0850713.
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N-PSDB; AAS07155.
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prostate tissue,
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02-MAY-1997;
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delivery agents for therapeutic agents as well as for diagnostic tests and for screening for diseases or conditions associated with PS108, especially cancer. The antibody is also useful for generating chimeric antibodies for therapeutic use, for inhibiting the biological activity PS108, in therapy (for e.g. to treat prostate tissue disease including prostate cancer and its metastases), and to detect the presence of any polypeptide in a test sample which shares one or more antigenic determinants with the PS108 polypeptide.
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AAE01423 standard; Protein; 252 AA.
                                                                 AAE01423;
RESULT 32
                 AAE01423
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SEQ ID NO:147. Human secreted protein variant,

(first entry)

18-JUL-2001

Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foctal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia: skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzhaimer's disease; food additive; angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification; gene therapy

Homo sapiens

'note" "Corresponds to any of the naturally occuring naturally occuring naturally occuring naturally occuring the to any of the to any of the оę any ដ /note= "Corresponds L-amino acids" /note= "Corresponds Location/Qualifiers /note= "Corresponds L-amino acids" L-amino acids" L-amino acids" Key Misc-difference Misc-difference Misc-difference Misc-difference

WO200134629-A1

08-NOV-2000; 2000WO-US30654 17-MAY-2001

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12-NOV-1999; 99US-0164835. 27-JUL-2000; 2000US-0221142.

(HUMA-) HUMAN GENOME SCI INC

Baker Fiscella M, Wei P, Komatsoulis GA, Ruben SM,

2001-308779/32

New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autolmmune disease and cancer, and used as a food additive or preservative -

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Disclosure; Page 476-477; 490pp; English.

AAD05220-AAD05282 represent cDNAs corresponding to 21 human secreted protein genes, and AAE01352-AAE01413 represent the proteins they encode. AAE01415-AAE0143 represent thuman secreted proteins they encode. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the 21 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoletic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),

1789

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1730 GTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCC

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1850 TATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTA 1909

1790 CAGGTGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCC

1910 TTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGG 1969

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Mismatches:
Indels:
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Matches:
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21 Phe***LysSerAspLeuAla-AsnThrGlnArgArg-AsnPheGln***IleGlyVal* 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               libraries. The patterns of both gene sets are compared to identify genes of unknown function with similar expression patterns to the prostate cancer-specific genes. The biomolecules identified by the method form pharmaceutical compositions useful for the diagnosis and treatment of diseases associated with cell proliferation. Such diseases include cancer of the adrenal gland, bladder and bone, but especially prostate cancer. The method may also be applied using other diseases specific genes. The prostate cancer-specific genes facilitate the diagnosis and treatment of cell proliferation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "potential casein kinase II phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying biomolecules for the diagnosis and treatment of diseases associated with cell-proliferation {}^{-}
                                                                                                                                                                                                                                                                                 Prostate cancer-associated gene; Incyte clone 1864683; bone cancer; cell proliferation; cancer; adrenal gland cancer; bladder cancer;
                                                                                                                                                                                                                                                   Amino acid sequence of a prostate cancer-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "potential transmembrane domain"
                                                   1970 AGGGCCTGCCTCACTGGGTCCCAGCTCCCCGCTCCTGT 2007
                                                                   240 **GlyLeuProHisTrpValProAlaProCysSerCys 252
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                                                                                                                                                  AAY54369 standard; Protein; 231
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                                                                                                                                                                                                                                                                                                                        prostate cancer.
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                                                                                                            ATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATG 1309
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                                                                                                                       Prostate cancer-associated gene; bone cancer; cell proliferation; cancer; adrenal gland cancer; bladder cancer; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a prostate cancer-associated protein.
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Mismatches:
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          Length:
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                                                                                       US-09-759-143-110 (1-3410) x AAY54369 (1-231)
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          1.01e-78
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Alignment Scores:
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                        Score:
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Homo sapiens

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The prostate cancer associated gene composed cancer associated gene. The prostate cancer associated gene composed to the invention. The specification describes a method for identifying biomolecules for the diagnosis or treatment of diseases associated with cell proliferation. The method comprises examining polynucleotides, consisting of prostate cancer-specific genes, and genes of unknown function, expressed in cDNA libraries. The patterns of both gene sets are compared to identify genes of unknown function with similar expression patterns to the prostate cancer-specific genes. The biomolecules identified by the method form pharmaccutical compositions useful for the diagnosis and treatment of diseases sociated with cell proliferation. Such diseases include cancer of the adrenal gland, bladder and bone, but especially prostate cancer. The method may also be applied using other disease-specific genes. The prostate cancer-specific genes are prostated cancer-specific genes facilitate the diagnosis and treatment of cell proliferation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 AIGGICAIGAACIICTCCICIACCCCCACIICCAGCAGCAGAGGCGGCACAIAGGIGAIG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGGCT 328
                                                                                                                                                                "potential protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 ITCCGGTGCCGCAGCAGCGGCTCACCCACGAGCTTGGACCATAGTGGGGCCAGGCGGGT 268
                                                                                         "potential protein kinase C phosphorylation site"
                                                                                                                            "potential protein kinase C phosphorylation site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is encoded by a prostate cancer-associated gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying blomolecules for the diagnosis and treatment of diseases associated with cell-proliferation \boldsymbol{\cdot}
                                                                                                                                                                                                   "potential CAMP and cGMP dependent protein
kinase phosphorylation site"
                                                                                                                                                                                                                                                      "potential BLOCK signature of Ly-6/u-PAR"
                                                   'note "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sprinzak EA;
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                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 51-52; 52pp; English.
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Domain
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Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foctal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoinmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psorlasis; sepsis; dlabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification;
                                                                                          267 AGGGCTCAGGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAG 208
                                                                                                                                                                                                                 CTGCGGCCTCTCCTTGCTGCTGCCGAACTGCCTAGGAATCAGCCAGGCGCCCATTTCT 148
66
                                                                                                                                                                                                                                                  New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autoimmune disease and cancer, and used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene 11 encoded secreted protein HWBAR14, SEQ ID NO:118.
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27-JUL-2000; 2000US-0221142.
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Tue Jun 10 11:28:19 2003

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AMD05220-AAD05282 represent cDNAs corresponding to 21 human secreted protein genes, and AAE01352-AAE01413 represent the proteins they encode. AAE01413 represent human secreted protein fragments or variants. CC The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. The secreted proteins and their genes are useful for preventing, treating corresponding to on the tissues in which they are most highly expressed, and include the new genes. Specific uses are described for each of the 21 genes. The new genes. Specific uses are described for each of the 21 genes. The new genes. Specific uses are described for each of the 21 genes. The new genes. Specific uses are described for each of the 21 genes. The composition of the diagnosis or treatment of proliferative disorders, diseases of the immune system, AIDS, autoimmune disorders, cancer, theumatoid arthritis), inflammation, allergies, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, conditive disorders (e.g., Alzheimer's disease, Parkinson's disease), conditive disorders, alabetes, atherosclerosis, cardiovascular disorders, pregnancy-related disorders, and disorders, and independent tissues, the dentify disorders, asthmic and also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding carters, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a content the invention can be used in allevatating symptoms associated with the disorders mentioned above, and in diagnostic immunoassay erg, the present sequence represents a human secreted protein of the invention of the invention of the human secreted protein of the invention of the invention of the invention of the invention of the inventi
Claim 11; Page 456-457; 490pp; English.
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129 AA; Seguence

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2974 AAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCCAACTTTCCCCACC 3033
                                                                                                                                                                                                                                                     3034 AGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAA 3093
                                                                                                                                                                                                                                                                                                   3094 GCCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCGTTGGGGAATCTCACACAGAAACT 3153
                                                                                                                                                                                                                                                                                                                                                   3154 CAGGAGCACCCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGTTTAAGTGCC 3213
                                                                                                                                                            GGCCCAGCCTGGTTCCCCCCACTTCCACTCCCCTCTACTCTTCTAGGACTGGGCTGATG 2973
                                                                                                                                                                                                                                                                                                                 1 GlyProAlaTrpPheProProLeuProLeuProSerThrLeuSerArgThrGlyLeuMet 40
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129
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          Length:
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Alignment Scores:
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Query Match:
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RESULT 36

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2854 AGGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCTTT 2913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and disgnosing disorders such as cancer, reproductive disorders, disease, also crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzhaimer's, Parkinson's, Creutzfeldt-Jacob disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to albumin fusion proteins comprising
                                                                                                                                               Albumin fusion protein; therapeutic protein X; human albumin; HA, human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haemactopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion protein for treating disease e.g. diabetes comprises albumin fused to a therapeutic protein -
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1016-1017; 2102pp; English.
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              ABG64102 standard; Protein; 129 AA
                                                                                                                  Human albumin fusion protein #777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2000; 2000US-229358P.
25-APR-2000; 2000US-199384P.
21-DEC-2000; 2000US-256931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2001; 2001WO-US11988
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100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                               WO200177137-A1.
                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                 27-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-2001
                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sedneuce
                                                 ABG64102;
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ABG64102
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599 AA;

Sequence

	LysAlaLeuProLysIleSerProThrProAsnPheProLeuProProThrPheProThr 60 AGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAGTGCGGTTTCCCAA 3093	GCCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAACT 3153 	CAGGAGCACCCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGTTTAAGTGCC 3213 	GTTTGCAATAATGTCGTCTTATTTATT 3240 	lard; Protein; 599 AA.	first entro)	melanogaster polypeptide SEQ ID NO 8919.	developmental biology; cell signalling; insecticide; al.	melanogaster.			2001WO-US09231.	2000US-191637P	P NY.	Adams M, Li PWD, Myers EW;	56860/75. 04812.	ed nucleic acid detection reagent for detecting 1000 or more Drosophila and for elucidating cell signalling and cell-cell ns	SEQ ID NO 8919; 21pp + Sequence Listing; English.	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cellcell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed the specification, but was obtained in electronic format directly from urbo
2314 GCC 21 G1yP 2974 AAGG	41 LysA 3034 AGCT 61 SerS	3094 GCCT 	3154 CAGG 101 GlnG	3214 GTTT 21 Valc	r 37 709 ABB60709 standard	ABB60709; 26-MAR-2002	Drosophila me	Drosophila; de pharmaceutical	Drosophila me	WO200171042-A2	-SEP-2001.	3-MAR-2001;	-MAR-2000;	(PEKE) PE CORP	enter JC, A	WPI; 2001-656860 N-PSDB; ABL04812	New isolated r genes from Dro interactions	Disclosure, SP	The invention relates capable of detecting useful in development cell-cell interaction insecticides, theraped discloses genomic DNA discloses genomic DNA (ABB57737-ABB72072). The sequence data for specification, but was

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977 CTGTCGGCCCCCTCCTTGTCGCCC------ 1000
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                                                                                                                                        317 CGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGTAACCTTTGGCCTGGAGGTGTGT 376
                                                                                                                                                                                                                                                                         146 LeuLeuGlyAspAlaGlyTyrThrTyrAlaGluSerAlaLeuAsnPheThrSerSerSer 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                599 GCCGGCTGGCTAGCAGGGCTGCTGTGC 640
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166 GlyGlySerValAlaAlaLeuValSerGlyGluAlaThrThrGlyProSerAlaSerAsp 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641 CIGGAGCTGGCA-----CTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAG 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 ThrCysGlnThrProAlaArgThrTyrLeuLeuAspMetCys---ValProGluGluGln 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 755 CGCCAGGCCTACTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTC 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 875 TGCCTCTTTGGCCTGCTCACCTGATCTTCCTCACCTGCGTAGCAGCCACACTG---- 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 IleGlyGlyValAspTrpGluThrThrHisIleGlySerPheMetGlyGlyAsnIlePro 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 :::111 325 ThrGlnLeuGluLeuGlnMetAlaSerAspAspProLysArgLeuGluAlaLeuGlnGly 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 PheArgGlulleProLeuProLeulleGluGlnAspGluLeuLeuArgProLeuSerGlu 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 GlnAlaIleLysLysGluLeuLysLysLysAsnAsnThrIleTyrTyrIleGlnGluThr 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ACCGAGCCAGCAGAAGGG 976
                                                                                                                                                              46 ArglysThrArgPheGluMetPheArgLeuSerAlaIleAlaMetAlaIleGluPheAla 65
                                                                                                                                                                                             377 TIGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAAAG
                                                                                                                                                                                                              |||||||
66 TyralaalaGluThrSerPheValSerProlleLeuLeuGlnIleGlyValaspHisLys
                                                                                                                                                                                                                                                                                                                                                                   437 ITCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTA
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                                         Conservative:
Mismatches:
Indels:
              Length:
Matches:
                                                                                                            US-09-759-143-110 (1-3410) x ABB60709 (1-599)
        8.24e-31
519.50
39.43%
23.66%
8.09%
                                     Percent Similarity:
Best Local Similarity:
Query Match:
Alignment Scores:
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345 SerTyrGlnAsnGlyTyrSerProAlavalGluLysGlnGlyLysSerClnAspLeuGlu 90 1001 ————————————————————————————————	aValGluLysGlnGlyLysSerGlnAspLeuGlu 364	CACTGCTGTCCATGCCGGGCCCGCTTGCCTTTCCGGAACCTGGCGCC 1048	SerLeuLysAlaTyrLeuLysSerIlePheIle 384	GCTCTTC 11	metProTyrSerMetArgMetLeuAla 393	GTGCCTGACCTGTCCAGCTGGATGCCACCATGACCTCTTTACACGGATTTC 1168 :::	1	GTGGGCGGGGTGCCCAGAGCTGGGGGGGGGGGGGGGGGG	12	::: SysTrpGlyMetAlaileTyrAlaPheSerCys 453	13	4	GCTGCCGGTGCCACATGCCTGTCC 1399	SlyMetLeuValLeuGlyLeuTrpProThrLys 493	::: :::	CAGATCCTGCCCTACACACTGGCCTCCTACTACCACGGGAGAAGCAGGTGTTCCTGCCC 1519 ::: ::: ::	GACAGCCTGATGACCAGCTTCCTG 15	530	CCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGC 1639	AsnGly 532	CTGCTCCCACCTCCACCCGCGCTCTGGGGGGCCTCTGCCTGTGTTCTCCGTACGTGTG 1699	532	GTGGTTCCGGGCCGGGCATCTGC 1750	-GluileValProLeuLysGlnAlaArgGlyLeuGly 544	Η .	VAIRTICITED TACTOR PROCESS TO TO TO THE TACTOR TO	584	1912	598		_
	 5 SerTyrGlnAsnGlyTyrSerProAl	001	10	o 1	n			~ -					349		94		520	530	580	531	640		700 GIGGIGGGIGAGCCCACCGAGGC	3	751	811		871 C	585	38 27 MM40227 standard; Protein; 748	

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification.
                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ren F, W.
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qian XB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang Y,
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1173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; SEQ ID NO 3372; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
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                                 Human polypeptide SEQ ID NO 3372.
                                                                                                                                                                                                                                                                                                    2000US-05488725.
2000US-0552317.
2000US-0598042.
2000US-0653450.
2000US-0653450.
2000US-0653450.
2000US-0653450.
                                                                                                                                                                                                                                                                         26-DEC-2000; 2000WO-US34263
22-OCT-2001 (first entry)
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466.00
34.00%
22.97%
7.26%
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N-PSDB; AAI59383.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
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                                                                                                                                                                                                           WO200153312-A1.
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14-SEP-2000; 2
19-OCT-2000; 2
                                                                                                                                                                               Homo sapiens.
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09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                     19-JUL-2000;
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                                                                                                                                               Leukaemia.
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Zhao QA,
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222 CCGAGACGAGCAGTTCTGGAGTGCCTGAACGGCCCCTGAGCCCTACCCGCCTGGCCCA 281

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0 ProlysargarglysCyslleargProSerProProProProProAsnThrProCysPro 69	2 CTATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCC 331	2 CAGCTCTTGCTGGTCAACCTGCTAACCTT ::: 6 GluLeuLeuPheAsnGlyCysIleLeuPh	ACCTATGTGCCCCCTCTGCTGCAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTG 4	2 CTGGGCATTGGTCCAGTGCTGGGCCTGGTGTCCCGCTCCTAGGCTCAGCCAGTGAC 51			2CCCAGGCCCCTGGAGCTGGCACTGCTGGGGGTGGGGCTGCTGGAC 682	TTCTGTGGC PheSerAla	3 CCGGACCACTGTCGCCAGGCCTACTTGTGTCATGATCAGTCTTGGGGGCTGC	3 CTGGGCTACCTCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGC 862	3 ACCCAGGAGGAGTGCCTCTTTGGCCTGCTCATCTTCCTCACCTGCGTA 916	7 GCAGCCACACTGCTGGTGGCTGGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGGG 976	CTGTCGCCCCCTCCTTGTCGCCCCACTGCTGTCCA		3 GlyAspSerLeuProSerHisThrAlaThrAsnPheSerSerProlleSerProProSer 342	2 1012	3 ProLeuThrProLysTyrGlySerPhelleSerArgAspSerSerLeuThrGlylleSer 362	DBL	3 GluPheAlaSerSerPheGlyThrAlaAsnIleAspSerValLeuIleA	5 1015	6	CGGGCCGGCTTGC	
50	282	332	392	452	512	572 166	632	683	743	803	863	917	977	1012	323	1012	343	1013		1015	383	_ (403
οg	Qy Dp	oy op	Qy	Oy Dp	Qy Dp	Qy Db	Qy Db	QD	Qy Db	Qy	Qy Dp	ري م	Qy Dp	Οy	qq	Qy	qq	οy	qq	οy	qq	oy d	a ,,

74	1043	GGCGCCCTGCTT 1054
ą	423	GluGlyAlaLeuThrSerGlyCysAspGlyAspIleLeuArgValGlySerLeuAspThr 442
γ	1055	1060
q	443	
λλ	1060	1060
ą	463	AlaGlyGlyGlyGlyProGluThrSerArgArgArgAsnValThrPheSerGlnGlnVal 482
λi	1060	1060
ą	483	AlaAsnIleLeuLeuAsnGlyValLysTyrGluSerGluLeuThrGlySerSerGluArg 502
λí	1061	
q	503	AlaGluGlnProLeuSerValGlyArgLeuCysSerThrIleCysAsnMetProLysAla 522
λī	σ	SACCITCACGCTG 11
ą		LeuArgThrLeuCysValAsnHisPheLeuGlyTrpLeuSerPheGluGlyMetLeuLeu 542
λ	Ŋ	AGCTGAGCCGGGC 12
ð	543	PheTyrThrAspPheMetGlyGluValValPheGlnGlyAspProLysAlaProHisThr 562
Δį	\vdash	a
ð	563	rGluAlaTyrGlnLysTyrAsnSerGlyValThrMetGlyCysTrpGlyMetCysTl
λí	1274	CAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGC 1333
Q	583	TyrAlaPheSerAlaAlaPheTyrSerAlaIleLeuGluLysLeuGluGluPheLeuSer 602
λ	1334	ACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGC 1393
ą	603	ValkrgThrLeuTyrPheIleAlaTyrLeuAlaPheGlyLeuGlyThrGlyLeuAlaThr 622
≱ q	1394	CTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCA 1453 ::::: ::: LeuSerArgAsnLeuTyrValValLeuSerLeuCysIleThrTyrGlyIleLeuPheSer 642
<u>></u>	1454	5
- Q	64	hrieucysThrieuProTyrSerLeuLeuCysAspTyrTyrGlnSerLys 659
Ā	1514	CTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGC 1573
Q	099	
Ž.	1574	TTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGC 1633
ą.	670	019
. <u>A</u>	1634	CTG
ą	670	010
γ	1694	CGTGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTG 1753
q	671	
γ̈́	1754	CTGTTT
ą	929	spileSerLeuLeuSerCysGlnTyrPheLeuAlaGlnIleLeuValSerLeuValL
۲.	1814	GGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTG 1873
д	969	GlyPro

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21 GlyLeuTrpSerTrpTrpGlyLySLeuGlyValGlyGluMetLeuGlyValGlyGluIle

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3046 GGGTTGTGGAGCTGGTGGGGAAAGTTGGGGGTAGGGGAAAG-TTGGGGGTAGGGGAAATT

2927 AACCAGGCTGGCCCAAGAGAGAGGGGTGGTTAGGGAAGCCGTTGAGACCTGAAGCCCCA 2868

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antaqonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and the proteins are useful in genetic vaccination, testing and the proteins are useful in agentic vaccination, testing and the concress stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding a range of human polypeptides, useful in genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
1874 GGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTT 1912
                                         alaAsnGlyValMetTyrPheSerSerLeuValSerPhe 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted protein #843
                                                                                                                                                                                                               AAU30352 standard; Protein; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Táng YT, Liu C, Drmanac RT)
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polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                       Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, SR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated prostate-specific
2867 CCCTCTACCTTCCAACACCCTAACCTTGGG 2835
             Human prostate cDNA encoded protein #67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 486-487; 579pp; English.
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                                                                                     AAU69873 standard; Protein; 123
                                                                                                                                                                                                                                                                                                                                                                   20000S-0568100.
20000S-0570737.
20000S-059793.
20000S-0636218.
20000S-0631236.
20000S-0651236.
20000S-0671236.
                                                                                                                                                                                                                                                                                                                            27-MAR-2001; 2001WO-US09919.
                                                                                                                                              30-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639232/73.
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                                                                                                                                                                                                                                                                  WO200173032-A2
                                                                                                                                                                                                                                                                                                                                                                   09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
10-AUG-2000;
29-AUG-2000;
06-SEP-2000;
                                                                                                                                                                                                                                       Homo sapiens.
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Fanger (
Li SX,
                                                         RESULT 40
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1310 GACCGCCTGGTGCAGCGATTCGGCACTCGAGCTCTATTTGGCCAGTGTGGCAGCTTTC 1369
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                                                                                                                                                                                                                                                                             The present invention describes polynucleotide sequences (I) which encode
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                                                                                                                                                                                                        New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW;
detecting cancer. The present sequence is a prostate specific polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate cancer; prostate-specific; diagnosis; vaccine;
                                                            123
87
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                                                                                Conservative:
Mismatches:
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                                                                                                                                US-09-759-143-110 (1-3410) x AAU69873 (1-123)
                                                                                                               Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; gene therapy; metastasis
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426.00
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94.57%
6.64%
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Kalos MD, Fanger GR, Day
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang A, Meagher MJ;
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                              123 AA;
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Best Local Similarity:
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                                                 Alignment Scores:
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DB:
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1250 ATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTTGTGGTCATG 1309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and isolated
T calls prepared using (I) or (II) are used treat cancer in a patient.
(I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) and (II) can be used for monitoring the progression of cancer in a patient.
(I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1490 TACCACCGGGAGAGCAGGTGTTCCTGCCCAAATAC 1525
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Conservative:
Mismatches:
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980S-0020956.
980S-0030607.
980S-0115453.
980S-0159812.
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                                                                                                                                                                                                      Sequence 123 AA;
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Best Local Similarity:
Query Match:
DB:
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09-FEB-1998;
25-FEB-1998;
14-JUL-1998;
23-SEP-1998;
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Tue Jun 10 11:28:19 2003

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2347 GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCT--- 2291
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                                                          Pendent group; repeating unit; enzyme recognition site; sealant; fibrin; enzymatic cross-linking; blocompatible material; structural integrity; medical adhesive; wound closure; tissue repair; transglutaminase.
         The amino acid sequence of the protein polymeric adhesion substrate (PPAS) 1-B. The protein comprises 10 repeats of the PPASI-B monomeric repeat (AAR80326) which consists of the CLP 3.7 gene encoded sequence (AAR80321) linked to the human fibrin cross-linking substrate peptide 93.2 sequence (AAR80316). The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 GlySerProGly------AlaProGlyThrProGlyGluGlyGlnGlnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - capable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein polymers comprising repeating units and sequences of enzyme-catalysed covalent bond formation useful as a blocompatible material for wound closure and tissue repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   762
257
38
298
263
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                                                                                              1490 TACCACCGGGAGAGCAGGTGTTCCTGCCCAAATAC 1525
                                                                                                             81 TyrHisArgGluLysGlnValLeuileGlyGlnTrp 92
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Matches:
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                                                                                                                                                                                                                                                 Protein polymeric adhesion substrate 1-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEIN POLYMER TECHNOLOGIES INC
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                                                                                                                                                                         AAR80327 standard; Protein; 762
                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0205518
                                                                                                                                                                                                                         (first entry)
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34.50%
30.06%
6.35%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             762 AA;
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                                                                                                                                                                                                                                                                         Pendent group;
enzymatic cross
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                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                         18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                             08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                 AAR80327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1370 CCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCC 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTC 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillon DC, Mitcham JL, Harlocker SL, Jiang Y,
GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
Wang A, Skeiky XAW, Hepler WT, Henderson RA;
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 706; 87pp; English.
15-JAN-1999; 99US-0232149.
09-APR-1999; 99US-0288946.
13-JUL-1999; 99US-0435116.
18-NOV-1999; 99US-043313.
18-NOV-1999; 99US-043313.
14-JAN-2000; 2000US-048367.
27-MAR-2000; 2000US-048367.
09-MAY-2000; 2000US-058100.
12-MAY-2000; 2000US-0593793.
27-JUN-2000; 2000US-0593793.
27-JUN-2000; 2000US-0593793.
27-JUN-2000; 2000US-055136.
06-SEP-2000; 2000US-0651236.
06-SEP-2000; 2000US-0651236.
06-SEP-2000; 2000US-0657279.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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HARLOCKER S L.
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DAY C H.
VEDVICK T S
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RETTER M W.
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                                                                                                                                                                                                                                  DILLON D C.
                                                                                                                                                                                                                                                                       JIANG Y.
KALOS M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 AA;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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Li SX, Wan
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(KALO/)
(FANG/)
(RETT/)
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(HARL/)
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(HEPL/)
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sepvalGlys	111 GlybroGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 126	2179 CCCTTGGAAGGCCTCCAGTCAGGGAGCCCCTAGAGACTGGGGAGAGAGGAGGAGGACCCCC 2120	CAGCCCCAGCTGCGCACCTCAGCAGCACAGGGTGGCAGCAGGGGGGGGGG	ProGlys	2065 CCACATTAGTTGGCAGCAACAGAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAAC 2006	2005 AGGACCGGGAGCTGGACCCAGTGAGGCAGGCCCTCCACCCCAATGTGCTGGAAGTTTT 1946 ::::::::::::::::::::::::::::::::::::	CTACGCTGACTATTTGGCCAAGTCGCTCTTGTCAATTTTTTTT	182 187	1885 GGCGACCAGGCCTGCGGCAACACCATATAGGCACTGACAGACTGGCTGAGCTG 1826 188GlySerProGlyAlaProGlyHrProGlyProGlyProGly	GACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGAAGGCACTATCCAG	:::	1765 GATGGCGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCCTGGCCTC 1718	GGTGGGCTCACCCACCACCACACGTACGAGACATCACAGGCAGAGGCCCC	AspVa	1666 GCAGAGCGCGGGTGGAGGTGGGAGCAGCCACTCCAGCACCCACGTGTCCATTAGG 1607	CGAPGRACTOCALY III. FLOCALY FLOGALIGAY BERTAGATOA VOCARGRACIA COLORIO A COLO	262GlyAlaProGlyThrProGlyProGlnGlyLeu-ProGlySerPro 276	1546 AGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGG 1487	GGAGGCCAGTGTGTAGGGCAGCATCAGGGGTGAAGGTGAACCCGGTGAGGGGGG	286 lyLeuProGlySerProGlyAla-ProGlyThrProGlyGluGly 300	1426 TGAAGCTGTCACCACGCCACACTGTGGACAGCATGTGGCACCGGCAG 1377	GINGTHIADHIADHUACHYGLYAIBHIGGINABGTAGATABAGATAGACTAGAAAAGTAGCAAATAGACTAGAAAGAGCAAAAAAAA	ProGlyThrProGlyProGlnGlyLeuProGlySerPro	CGAATCGCTGCACCGGTCCATGACCAGAGAGAGCCAGGGAGATGGCGCACTGCA	GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 350	1271 GGACA
Oy Oy	QQ	Qy Pp	٥y	qo	Qy Dp	۷٥ باد	ò	qq	oy Og	δλ	qq	Qy	3 6	qq	ر م	3 8	S 6	oy Db	οy	qq	VO 40	3 8	qq	Οy	qq	, oy

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1244 CGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCA-----CGC 1191
                                                                                                                                                                                                                                                                                                                                                                                                              1070 GCTGGTGCAGCCGGGGAAGCAGGCGCCCCAGGTTCC---GGAAAGCCAAGCGGGCCCGGC 1014
                                                                                                                                                                             1190 CCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA 1131
                                                                                                                                                                                                                                                                                            1130 TCCAGCTGCACAGGTCAGCCACGAAGAGCCGGCGCGAGGGTGCGGGGCATGCGGCAGCACA 1071
351 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGlu 370
                                                                                                  371 GlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAla 390
                                                                                                                                                                                                                                       401 GlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                   998 GCGACA---AGGAGGGGCCGACAGCCCTTCTGCTGGCTCGGTGGGGCCCAGGGCTGCCT 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        728 CAGAGAGCAGGCCTCCAGTGGAGTGAAGCACACTGGCCACAGAAGTCCAGCAGCACCA 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    668 CGCCCAGGATGAGCAGTGCCAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCCCTGCTA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    625 ------GlnGlyLeuProGlySerProGlyAla------ 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1013 ----ATGGACAGCAGTGG 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 GluGlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGly 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      941 CCTCAGCCACCAGCAGTGTGCCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAA 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          782 TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGT---CCCGGAAGAGGT 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        881 AGAGGCACTCCT------CCTGGGTGCCCAGGTAGGGGGCCAGGGCACTGG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        585 GlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAlaPro 604
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302 CCCACAGCCT 672 ProGlyAlap 672 ProGlyAlap 245 CACTCCAGAA 1611	CCCACAGGCTCTGGACCATAGTGGGCGGGGGGGGGGGGG		CCGCCAACTACGGGAATCAGCAGCGCCCATTTCTGCCAGCTTGGTGCGGGTCC 126	ProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGl 725	AGCITCTCAGCCCATGCTCAACACCTGCTGTGGGGCACCTCAGTGGGGACACGTCTC 66	CTCAGATCCTGGCCGA 46 :::	; Protein; 762 AA.		dhesive substrate PPASI-B.	dhesive substrate; PPAS1-B; sealant; P 3.7; collagen; human.				US-0205518.	US-0397633. US-0205518.	OLYMER TECHNOLOGIES INC.	•	33.	rotein polymers – containing naturally occurring for crosslinking by enzymes, useful as medical lants, depots and matrices	27; 70pp; English.	Protein polymer adhesive substrate PPASI-B comprises 10 repeats of a monomer (see AAW49714) consisting of human fibrin gamma chain peptide 93.2 (see AAW49708) inserted into a structural backbone of collagen repeat motifs (see AAW49711). The 68 kDa PPASI-B FOLYMER has been expressed in Escherichia coll HBIO1 transformants using plasmid pPT0324. Claimed recombinant protein polymers are capable of covalent crosslinking by enzymatic reaction to form products which set quickly and have good adhesive properties and high strength. CLP (collagen like protein) polymers are extremely soluble in water, allowing protein solutions of over 10 wt.% to be formed while maintaining good flow properties. CLP polymers have good adhesion to hydrophilic surfaces and therefore may adhere well to tissue. The fibrin peptide 93.2 inserts of PPASI-B provide glutamine donor sites for Factor XIIIa mediated cross-linking.
302 672 672 691 185 710 725 65 727 741 741 771 741 741 741 741 771 741 74	302 CCCACAGCCTCTGGACCAT 672 ProGlyAlaProGlyThr-	245 CACTCCAGAACTGCTTCGT 691 yThrProGlyProGlnGly		1	125 AGCTTCTCAGCCCATGCTCAAC 	ProGlyAla		, to	ymer adhesive	Protein polymer adhesive subs Wound healing; CLP 3.7; coll	Synthetic. Homo sapiens.	US5773577-A.	30-JUN-1998.	03-MAR-1994; 94US-0205518.	(-1995; 95US-0397633. (-1994; 94US-0205518.	PROTEIN POLYMER TECHN		1998-387091/33.	New recombinant protein polymers - repetitive units for crosslinking adhesives and sealants, depots and	4; Column 27; 70pp; E	Protein polymer adhesive subs of a monomer (see AAW49714) copptide 93.2 (see AAW49708) is collagen repeat motifs (see Phas been expressed in Escheriplasmid pPT0324. Claimed recognishing by ewhich set quickly and have go strength. ClP (collagen like in water, allowing protein symbol. The maintaining good flow father maintaining good flow fathers on hydrophilic surfatissue. The fibrin peptide 9glutamine donor sites for Fac

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2290 CAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCA------GAG 2240
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                                                                                                                                                                                                                                                                                                                                           2179 CCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGGAGAGAGGAGAGGACGCCC 2120
                                                                                                                                                                                                                                                                                                                                                                                                   2119 CAGUCCCCAGCTGTGCAGCTACGCACCTCAGCACAGGGT-----GGCAGCAGAGAG 2066
                                                                                                                                                                    2347 GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCT--- 2291
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2065 CCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAAC 2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1945 CTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAAT 1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1885 GGCGACCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTG 1826
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                                                                                                                                                                                                                                                      91 HisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAlaProGlyThrPro 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1606 GAAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCT 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1546 AGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAG 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1486 GGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGC 1427
                                                                                                                                                                                                                                                                                                     160 GlnHisHisLeuGly------GlyAlaArg 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 Gly-----GlnGlnHisHisLeuGlyGly-AlaArgGlnAlaGlyAspValGlySerPr 246
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                                                                                                                                                                                       188 -----GlySerProGlyAlaProGlyThrProGlyProGln------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       762
257
38
298
263
52
                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                    US-09-759-143-110 (1-3410) x AAW49715 (1-762)
                                       2.42e-21
395.00
34.50%
30.06%
6.35%
                                                                 Percent Similarity:
Best Local Similarity:
762 AA;
                           Alignment Scores:
 Seguence
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qa Vo		Db 605 GlyThrProGly Qy 506 TGGCTGAGCCTA Db 615SerPro	rProGly SAGCCTA
Db Qy	301GlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAla 319 1376	Qy 446 TGGTCATGAACT	AACT
qq		Oy 386 CIGGGCCAAAC	'AAAC
Qy	1331 CGAATCGCTGCACCGGGTCCATGACCAGAGAGACCAGGGAGATGGCGCACTGCA 1272 	634	ogly
& &	1271 GGAACA	326 652	uGly
G 60	CGCCTTCATCATAGTGTCTCCGGGCTCGGTGCCCGGCTCTGGGCACGC	Oy 302 CCCACAGCCTCT	CCTC1
da oy	<pre>lnAlaGlyAspValGlySerProGlyAla GTAAAACAGCGTGAAGGTCATGAGTGCCA ::: </pre>	Qy 245 CACTCCAGAACT	3AAC1
g ::	391 ProGlyThrProGlyProGlnGly	Qy 185 CCGCCAACTGCC	7160
S G	GlySerProGlyAlaProGlyThrProGlyProGlyProGlyLal	Db 710pr	14
ογ	GCTGGTGCAGCCGGGGAAGCAGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGC		31nH
qq	ProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyInrFroGly	Qy 65 ATCA	:
Oy Dp	1013ATGGACAGCAGTGGG 999 1013	Db 741 ySerProGlyAl	GlyA
\$ 5	998 GCGACAAGGAGGGGCCGACAGCCCTTCTGCTGGCTCGGTGGGGCCCAGCGCTGCT 942	57.	. Ou
3 3	A CONTRACT C	AC AAW57668;	
o d	GlythrProGlyProGlyProGlySerProGlySerProGlyAlaProGlyThrProGlyPro	DT 27-AUG-1998 (first exx xx Collagen-like polymen	rst
oy Db	881 AGAGGCACTCCT	XX XX KW Collagen-like polymen KW prosthetic device; CG	polyme ice; ca
δλ	836 TGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCA 783	OS Synthetic.	
qa	518 LeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAlaPro 533	PN US5773249-A.	
ογ	782 TGAAGGCATAGACAGACATGGCGACACTGGTCCGGGTCCCGGAAGAGGT 729	30-JUN-1998. 02-MAY-1996:	-sn96
8 8		02-MAY-1996;	-sn96
영	549 GlyhrproGlyProGlnGlyLeuProGlySerProGlyAlabroGlyThrPro 566	04-NOV-1986; 29-OCT-1987; 09-NOV-1988;	60S- 70S- 80S-
Οy	CGCCCAGGATGAGCAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCTGCTA	06-NOV-1990; 12-NOV-1991;	900S-
QQ	lyAlaProGlyThrProGlyGluG1y	22-DEC-1995;	50S
Qy Db	608 GCCAGCCGGCCCTTGGGATGAGAAGAGGCTCAGCAGGATGCCCA 564	(PROT-) PROTE	POLY
ογ	563 AGGACAGTGCCCAGATGAAGGGCGGGGGGGGGCATAGCGTCCACGCCAGTGGTCAC 507	XX XX DPELLO J, FEFFATI XX DR WPI; 1998-387004/33.	/33
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CTGGACCATAGTGGGCCAGGCGGG---TAGGGCTCAGGGGCCGTTCAGG 246
                                                                                                                                                                                                                                                                                                                              TECTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTG 186
                                                                                                                                                                                                                                                                                                                                                   CCTAGGAATCAGCCAAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCC 126
                                                                                                                                                                                                                                                                                                                                                                                                              yGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySer 671
                         AGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCA 447
                                       -GinglyLeuProGlySerProGlyAla-------633
                                                                                                                                               CACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGGCTT 327
                                                                                                                                                                    ------GCCGCAGCAGCGGCTCA 303
                                                                                      TTCTCCTCTACCCCCACTTCCAGCAGCAGAGGCGGCACATAGGTGATGC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATGCTCAACACCTGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ner; synthetic polymer; fibre coating;
catalytic substance.
yProGlnGlyLeuProGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alaMet-AspProGlyArg 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---CTCAGATCCTGGCCGA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide; 762 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5-0642255.
5-0927258.
5-0114618.
5-0269429.
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-0972032.
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This sequence represents a unnatural collagen-like polymer of the invention. The products may be used as films, fibres, moulded objects and admixed with other natural or synthetic polymers or coatings on fibres, films, labware or other surfaces, e.g. prosthetic devices. The polymers may be used for binding a wide variety of specific binding materials, as catalytic substances (where the amino acid sequence may specifically chelate a wide variety of elements), as purification media, composites, laminates or adhesives. They may also be combined with inorganic or organic materials such as carbon fibres, nylon fibres, nitrocellulose, etc., as flask coatings or in synthetic matrices for the growth and study of cells, as affinity columns or as supports for blological materials. The polymers have collagen-like properties, but may sequences can be tailored to give the desired properties.
             Recombinant collagen-like polymers - useful for making gels, films, fibres, etc.
                                                                                                Example 7; Column 51; 93pp; English
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762 AA; Sequence

Alignment Scores: 2 428-21 Length: 762	
69-129	2.42e-21 Length: 395.00 Matches: 34.50% Conservative: 30.06% Mismatches: 6.35% Indels:
	SARACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCT 2291
	ACTAGGAGGCTAGCTGTTAACCCTGAGCTAATCCACCTGCAGAG 2240
	sLeuglyglyAlaArgGlnAlaGlyAspValGlySerProGlyAlaProGlyThrPro 110
	SCCGCATTCCAGTGCATGGAGCCCTTCTGGCTCCTGTATAAGTCCAGACTGAAACC 2180
	TTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGGAGGGAG
	5GlnGlyLeuProGlySerProGlyAlaProGlyThrFro 140
	SCCCCAGCTGTGCAGCTACGCACCTCAGCACAGGGTGGCAGCAGAGAG 2066
	ACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAAC 2006
	:::
	GAGCGGGGAGCTGGGACCCAGTGAGGCAGGCCCTCCACCCCAATGTGCTGGAAGTTTT 1946
	nalaglyaspvalglySerProGlyalaProglyThrPro 181
	ACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAGTAAAT 1886
	CGACCAGACCCAGGCCTGCGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTG 1826
	GlySerProGlyAlaProGlyThrProGlyProGln199
	CAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACGCAGGAAGGCACTATCCAG 1766

oy	65	111
gg .	507	OGINGIYLEURIOGIYSEI FI OGIYALBRIO GIYIII FI OGIYGIG 26.
Qy Db	1717 (AspvalGlySerPr 246
ΟŸ	99	3AGCGCGGTGGAGGTGGGAGGCCACTGCTCCAGCACCACGTGTCATTAGG 16
QQ	246	odlyalaprodlyThrProdlyProGlnGlyLeuProdlySerPro 261
Oy	1606	AGGGAGCTCCAGGCTTAGGGCCTGCAGGAAGCTGGTCATCAGCTGTCCTCACTG
QQ	262	- 6
Qy	1546 /	CCAGTGTCCCCTCGGTATTTG
qq	277	ш.
Qy	1486 (C 1
QQ	286	GlySerProGlyAla-ProGlyThrProGlyGluGly
Qy	vo	GAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGGCACCGGCAG 13
qq	301	GlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAla 319
Qy .	97	CACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGC 13
qq	320	256 -
QY	1331	AATCGCTGCACCAGCCGGTCCATGACCAGAGACAGGGAGATGGCGCACTGCA 12
οĎ	333	lyAlaProGlyThrProGl
Qy.	71	
QQ	51	oglyproginglybeuProglyserProglyAlaProglymmFroglybiu 5/70
Qy	1244	CGC 11
qq	371	GlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAla 390
Qy	0	CCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA 1131
qa	391	ProGlyThrProGlyProGlnGly
QY	1130	SCTC
QQ	401	GlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 420
Qy	1070	GCTGGTGCAGCCGGGGAAGCAGGGCGCCCAGGTTCC~~-GGAAAGCCAAGCGGGCCCGGC. 1014
qq	421	5
Οy	1013	-ATGGACAGC
Db	441	pvalGlys
Οy	866	GCGACAAGGAGGGGCCGACACCCTTCTGCTGGCTCGGTGGGGCCCCACCGCTCGT 942
qq	461	AlabroGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 477
Qy	941	CCTCAGCCACCAGCAGTGTGGCTACGCAGGTGAGGAAGATGAGGTGAGCAGGCCAA 882
Db	478	49
Qy	881	SAGGCACTCCT
qa	498	lySerProGlyAl
Qy	836	TGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCA 783

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518 LeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAlaPro53	782 TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGGTCCCGGAAGAGGT 72	534GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 54	728 CAGAGAGGCCTCCAGTGGAGTGAAGCACACTGGCCACAGAAGTCCAGCAGCGCCCA 669		668 CGCCCAGGATGAGCAGTGCCAGGGGCCTGGGATCCGGGCACAGCAGCTGCTA 609	567 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGly 584	608 GCCAGCCGGCCCTTGGGATGAGAAGAGGCTCAGCAGGATGCCCA 564		563 AGGACAGIGCCCAGAIGAAGGGCCGGCGGCGGCCAIAGCGICCACGCCAGIGGICAC 507	605 GlyThrProGlyProGlyLeuProGly 614	506 TGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCA 447	615SerProGlyAlaProGlyThrProGlyPro	446 TGGTCATGAACTTCTCCTCTTCCCCACTTCCAGCAGAGAGGCGCACATAGGTGATGC 387	625GlnGlyLeuProGlySerProGlyAla63	386 CTGCGGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTT 327	634ProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr 651	326 TCCGGTGCCGCAGCAGCAGCTCA 303	 ProGlyGluGlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySer 671	302 CCCACAGCCTCTGGACCATAGTGGGCGAGGCGGGTAGGGGTCAGGGGCCGTTCAGG 246	672 ProGlyAlaProGlyThr-ProGlyProGlnGlyLeuProGlySerProGlyAlaProGl 691	245 CACTCCAGAACTGCTTCGTCTCGGCTCTGCAGAAGGTGCGGCCTCTCCTTGCTG 186		185 CCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTCTGCCAGCCCTTTGGTGCCGGTCC 126		125 AGCTICTCAGCCCATGCTCAACACCTGCTGTGGGGCACCTCAGTGGGGACACGTCTC 66	725 uGlyGlnGlnH18H1SLeuGlyGlyAlaArgGlnAlaGlyAspValGl 741	65 ATCACTCAGATCCTGGCCGA 46	741 ySerProGlyAlaMet-AspProGlyArg 750
- 7			-	=*	-		_	••	.,	•		v	4	¥	(*)	¥	m	9	en .	9	2	9	1	7	1	7		7
QQ	δ	QQ	Qy.	qq	ΟŻ	Dp	ò	QQ	οy	qq	δ	QQ	δy	QQ	οy	ρp	δ	QQ	Οy	qq	δy	qq	δy	QQ	οy	qq	οy	qq

Search completed: June 9, 2003, 22:24:42 Job time: 166.5 secs

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(without alignments)
10831.191 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 ; 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                             2185239 seqs, 1125999159 residues
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/SIDS2/gcgdata/geneseg/genesegn-embl/NA2000.DAT:*/ /SIDS2/gcgdata/geneseg/genesegn-embl/NA2001A.DAT /SIDS2/gcgdata/geneseg/genesegn-embl/NA2001B.DAT /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:* /SIDS2/gcgdata/geneseq/genesegn-emb1/NA2002.DAT: /SIDS2/qcqdata/qeneseq/qeneseqn-embl/NA1999.DAT: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT: /SIDS2/gcgdata/geneseq/genesegn-emb1/NA1987;DAT: /SIDS2/gcgdata/geneseg/genesegn-emb1/NA1988.DAT: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT /SIDS2/gcgdata/geneseg/genesegn-embl/NA1994./SIDS2/gcgdata/geneseg/genesegn-embl/NA1995./SIDS2/gcgdata/geneseg/genesegn-embl/NA1996. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1989. /SIDS2/gcgdata/geneseg/genesegn-emb1/NA1993. /gcgdata/geneseg/genesegn-emb1/NA1998. /SIDS2/gcgdata/geneseg/genesegn-emb1/NA1992 /SIDS2/gcgdata/geneseg/genesegn-embl/NA1997 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA19 /SIDS2/gcgdata/geneseg/genesegn-embl/NA19

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Full length cDNA s	Prostate tumour sp	cDNA sequence of h	Human prostate cDN	Human prostate tum	Human prostate-spe	Human prostate-spe	Prostate tumour an	Human L1-12 cDNA s
SUMMARIES	ΩI		AAV58586	AAC79473	AAS63557	AAS10108	AAH93465	AAH84779	AAH02530	ABL94929
	DB	19	19	21	22	22	22	22	22	24
	Query e Match Length DB]	3410	3410	3410	3410	3410	3410	3410	3410	3410
æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	3409.6	3409.6	3409.6	3409.6	3409.6	3409.6	3409.6	3409.6	3409.6
	Result No.	-	7	m	4	S	9	7	80	6

	Human prosate cDNA P553S cDNA splice Human p553S splice Human p553S splice Human p553S splice Human secreted pro Consensus sequence Clone 1711346IH, t	CDNA sequence of a Human prostate gene PS10 Human prostate rel Prostate gene PS10 Human mast cell re Human prosate CDNA P553 SDICE Human mast cell re Human mast cell refluman mast cell	Human Secteted pro Human /W. tubercul Ral2-P5015-E2 cons Ral2-P5015-E2 cons 3' CDNA sequence o 3' fragment of pro Human immunogenic Human prostate CDN
ABK29017 AAA06349 AAS14962 AAS64040 AAH93868 ABK95411	AAS64039 AAB193867 ABL95410 AAS64038 AAH93866 ABL95409 AAD05230 AAV71180	AAZ45677 AAC64928 AAC64927 AAS07601 ABN81320 ABN81320 ABN81320 ABN81324 ABN81324 ABN81283 ABN91284	AADU 2264 AAS64153 AAH33917 ABL95524 AAV61144 AAV58487 AAS63458
24 22 22 22 24 24 24	20222222	222222222222	222 222 222 222 222 223
3410 3410 3320 4034 4034 4034 2582	2904 2904 2904 4894 4894 4894 2152	2462 2133 2124 2124 2124 3663 6976 6976 6976 1662	1019 1203 1203 1203 789 789 789
	64.4 64.4 62.8 62.8 62.8 62.7 62.7	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	27.1 23.3 23.3 23.3 19.7 19.7
3409.6 3408 3292.4 2585.4 2585.4 2585.4 2486.4	2196.4 2196.4 2196.4 2142.8 2142.8 2142.8 2136.8 2136.4	2065.4 1915.4 1899.8 1899.8 1815.8 1815.8 1815.8 1662.2	925.2 794.6 794.6 673.4 673.4 673.4
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Polypeptides comprising immunogenic portions of prostate proteins -
                                                                      Full length cDNA sequence of prostate tumour clone L1-12.
                                                                                         Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
                  AAV61201 standard; cDNA; 3410 BP
                                                                                                                                                                                98US-0020956.
97US-0806099.
97US-0904804.
                                                                                                                                                                98WO-US03492.
                                                     06-JAN-1999 (first entry)
                                                                                                                                                                                                                                                          WPI; 1998-609886/51.
P-PSDB; AAW71869.
                                                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                                                                                                                                                                         Oillon DC, Xu J;
                                                                                                                                                                25-FEB-1998;
                                                                                                           Homo sapiens
                                                                                                                           409837093-A2
                                                                                                                                                                                  09-FEB-1998;
                                                                                                                                                                                           25-FEB-1997;
01-AUG-1997;
                                                                                                                                              27-AUG-1998
RESULT 1
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of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library. cancer prostate οţ Claim 3; Page 79-80; 130pp; English the ņ nseq

Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

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ö 120 240 300 300 360 360 420 480 480 540 540 900 009 780 9 9 GGGAACCAGCCTGCACGCGTGGCTCCGGGTGACAGCCGCGCGCCTCGGCCAGGATCTGA GTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG **AAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCCGCCTGGCTGATTCCTAGGCAGTT** GCCGCCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTG GAGTGCCTGAACGGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG GAGTGCCTGAACGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG GGTGAGCCGCCTGCTGCGCACCGGAAAGCCCCAGCTCTTGCTGGTCAACCTGCTAACCTT TGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT GGGGGTAGAGGAGGATCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCG GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGC CGCCTGCCTAGCAGGGCTGCTGTGCCCGGATCCCCAGGCCCCTGGAGCTGGCACTGCTCAT CCTGGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT GCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTT Gaps 3410; ö Length Indels 19; ; 0 DB Score 3409.6; Pred. No. 0;); Mismatches ó 100.0%; 100.0%; Best Local Similarity 100. Matches 3410; Conservative 61 121 121 181 181 241 301 301 361 361 421 421 481 181 541 541 601 Match 601 661 721 781 661 721 g ò ö g g Q

1020 1020 1080 1140 1260 1380 1440 1680 1080 1380 1500 1560 1740 1680 GAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAG 1560 1800 1800 1860 1860 900 960 096 TGCCCTGGCCCCCTACCTGGCCACCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCAT CTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCAC CCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCTGTGCTGCCG CATGCCCCGCCACCCTGCGCCCGCTCTTCGTGGCTGTGCAGCTGGATGGCACTCAT CGAGCCAGCAGAAGGGCTGTCGGCCCCTTCTCGCCCCCACTGCTGTCCATGCCGGGC GACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAG AGCTGAGCCGGGCACCGGGGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGG CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT GGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGGGGCTCTGCGGGGCCTCTGCCTG TGATGTCTCCGTACGTGTGGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCG TGATGTCTCCGTACGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCG GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC TGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG ATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 1021 1141 841 961 1021 1081 1081 1141 1201 1201 1441 841 901 901 961 1261 1441 1321 1321 1381 1381 1501 1621 1261 1501 1561 1621 1681 1681 1741 1741 1801 1801 1921 Ω ò · q ò g ò g ò g δy g ò Q Qγ qq qq ò αq QQ qq δ οy ŏ à g qq Q Op g Ωy δ ò g δ à à

Db	3241 3301 3301 3361	/58586 AAV58586 standard; cD AAV58586; 08-DEC-1998 (first e Prostate tumour speci	rostate therapy; somo sapie ey by 09837418-7-AUG-199	PF 25-FEB-1998; 98WO-USO3 XX PR 09-FEB-1998; 98US-0904 PR 25-FEB-1997; 97US-0904 XX XX PA (CORI-) CORIXA CORP. XX XX XX XX DR WPI; 1998-480805/41. DR WPI; 1998-480805/41.	PT Novel human prostate sperarion of detecting and treating the for detecting and treating by Claim 1; Page 84-85; 141 XX CC This sequence represents CC be used in the method of CC prostate cancer comprise CC able to bind an immunoge CC encoded by this sequence
	161 ACTGGAGGCCTTCCAAGGGGTTTCAGTCTGACTATACAGGAGGCCAGAAGGGCTC 220 1	240 246 246 246 252		GGTCCCTGAG 	2881 CTCAACGCTTCCCTAACCACCCTCTTCTTGGCCCAGCTTGCTCCCCCCACTTCC 2940 [
90 O O O O O O O O O O O O O O O O O O O	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	64 64 65 64 65 65 65 65 65 65 65 65 65 65 65 65 65	8 6 8 6 8 8	69 69 69 69	δδ φα δδ ,

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PACCCCCAACTTTCCCCACCAGCTCCACAACCCTGTTTGGAGCTACT 3060
                                                                                                                                              This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pecific tumour protein and fragments - useful ting prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ic gene; human; prostate cancer; detection;
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- AGC -	3CAGAAGGGCTGTCGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGC 10
GAGC	AGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGC 10
SCTT	GGCTTTCCGGAACCTGGGGGCCCTCCTCCCGGGTGCACAGCTGTTGCTGCTCCG 10
76C 111	CGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCAT 11
E E E	CACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTGTACCAGGCGTGCCCAG 12
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<u> ე</u> — ე	TPCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCG
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CGGTGCC	CATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGG
TTCAC TTCAC	TTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC
GAAGCAC GAAGCAC	GTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAG
CCTGATG CCTGATG	COAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCT
GGGTGCT GGGTGCT	AGGCAGTGGCCTGCTCCCACCTCCACCGGCGCTCTGCGGGGCCTCTGCCTG 16
TGATGTCT TGATGTCT	CCGTACGTGGGGGGGGGGGGGCCCACCCAGGCCAGGGGGGTTCCGGGCCG 17
GGCAT GGCAT	GCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 1
ATCCCTG 	TTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 18
GCCGCA	CCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 1
Ř=Ř	GCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT
CACTGGG' CACTGGG	TCCCAGCTCCCGGTCCTGTTAGCCCCATGGGGCTGCCG

QY 3121 ATATCTGGGGAATCTCACACAGAAACTCAGGGGCACCCCTGCTGAGG 3180 Db 3121 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 3 AAC79473 ID AAC79473 ID AAC79473 standard; cDNA; 3410 BP. XX AC AAC79473; XX DT 07-FEB-2001 (first entry) XX DE cDNA sequence of human breast tumour clone P501S. XX W Human; breast tumour antigen; cytostatic; immunotherapy; XX XX XX XX XX XX YX YX YX YX YX YX YX	XX XX XX XX XX	oue Ses Tat
2041 TTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCCCCTGTGCTGCTGGGGGCGTA 2100 2041 TTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCTGCTGCTGCTGGGGGCGTA 2100 2041 TTCTGTTGCTGCCCAAAGTAATGTGCTCTCTCCTGCTGCTGCTGCTGGGGTGCCTA 2100 2101 GCTGCACAGCTGGGGGCTGGGGCTCCTCTCTCCCCAGTCTCTAGGGTGCCTG 2160 2101 GCTGCACAGCTGGGGGCTGGGGCTCCTCTCTCTCCCCAGTCTCTAGGGCTGCTG 2160 2101 GCTGCACAGCTGGGGGCTTCCAGTCTGTCTTTTTTTTTT		281 TCGAARGCCCAAACCAAACTTTAATTTAACAAAGTAAAAGGGGA 2641 TGCTAGCTTTCTGTGTGTGTGTCTAATTTTGGGTAGGGGGGGTCCCAA 2641 TGCTAGCTTTCTGTGTGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAA 2641 TGCTAGCTTTCTGTGTGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAA 2701 GGTCCCCTGAGATAGCTGGTCATTGGGCTGGTAGGGTAG	2821 TCCAAATGCTGTTTTTTTTTTTTTTTTTTTTTTTTTTTT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising an immunogenic portion of a .n the detection and treatment of breast
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Pred. No. 0;
Mismatches 0; Indels 0; GZ
cytostatic; immunotherapy;
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                                                                                                                                                                                                                                                                                     tumour clone P501S.
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Db 1081 CATGCCCGCACCTGGGCGGGTTTTGTT Qy 1141 GACCTCACGCTGTTTTACACGGATTTCGT	1141	1201	61 61	21 60	1 CGGTGCCACATGCCTGTC(1441	1501 GAAGCAGGTGTTCCTGCCCAAN 	1561 CCTGATG 	1 GGGTGC 	Qy 1681 TGATGTCTCCGTACGTGTGGTGGTGGGTGA 	1741 GGGCATCTGCCTGGACCTCGCC	1801 ATCCCTGTTTATGGGCTCCATTGTCCAGC	1861 TGCCGCAGGCCTGGGTCTGGT 	Oy 1921 CGACTTGGCCAAATACTCAGCGTAGAAAAC	1981	OY 2041 TTCTGTTGCTGCCAAAGTAATGTGGCTCTC	Oy 2101 GCTGCACAGCTGGGGGCTGGGGCGTCCCTC	Oy 2161 ACTGGAGGCCTTCCAAGGGGTTTCAGTCT
	ol Grafichkardistroccontrakeistoccontrakeisteritakeititakeitista. 	121 AAGCTGGACCGGCACCAAAGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTT 180	181 GCCGGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAAGCAGCAGCAGCAGCAGCTTCTG 240	GAGTGCCTGAACGCCCTGACCCTGGCCCACTATGGTCGAGAGGCTGTG 1 1 1 1 1 1 1 1 1 1	GGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTT 3	TGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT	421 GGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT 480	481 CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGACGCTATGGCCGCCG 540	541 GCCTTCATCTGGGCACTGTCGTTGGCCATCCTGCTGAGCCTCTTCTCATCCCAAGGGC 600	CGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCAT	CCTGGGGGTGGGGGCTGCTGGACTTCTGTGGCGAGGTGTGCTTCACTCCACTGGAGGCCCT	721 GCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTT 780 11	781 CATGATCAGTCTTGGGGCTGCCTGGGCTACCTGCCTGCCATGGCTGGGACACCAG 840	GCCCCCTACCIGGGCACCCAGGAGGAGIGCCTCTTTGGCCTGCTCACCTCAT 90	TECCCIGENCECCIALCIAGESCACCEAGEAGETGCCICTITIGECCIGETCACCCICAT FOR CITTCECCACCCICATE FOR THE CITTCECACCCICATE FOR THE CITTCECACCTGCGCACGCCCCCAC FOR CITTCECACCACCACCACCACCACCACCACCACCACCACCACCA	961 CGAGCCAGCAGAGAGGGTGTCGCCCCTCCTTGTCGCCCCCACTGCTGTCCATGCCGGGC 1020	21 CCGCTTGGCTTTCCGGAACCTGGGCCCCTTCCCCGGCTGCAGCTGCTGCTGCCG 108	11
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Query Match
Best Local Similarity
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29-AUG-2000;
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13-JUN-2000;
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                                              CTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTG
                                                                              GITICCCAICICIAAGCCCCTIAACCIGCAGCTICGITIAAIGIAGCICTIGCAIGGAG
                                                                                                             TITCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA
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polynocleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding the antigen-presenting cells are useful for stimulating and/or expanding of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune assponse, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
                           human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer , ,
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Carter D;
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                                                                                                                                           Human; prostate cancer; ss; cytostatic; immunostimulant; tumour
                                                                                                               Jillon DC, Mitcham JL, Harlocker SL, Jiang Y, SR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate cDNA sequence #109.
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GR, Rette
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Matches 3	3410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	-	
Ολ	GGGAACCAGCCTGCACGCGCTGGCTCCGGGTGACAGCCGCGCGCCTCGGCCAGGATCTGA 60	Oy 40	1081 CATGCCCCGCA(
qq	1 GGGAACCAGCCTGCACGCGTGGCTCCGGGTGACACCCGCGCCCTCGGCCAGGATCTGA 60	. ·	TOOT CATGUCCUGUA
oy do	61 GTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG 120	QY DP	1141 GACCTTCACGC
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0y 1	1 (Qy	1261 GGGGCTGTTCC
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Qy 2,	30	٥y	1321 GCAGCGATTCGC
Db 2,	241 GAGTGCCTGAACGGCCCCCTGACCCTACCGCCTGGCCCACTATGGTCCAGAGGCTGTG 300	qq	21
9. 3.	GTGAGCCGCCTGCTGCGGGACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTT 36	y da	1381 CGGTGCCACATC
	SOLUTION CONTROLLING TO THE STATE OF THE STA	٥y	1441 GTTCACCTTCTC
		qa	1441 GTTCACCTTCTC
ον 4.	48	QY	1501 GAAGCAGGTGTT
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Qy 54	541 GCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGG 600 	G · q	
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99 qa	661 CCTGGGCGTGGGGCTGCTGTTCTGTGGCCAGGTGTGCTCCACTCCACTGGAGGCCCT 720	qq	GGGCAT
	721 GCTCTCTGACCTCTTCCGGGACCCGGACCAGGCCTACTGTCTGT	Oy Ph	1801 ATCCCTGTTTAT
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Oy 78	81 CATGATCAGTCTTGGGGCTGCCTGGGCTACCTCCTGCCTG	දි සි	1861 TGCCGCAGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                         lynucleotide encoding polypeptide comprising a portion of tumour protein useful for inhibiting development of prostate
DB 22; Length 3410;
                                                                   partial tumour protein. The DNA is useful for inhibiting the der
of prostate cancer or for treating prostate cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is a human prostate tumour cDNA which encodes a partial tumour protein. The DNA is useful for inhibiting the
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                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer or for treating prostate cancer in a patient
                                                                                                                                                                                                                   Human; prostate tumour protein; prostate cancer;
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                                                                                                               Human prostate tumour cDNA L1-12
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97US-0904804.
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Matches 3410; Conservative
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GGCGCAGCAAGGAGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTG 240 GAGTGCCTGAACGCCCCTGAGCCCTAGCCGCTGGCCAGAAGGTGTG 300		301 GSTGAGCCGCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTT 360 111111111111111111111111111111111111	, 4, -	* * *	CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCTTGGCTGATGGCTGCTGGGGGGGG	009				ω ω						CGTGCCCAG 120	1	13
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٥y	1381	GGTGCCACATGCCTGTCCCACAGTGTGGCGTGGTGACAGCTTCAGCCGCCCTCACCGG 144
qa	1381	CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGACAGCTTCAGCCGCCTCACCGG 1440
οy	1441	GTTC
qq	1441	GITCACCITCICAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTTACCACCGG
Qy Db	1501	GAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGAGAG 1560
Qy	1561	CTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 162
QQ	1561	62
Qy	1621	GGTGCTGGAGGAGTGGCCTGCTGCTCCACCTCCACCCGCGGTCTGCGGGGCCTCTGCCGT
qa	1621	GTGCTGGAGGCAGTGGCCTG
Qy	1681	GGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGGC
qa	1681	GATGTCTCCGTACGTGTGGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCG 1
٥y	1741	TGCTGTCCCAGGTGGCCC
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Qy	1801	ATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGT
QQ	1801	TCCCTGTTTATGGGCTCC
Qy	1861	SCCGCAGGCCTGGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGA
qq	1861	TGCCGCAGGCCTGGGTCTGGTCGCCATTACTTTGCTACACAGGTAGTATTTGACAAGG 1920
Qy	1921	TGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGC
Dp	1921	GACTIGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATIGGGGTGGAGGGCCTGCCT 1
Qy	1981	ACTGGGTCCCAGCTCCCCGCTCTTAGCCCCCATGGGGCTGCCGGGCTGCCCAG
qq	1981	CTGGGTCCCAGCTCCCCGC
Qy	2041	AATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGT
qa	2041	CIGITGCIG
Qy	2101	CTGCACAGCTGGGGCCTGGGGCGTCCCTCCTCCTCCCCAGTCTCTAGGGCTGCCT
QQ	2101	TGCACAGCTGGGGCTGGGGCGTCCCTC
ΟŊ	2161	CTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTC
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QY	2221	GGACTCTGCAGGTGGATTACCCCAGGCTCAGGGTTAACAGCTAG
qq	2221	SCACTGGAATGCGGGGA
οy	2281	TTTGGGAGCTGAATAAACTCAGTCACCT
qq	2281	TCCTAGTTGAGACACCTAGAGAAGGGTTTTTG
δλ	34	GTITCCCATCICTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAG 2400
QQ	2341	TTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes polynucleotide sequences (I) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SL, Jiang Y, Reed SG; , Stolk JA, Skeiky YAW;
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100.0%; Pred. No. 0;
iive 0; Mismatches
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Retter MW,
                                                                                                                                                                                                                 cytostatic; gene therapy; metastasis; ss.
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CH,
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1381 CGGTGC 	1441	1501 GAAGCA 1501 GAAGCA	1561 CCTGATGACCAGCTTCCTGCCAGG 	Qy 1621 GGGTGCTGGAGGCAGTGGCCTGCTCCCACCI	Qy 1681 TGATGTCTCCGTACGTGGGTGGTGGTGGCTGAC	QY 1741 GGGCATCTGCCTGGACCTCGCCATCCTGGAN	QY 1801 ATCCTGTTTATGGGCTCCATTGTCCAGCTC	Oy 1861 TGCCGCAGGCCTGGGTCTGGTCGCCATTAC	Qy 1921 CGACTTGGCCAAATACTCAGGGTAGAAAC7 	1 CACTGGGT CACTGGGT	QY 2041 TTCTGTTGCTGCCAAAGTAATGTGGCTCTC:	2101	2161	Oy 2221 ATGCACTGGAATGCGGGACTCTGCAGTGC	1 CTCCTAGTTGAGACACCCTAGAG; 	Qy 2341 GTTTCCCATCTCAAGCCCCTTAACCTGCACACACACACAC	Oy 2401 TTTCTAGGATGAACACTCCTCCATGGGAT'	1
301 GGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTT 360	361 TGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT 420 	421 GGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT 480	CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCG 5	GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGC 60	CGGCTGCTAGCAGGCTGCTGTGCCGATCCCAGGCCCCTGGAGCTGCACTCTCAT 6	CCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT 7	GCTCTCTGACCTCTTCCGGGACCCGGACCAGTGCCCAGGCCTACTCTGTCTATGCCTT	CATGATCAGTCTTGGGGGGTGCCTGGGTACCTGCTGCGTGCG	TGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGCCTGCTGCACCTCT TGCCCTGGCCCCCTACCTACCTGGGCACCCCAGGAGGAGTGCCTCTTTGCCTGCTCTCACCTCT TGCCTGGCCCCCTACCTGGGCACCCCAGGAGAGTGCTCTTTGGCCTGCTCACCTCAT TGCCCTGGCCCCCTACCTGGGCACCCCAGGAGGAGTCCTTTTGGCCTGCTCACCTCAT TGCCCTGGCCCCCTACCTGGGCACCCCAGGAGGTCCTCTTTGGCCTGCTCACCTCAT TGCCCTGCTCACCTGCTCATCCATCATCATCATCATCATCATCATCATCATCATC	CTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGAGGAGGCAGCGTGGGCCCCAC 9	TTGTCGCCCCACTGCTGTCCATGCCGGGC	CGGCTTGGCTTTCCGGAACCTGGGCGCCTGCTTCCCCGGCTGCACCTGTGCTGCG 108	1081 CATGCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCAT 1140	1141 GACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCCTGTACCAGGCGTGCCCAG 1200 	AGCTGAGCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT	1261 GGGCTGTTCCTGCAGTGGCCATCTCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGT 1320 1101	21 GCAGCGATTCGGCACTCCAGCCAGTCGCCAGTGTGGCCAGCTTTCCCTGTGGCTGC 138	
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	CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGACAGCTTCAGCCGCCTCACGG	1440
	TCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACACTGGCCTCCCTTCTACCACC	
	GITCACCTICTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC	1500
	CAAATACCGAGGGACACTGGAGGTGCTAG	1560
	ATGACCAGCTTCCTGCCAGGCCCTAAGCCTGCAGCTCCCTTCCCTAATGGA	2
	CTGCCAGGCCCTAAGCCTGGAG	~
	GGAGGCAGTGGCCTGCTCCACCTCCACCCGCGCTCTGCG 	1680
	GATGTCTCCGTACGTGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCC	74
Н	GATGTCTCCGTACGTGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCC	1740
	3GACCTCGCCATCCTGGATAGTGCC	1800
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61	GCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAG	
61	CGCGAGGCCTGGGTCTGGTCGCCATTACTTTGCTACACAGGTAGTATTTGAAAGA	1920
	STAGAAACTTCCAGCA	œ
	GACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCC	œ
81	CACTGGGTCCCAGCTCCCGGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGT	2040
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01	regeggctggggcgtcctctctctcccagtcttag	9
01	CTGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCCCCCAGTCTCTAGGGCTGCCT	
61	TTCAGTCTGGACTTATACAGGGA	
61	CTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTTC	2220
21	SCACTGGAATGCGGGACTCTGCAGGTGGATTACCCAGGCTCAG	2280
21	ACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAG	2280
	DCTAGTTGAGACACACTAGAGAAGGGTTTTTGGGAGCTGAATA	34
81	TCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCT	2340
1 1	TAACCTGCAGCTTCGTTTAA	40
7	ICCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGA	40
01	CATGGGATTTGAACATATGACT	46
_	ttctaggatgaaacactcctccatgggatttgaacatatgacttatttgtaggggaag	2460
Н	GTCCTGAGGGGCAACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTTGCT	2520

chromosome 22q11.2; prostate-specific protein; chromosome 1; prostate specific antigen; PSA; ss.

WO200134802-A2

09-NOV-2000; 12-NOV-1999; 18-NOV-1999;

17-MAY-2001

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GATCCACCCCCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA
                                                            CAGAGACACAGGCATTTAAATATTTAACTTATTTAATTTAACAAAGTAGAAGGGAATCCAT
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The present invention describes an isolated polypeptide (P1) comprising to least an immunogentc portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P77FP and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent

Seguence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

the present invention.

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Isolated polypeptide comprising at least an immunogenic portion corrects.

Claim 5; Page 164-165; 325pp; English.

prostate cancer

Harlocker SL, Jiang Y, , Day CH, Skeiky YAW,

Retter MW, Stolk JA, Mitcham JL,

WPI; 2001-308785/32.

99US-0439313

(CORI-) CORIXA CORP.

Dillon DC,

Xu J,

Kalos MD,

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                                     0; Indels
100.0%; Score 3409.6;
illarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                 Best Local Similarity
Matches 3410; Conserv
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Human prostate-specific cDNA sequence L1-12/P501S.

(first entry)

25-SEP-2001

AAH84779

DX ZX Z X E

ВР

AAH84779 standard; cDNA; 3410

RESULT 7 AAH84779

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1441 GTTCACCTTC 1501 GAAGCAGGTC 1501 GAAGCAGGTC	1561 CCTGATGACC 1561 CCTGATGACC	1621 GGGTGCTGGA 1621 GGGTGCTGGA	1681 TGATGTCTCC 	1741 GGGCATCTGC 	1801 ATCCTGTTT 		1921 CGACTTGGCC 	1981 CACTGGGTCC 	2041 TTCTGTTGCT 2041 TTCTGTTGCT	2101 GCTGCACAGC 	2161 ACTGGAGGCC 					2461 GTCCTGAGGC 	2521 GATCCACCCC
90 03	QY DP	Qy Db	Ογ DP	Qy	do Db	Qy QD	Qy	da D	Qy	Qy Db	Qy	da da	Qy Dp	Qy Q	Qy Dp	Qy	Qy
	421 GGGGGTAGAGGAGATTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT 480 481 CTGTGTCCGCTCCTAGGCTCAGCCAGTGACCACTGGGCGTGACGCTATGGCCGCGCG 540 481 CTGTGTCTCTAGGCTCAAGCAAGTAACAACTAGACCACTGGAAGTAAAAAAAA	41 GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGGTCAGCTGTTTCTCATCCCAGGGC	CGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCAT	661 CCTGGGGGTGGGGCTGCTGCTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT 720	721 GCTCTCTGACCTCTTCCGGGACCGGGACCACTGTCGCGGGCCTACTCTGTCTATGCCTT 780	781 CATGATCAGTCTTGGGGCTGCCTGGGCTACCTGCCTGCCATGACTGGGACACCAG 840	841 IGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGACCCTCAT 900	CTTCCTCACCTGCGTAGCAGCACACACTGCTGGCTGGCTG	CAAGCCAGAAAGGCTGTCGGCCCCTTGTCGCCCCATGCTGTCGCCCCCCCC	CGCTTGGCTTTCCGGAACCTGGCCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCC	1081 CATGCCCGGACCCTGCGCCGGCTCTTCGTGGCTGTGCCAGCTGGATGGCACTCAT 1140	1141 GACCTTCACGCTGTTTTACACGGATTTCGTGGCGGGGCTGTACCAGGGCGTGCCCAG 1200	1201 AGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT 1260	1261 GGGGCTGTTCCTGCAGGGGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGT 1320 	1321 GCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGC 1380 	1381 CGGTGCCACATGCCTACAGAGTGGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGG	GTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC
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1441	GTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC	
1501	GAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGGGGGACAG 1560 	
1561	CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 1620	
1621	GGGTGCTGGAGGCAGTGGCCTGCTCCACCTCCACCCGGGCTCTGCGGGGCCTCTGCCTG 1680	
1681	TGATGTCTCCGTACGTGGTGGTGGTGACCCCACCGAGGCCAGGGTGGTTCCGGGCCG 1740	
1741	GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 1800	
1801	APCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 1860	
1861	TGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGGTAGTATTTGACAAGAG 1920 	
1921	CGACTTGGCCAAATACTCAGGGTAGAAACTTCCAGCACATTGGGGTGGÄGGGCCTGCCT 1980 	
1981	CACTGGGTCCCAGCTCCCCGCTCCTGTTAGCCCCATGGGGTGCCGGCTGGCCGCCAGT 2040	
2041	TICTGTIGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTA 2100	
2101	GCTGCACAGCTGGGGGCTGGGGCGTCCCTCTCCTCCCAGTCTCTAGGGCTGCCTG 2160	
2161	ACTGGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGAGGCCAGAAGGGCTCC 2220 	
2221	ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGC 2280	
2281	CTCCTAGTTGAGACACACTAGAGAAGGGTTTTTGGCAGCTGAATAAACTCAGTCACCTG 2340 	
2341	GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGA 2400 	
2401	TITCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA 2460 	
2461	GTCCTGAGGGGAACACAAGAACAAGTCCCCTCAGCCCAAGGACTGTCTTTTGCT 2520 	
2521 2521	GATCCACCCCCTTTACCTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA 2580	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate tumour antigen determined full length cDNA sequence for L1-12.
                                                                                                                                                                                                                                                                                                                                                                     TAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCAACGGCTTCCCTAACCACCCCTCTTCTTCTTGGCCCAGCCTGGTTCCCCCCACTTCCA
                                                                                                                                                                                                                                                          CTCCCCTCTACTCTCTCTAGGACTGGCCTGATGAAGGCACTGCCCAAAATTTCCCCTACC
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CAGAGACACAGGCATTTAAATTATAACTTATTTATTTAACAAAGGTAGAAGGGAATCCAT
          CTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAAT
                                                                                                                                         CTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCAAATGATAAT
                                                                                                                                                                                                                         CTCAACGGCTTCCCTAACCACCCCTCTTCTTTGCCCAGCCTGGTTCCCCCCACTTCCA
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                                       <u> TGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCA</u>
                                                                                GGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTTCTGGGGT
                                                                                                                                                              Human; prostate tumour antigen; prostate tumour; therapy; diagnosis; prostate cancer; immunogenic; cytostatic; vaccine; ss.
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361 TGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT 420
                                                                                                                                                                                                                                                                                                                           The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or lits variant. (I) have eytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonocleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGATGAGACGTGCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT
                                                                                                                                                                                                                                               Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 3410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 3409.6; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                 Cheever MA;
                                                                                                                                                                                                                                                                                                Claim 4; Page 155-156; 276pp; English.
                                                                                                                                                                 Reed SG,
                                                                                                  99US-0157455
                                                                 04-OCT-2000; 2000WO-US27464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 3410; Conservative
                                                                                                                                                                                                WPI; 2001-245062/25.
P-PSDB; AAB74800.
                                                                                                                                CORI-) CORIXA CORP
                                                                                                                                                                   Skeiky YAW,
WO200125272-A2
                                                                                                 04-OCT-1999;
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Homo sapiens

Db 1561 CCTGATGACCAGCTTCCTGCCAGGO OY 1621 GGGTGCTGGAGGCAGTGGCCTGCTC	Oy 1741 GGGCATCTGCCTGGACCTCGCCATC	1921 CGACTTGGCCA 1921 CGACTTGGCCA 1921 CGACTTGGCCA 1921 CGACTTGGCCA 1981 CACTGGGTCCC	Qy 2041 TTCTGTTGCTGCCAAAGTAATGTGGG	2221 2221 2281 2281 2341	Qy 2401 TTTCTAGGATGAAACACTCCTCCATG Db 2401 TTTCTAGGATGAAACACTCCTCCATG Qy 2461 GTCCTGAGGGGCAACACACACAGAACC Qy 2461 GTCCTGAGGGGCAACACACACAGAACC Qy 2521 GATCCACCCCCCTTTATTTATT Db 2521 GATCCACCCCCCTTTAACTTTATT Qy 2581 CAGAGACACCCCCTTTAATTTATTTTTTT Db 2581 CAGAGACACAGGCATTTAAATATTTTT Qy 2641 TGCTAGGATTTCTGTGTTGGTGTCTA Db 2641 TGCTAGGATTTTCTGTGTTGGTGTCTA Db 2641 TGCTAGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
	CCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT 72	781 CATGATCATTTTGGGGGCTGCTGGGGTACCTCCTGCCTGC	CGAGCCAGCAGAAGGGCTGTCGGCCCCTCTGTCGCCCCCCTGTCCTGTCCATGCCGGGC	CTGCGCCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATG STTTACACGGATTTCGTGGCCAGGGGCTGTACCAGGG IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TATTTGGCCAGTGTGCAGCTTTCCCTGTGGCTGC 138
90 40 60	da da da	, oy oy	60 60 60 60	8 6 6 6 6 6	

	1561	1 CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 1620
	62.	GGGTGCTGGAGGGAGTGGCCTGCTCCCACCTCCGCGCTCTGCGGGGCCTCTGCCTG 168
•	1621	GGGTGCTGGAGGCAGTGGCCTGCTCCACCTCCACCGGCGCTTGCGGGGCCTCTGCCTG 168
	1681	TGATGTCTCCGTACGTGTGGTGGTGGGTGAGCCCACGAGGCCAGGGTCCGGCCG 17
	74	GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 180
	1741	
	80	ATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 18
_	80	ATCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 186
	1861	TGCCGCAGGCCTGGGTCGGTCGCCCATTTACTTTGCTACACAGGTAGTATTGACAAGAG 1922
	1921	CGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT
	1981	CACTGGGTCCCAGCTCCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGGTGGCCGCCAGT 204
	04	TTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCCCTGTGCTGCTGAGGTGCGTA 210
	04	Trengtrecteccaaagraateresereresesecaecerereseseseseses 210
	2101	GCTGCACAGCTGGGGGCTGGGGCGTCC
	2161	ACTGGAGGCCTTCCAAGGGGGTTTCAG
	2221	ATSCACTGGAATGCGGGGACTCTGCAGGTGATTACCCAGGCTCAGGGTTAACAGGTAGC 228
	78	CTCCTAGTTGAGACACACCTAGAGAGGTTTTTGGGAGCTGAATAAACTCAGTCACCTG 234
	2281	
	2341	GTTTCCCATCTCTAAGCCCCTTAACCTGCAGTTCGTTTAATGTAGCTCTTGCATGGGAG 2401
	2401	TTCTAGGATGAAACACTCCTCCATGGGATTGGAACATATGACTTATTTGTAGGGGAAGA 246
	5 4	111.CIASGA1.GAAACACICCICCAIGSGAIITGAACAIAIGACITAITIGIAGGGGAAGA 246
	2461	GTCCTGAGGGGCAACACACAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCT 2520
	2521	GATCCACCCCCTCTTACCTTTAACAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA 2580
	2581 2581	TATTTAACTTATTTATTTAACAAAG
-	2641	TGTGTTGGTGTCTAATATTTGGGTAGGG

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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGATGAGACGTGTCCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24; Length 3410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New prostate-specific polynucleotides for diagnosing and treatir diseases, in particular prostate cancer, and as markers for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, 3R, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 3409.6;
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 110; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC, Mitcham JL,
                                                                                                                                                                                                                       20000S-0605783
20000S-0636215
20000S-0651236
20000S-0657279
20000S-067279
20000S-067826
             98US-0030607.
98US-0115453.
98US-0159812.
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Matches 3410; Conservative
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WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                                                                                                                                                                                                                                       MITCHAM J L.
HARLOCKER S
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RETTER M W.
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KALOS M D.
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DAY C H.
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٥y		GCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGC
QQ	1321	CAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCAGCTTTCCCTGTGGCTGC 138
Σγ		CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGG 1440
qa	1381	GGTGCCACATGCCTGTCCCACAGTGTGGCGTGGTGACAGCTTCAGCCGCCCTCACCGG 144
δy	44	CTCTACCACCGGGA 150
qo	1441	CTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC
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ογ.	ın i	62
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δά.		TGATGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCG 1740
q	œ	SATGTCTCCGTACGTGGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCG 174
۵y	4	SCCTGGACCTCGCCATCCTGGATAGTGCCTTC
qa	1741	GGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 180
οy	1801	AGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 186
qo	1801	CCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGT
οy	1861	AGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 192
qa	1861	SCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 192
۵y	1921	GCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGCCTGCCT
qq	1921	GACTIGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT
۵y	1981	STCCCAGCTCCCCGCTCCTGTTAGCCCCCATGGGGCTGCCGGGCTGGCCGCCAGT 204
qq	1981	SGGTCCCAGCTCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGT 204
ρλ	4	STTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGGTGGGTG
q	2041	GTGCCAAAGTAATGTGGCTCTCTGTGCTGCCTGCTGTGTGTG
۵y	2101	CTGCACAGCTGGGGGCTGGGGCGTCCCTCCTCCTCTCCCCAGTCTCTAGGGCTG
qa	2101	TGGGGGGCTGGGGCGTCCTCTCTCTCCCCCAGTCTCTAAGGGCTGCCT
ρλ	2161	SGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCCAGAAGGGCTCC 222
qo	2161	CAGAAGGCTCC 222
λά	2221	TTACCCAGGCTCAGGGTTAACAGCTAGC 228
qq	2221	ACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGC 228
ρy	2281	CICCTAGITGAGACACACCTAGAGAGGGITITITGGGAGCTGAATAAACTCAGICAG 2340
.qq	2281	TAGTTGAGACACACCTAGAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTGACCT
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TTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to polynucleotides encoding breast tumour polypeptides. The sequences are useful for treating cancer, preferably becast cancer, in a patient or for stimulating an immune response. The polynucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that bind to a breast tumour polypeptide, detecting in the sample an amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient. Sequences ABK28920-ABK29025 represent cDNA clones encoding human breast tumour polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGTGCCTGAACGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG
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                                                                                                                    Human; breast tumour polypeptide; gene; ss; breast cancer; cytostatic;
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o
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                                                                                     Human breast tumour polypeptide full length cDNA clone #3.
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100.0%; Pred. No. 0;
ive 0; Mismatches
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12-OCT-2000; 2000US-0687507.
06-FEB-2001; 2001US-0778381.
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Matches 3410; Conservative
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                                                                                                                                       immunostimulant.
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                                                                                                                                                                    Homo sapiens
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qα	241 GAGTGCCTGAACGGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG 300		
Qy	301 GGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTT 360	δλ	81 CGGTGCCACATGCCTGTCCCACAGT
qa	CTGCGCACCGGAAAG	g C	81 CGGTGCCACATGCCTGT
δ d	361 TGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT 420	ÅÖ qa	1441 GTTCACCTTCTCAGCCCTGCAGATCC
8 8	1 166CCTGCGGGGGGTTTGGCCGCGGGGATCACCTATGTGCCGCCTCTGCTGCTGGGAAGT 42	Oy	GAAGCAGGTGTTCCTGC
දු දු	421 GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT 480	ga a	1501 GAAGCAGGTGTTCCTGCCCAAATACC
ογ	CTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCG 54	QY	1561 CCTGATGACCAGCTTCCTGCCAGGCC
qa		qa	ATGAC
οy	9	Ολ	62
qq	GCACT	qa '	21 GGGTGCTGGAGGCAGTGGCCTG
Qy	601 CGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACGAT 660 1	da D	1681 TGATGTCTCCGTACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTG
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qq	661 CCTGGGCGCTGCGGCTCTTCTGTGGCCCAGGTGTGCTCCACTCCACTGGAGCCCCT 720	qa	ATCTGCCTGGACCTC
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δy	CTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGTGAGGAGGCAGCGGTGGGCCCCCAC 96	Oy	1981 CACTGGGTCCCAGCTCCCGGCTCTG
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q	961 GGAGCCAGCAGAAGGGCTGTCGGCCCCTCCTTGTTGTTTTTTTT	අ _ධ ,	41 TTCTGTTGCTGCCAAAGTAAT
oy Og	1021 CCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCG 1080 	da q	
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අු	1201 AGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT 1260	qa «	281 CTCCTAGTTGAGACACACCTAG
λō	GGGGCTGTTCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGT 1	λο qa	2341 GTTTCCCATCTCTAAGCCCCTTAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polynucleotides encoding the polypeptides can be used a a probe or the modulate the expression of the polypeptides. AAA06241 to AAA06691 and AAX82000 to AAX82000 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:110
                             prostate cancer; diagnosis; tumour; gene therapy; detection;
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                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide useful for treating and diagnosing prostate comprises an immunogenic portion of prostate tumor protein .
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 135-136; 263pp; English.
                                             immunogenic; cytostatic; vaccine; ss.
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98US-0116134.
98US-0159812.
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Matches 3409; Conservative
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Db 1381 CGGTGCCACATGCCTGTCCC	Oy 1441 GTTCACCTTCTCAGCCTGC, 	Qy 1501 GAAGCAGGTGTTCCTGCCCA 	Oy 1561 CCTGATGACCAGCTTCCTGC	Qy 1621 GGGTGCTGGAGCAGTGGCCT 	Qy 1681 TGATGTCTCCGTACGTGTGGT 	Oy 1741 GGGCATCTGCCTGGACCTCGC	Qy 1801 ATCCTGTTTATGGGCTCCAI	Oy 1861 TGCGCAGGCCTGGGTCTGG1	QY 1921 CGACTTGGCCAAATACTCAGG 	Oy 1981 CACTGGGTCCCAGGTCCCGGC	Qy 2041 TTCTGTTGCTGCCAAAGTAAT	Qy 2101 GCTGCACAGCTGGGGGCTGGG	Qy 2161 ACTGGAGGCCTTCCAAGGGGG 	Oy 2221 ATGCACTGGAATGCGGGGACT 	Oy 2281 CTCCTAGTTGAGACACACTA	OY 2341 GTTTCCCATCTCAAGCCCTT	Qy 2401 TTTCTAGGATGAAACACTCCT 	Oy 2461 GTCCTGAGGGCAACACAAA
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ξ. q	1441	GTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC
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λq		CCTGATGACCAGCTTCCTGCCAGGCCCTAGGCCTGGAGCTCCCTTCCCTAATGGCAGGT 162
λQ	1621	GGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGGGCTCTGCGGGGCCTC
γ q	1681 1681	TGATGTCTCCGTACGTGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCG 174
ъ q	1741	GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 18
>	1801	ATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGT 1860
ъ д	1861	TGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 1920
λ Q	1921 1921	STGGAGGCCTGCCT 19
	1981	CACTGGGTCCCAGCTCCCGGTCCTGTTAGCCCCATGGGCTGCGGGGTGGCGCCGGCAGT 2040
. <i>k</i> c	2041	TICTGTIGCIGCCAAAGTAAIGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTA 2100
	2101	GCTGCACAGCTGGGGGCTGGGGCGTCCCTCTCCTCCCCAGTCTCTAGGGCTGCCTG 2160
	2161	ACTGGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGGGGGCGGAGAGGGCTCC 2220
	2221 2221	ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGC 2280
	2281 2281	CTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTG 2340
	2341	GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTGTTTAATGTAGCTCTTGCATGGGAG 2400
	2401	TTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA 2460
	2461	GTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTTGCT 2520

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Location/Qualifiers 282..1943

SS.

cytostatic; vaccine;

Homo sapiens

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                                          CAGAGACACAGGCATTTAAATTTTAACTTTATTTAACAAAGGTAGAAGGGAATCCAT
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                                                                                                                                               Human; PROST 03; metastasis; prostate cancer; tumour; immune response;
                                                                   AAS14962 standard; cDNA; 3320 BP
                                                                                                                            DNA encoding human PROST 03.
                                                                                                        14-FEB-2002 (first entry)
                                                                                     AAS14962;
                                                RESULT 12
                                                        AAS14962
ID AAS:
XX
AC AAS:
XX
DT 14-1
XX
DE DNA
XX
KW HUM3
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The invention relates to an isolated PROST 03 polypeptide (I) and to the polynucleotide (II) encoding PROST 03. Fragments of (I) were used to generate antibodies (III) to PROST 03. (III) 1s useful for selectively destroying a cell expression of PROST 03. (III) 1s useful for selectively east-octated with expression of PROST 03 in a human patient. (III) is useful for diagnosing and treating diseases of cell proliferation such as prostate cancers. (I) is also useful for diagnosing and treating diseases of cell proliferation such as prostate cancers. (I) is also useful for generating antibodies to PROST 03. (III) is useful in detecting the levels of PROST, (3) polypeptides in cells and tissues, and in targeting drugs to primary and metastatic tumours. (I) is also useful for stimulating immune response to PROST 03 containing cells. (II) is useful in diagnostic assays for detecting the levels of polynuclectides encoding PROST 03 in cells and tissues. (II) is useful as DNA probes, as targets for antisense and ribozyme therapy, and as templates for the production of antisense polynuclectides. (I) and (II) are useful in research, biological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel PROST 03 polypeptides and polynucleotides useful in research, diagnosis and therapeutic applications, particularly for use in cancer
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                                                                                                                                                                                                                                                                                                                                                     Steinbrecher R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clinical and therapeutic purposes. The present sequence represents the coding sequence of human PROST 03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24; Length 3320;
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                                                                                                                                                                                                                                                                                                                                                       Schneider DW,
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Pred. No. 0;
0; Mismatches
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99.98;
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20-APR-2001; 2001US-0200065.
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Matches 3316; Conservative
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Wu J;
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P-PSDB; AAU10324.
                                                                                                                                                                                                                                                                                                                  (SCHD ) SCHERING AG.
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Van Héuit PT,
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Db 1321 AGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTG	Oy 1383 GTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGAC	Oy 1443 TCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTI	Oy 1503 AGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGG,	Oy 1563 TGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGC	Qy 1623 GFGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCCCCCCCC	Qy 1683 ATGTCTCCGTACGTGGTGGTGGCTGACCCACCGAC	1743 GCATCTGCCTGGACC 	LTAT	Qy 1863 CCGCAGGCCTGGGTCTGGTCGCCATTACTTTGCTACA	OY 1923 ACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCAC.	QY 1983 CTGGGTCCCAGCTCCCGGTCCTGTTAGCCCCATGGGC Db 1981 CTGGGTCCCAGCTCCCGGTCTGTTAGCCCCATGGGC	Qy 2043 CTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACC Db 2041 CTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACC	QY 2103 TGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCTCTCTC	Qy 2163 TGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATAC 	Oy 2223 GCACTGGAATGCGGGGACTCTGCAGGTGGATTACCAGC 11	Oy 2283 CCTAGTTGAGACACACCTAGAGAAGGGTTTTGGGAGG	Oy 2343 TICCCATCICTAAGCCCCTTAACCTGCAGCTICGTITA	Oy 2403 TCTAGGATGAAACACTCCTCCATGGGATTTGAACATAI
ε (TGAGCGCCTGCTGCGGCGCCCCGGAAAGCCCACTTGGCTCCAGAGGCTGTGGG TGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTG TGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	63 GCCTGGAGGTGTTTGGCCGCAGGATCACCTATGTGCGCCTCTGCTGCTGCAGGAGG 42 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	23 GGGTAGAGGAGAAGTTCATGACCATGGTGGCGATTGGTCCAGTGCTGGGCCTGGTCT 48	36CCGGC 5	9	TGCTCATCC 6	CTGC 7	723 TCTCTGACCTCTTCCGGGACCGGGACCACTGTCGCCACTCTGTCTATGCCTTCA 782	783 TGATCAGTCTTGGGGCTGCCTGGCTACCTGCCTGCCATTGACTGGGACACCAGTG 842	AGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATCT 90	367GGCTGAGGAGGCAGGCTGGGCCCACCG 96	rccargccgggcc 10	SCTGCCGCA 10		120	SCCTGG 12 SCCTGG'12	CCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGC 132	ပ္က
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TGGCAGCTTCCCTGTGGCTGCCG 1380 1442 1562 1560 CTCCCTTCCCTAATGGACACGTGG 1622 1682 CACAGGTAGTATTGACAAGAGG 1922 2040 CCCTGTGCTGCTGAGGTGCGTAGC 2102 2282 2280 2342 TGGCCTCCCTCTACCACCGGGAGA 1502 CGCTCTGCGGGGCCTCTGCCTGTG 1680 AGGCCAGGGTGGTTCCGGGCCGGG 1742 TCCTGCTGTCCCAGGTGGCCCCAT 1802 CTGTCACTGCCTATATGGTGTCTG 1862 CIGTCACTGCCTATATGGTGTCTG 1860 CATTGGGGTGGAGGGCCTGCCTCA 1982 CATTGGGGTGGAGGGCCTGCCTCA 1980 GGCTGCCGGGCTGCCGCCAGTTT 2042 GCTGAATAAACTCAGTCACCTGGT 2340 TAATGTAGCTCTTGCATGGGAGTT 2402 TAATGTAGCTCTTGCATGGGAGTT 2400 ATG--ACTTATTTGTAGGGGAAGA 2460 GGCTGCCGGGCTGGCCGCCAGTTT CAGCTTCAGCCGCCCTCACCGGGT GAGGTGCTAGCAGTGAGGACAGCC CGCTCTGCGGGGCCTCTGCCTGTG SCTGAATAAACTCAGTCACCTGGT

cancer; ss; cytostatic; immunostimulant; tumour

Human; prostate

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TCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGAAAGTTATTTGTAGGGGAAGA 2460
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               GTCCTGAGGGCCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTTGCT
                       GATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA
                                                                           CAGAGACACAGGCATTTAAATATTTAACTTATTTAATTTAACAAAGTAGAAGGGAATCCAT
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Human prosate cDNA P553S splice variant #3

(first entry)

29-JAN-2002

AAS64040

AAS64040
ID AAS6
XX
AC AAS6
AC AAS6
DT 29-J
XX
DE Huma

AAS64040 standard; cDNA; 4034

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The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, polypeptides for antigenic epitopes antibodies raised against the polypeptides for antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynocheotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The present sequence is a prostate specific detecting cancer. The present sequence is a prostate specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TGCCTGAACGGCCCCCTGAGCCCTACCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGT
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Carter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          illon DC, Mitcham JL, Harlocker SL, Jiang Y,
FR, Retter MW, Stolk JA, Day CH, Vedvick TS,
Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
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Pred. No. 0;
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2000US-0568100.
2000US-0570737.
2000US-0593793.
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2000us-0651236.
2000us-0657279.
2000us-067279.
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82.4%;
                                                                                                                                  27-MAR-2001; 2001WO-US09919
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dillon DC,
                                        WO200173032-A2
                                                                                                                                                                                                                                                                                               10-AUG-2000;
                                                                                                                                                                                                                                                                                                                  29-AUG-2000;
06-SEP-2000;
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10-OCT-2000;
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                                                                                                                                                                                                                                                                       27-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GR,
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ò	CACCGGAAAGCCCAGCTCTTGCTGGTCAACC	δλ	1240
අ		q ₀	89
λo i	CCTGGAGGTGTGTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGCTAGATGGG 4	da da	1240
Q	61 CCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCAGTGGG 4	٥٧	1240
දු දු	424 GGTRGAGGAGAAGTTCATGACCATGGTGGTGGGCATTGGTCCAGTGCTGGGCCTGGTCTG 483 	qa	1501 AGTCTAGAGGGAGTGGAGGAGTTAAGGCTG
ò	84	Qy	1240
G Q	81 TGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGCC	qu	1561 TGTGCCCTCTGCTCCCCCAACGACTTTCCA
ογ	544 CTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGG 603	λo t	
QQ	541 CTTCATCTGGGCACTGTCTTTGGGCATCCTGGTGAGCCTCTTTCTT	g à	1240
χο ε	604 CTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCT 663	දි අ	1681 GTCCTCACAGCTGAGACTCCCAGGAAACC
3 8	CLOCOLDOCAGOGCIOCIOLOCICCOGALCCCAGOCCCCIOGAGCIGGCACACIGGCACACIGCICAICCI	٥y	1240
5 A	661 GGGCGTGGGGCTGCTGGACTTCTGTGGCCCAGGTGTCCTCCACTCCACTGGTGCTTCTT 7.23	qq	1741 GGCGTTGCCCACATTCTCTGAGGGTCAGT
δλ		δy	1240
qq		qq	1801 GAAAGGGGAAGGGTGCTGGGGAGCAGGGC
ò	(3年でもの中ではのののできない) できない かんしゅん かんしゅん かんしゅん かんしゅん かんしゅん アンドラン かんしゅん かんしゃ かんしゅん かんしゅん かんしゅん かんしゅん かんしゅん かんしゅん かんしゅん かんしん かんし	Oy	1240
ga G		qa	1861 CTGTGGTTCCGCCTTCTCATCTCCCTGAGA
ογ	CCTGGCCCCCTACCTGGGCACCCAGGAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCTT 90	Qy	1240AGGCGTTC
QQ		qa	
Qy	904 CCTCACCTGCGTAGCCACACTGCTGGTGGCTGAGGAGCAGCACCGCACCGA 963	Qy	1278 GCGCCATCTCCTGGTCTTCTCTCTGGTCA
qq	901 CCTCACCTGCGTAGCAGCCACCACTGCTGGGTGAGGAGCAGCGCTGGGCCCCACCGA 960	gg :	
QY	964 GCCAGCAGAAGGGCTGTGGGCCCCTTGTCGCCCCATGCTGTCCATGCCGGGCCCG 1023	Å å	1338 GAGCAGTCTATTTGGCCAGTGTGGCAGCTT 1
QQ	961 GCCAGCAGAAGGGCTGTCGGCCCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCG 1020	2	
δ <i>δ</i>	1024 CTTGGCTTTCGGGAACCTGGGCGCCTGCTGCCCGGCTGCACCAGTGTGCTGCCGCTT 1083	q _Q	2101 CCCACAGTGTGGCCGTGACAGCTTCAC
3 8	CITGGCTITICCGCGCGCCCCTGCTITCCCCGGCIGCTGCCGGCTGCTGCCGCGCIGCTGCTGCTGCTTTTGCGCGCGC	Qy	1458 TGCAGATCCTGCCCTACACACTGGCCTCCC
7 원	GCCCCGCACCCTGCGCCGCTCTTCGTGAGCTGTGCCAGCTGGATGGCACTCATGAC 114	qa	-
ογ	1144 CTTCACGCTGTTTTACACGGATTTCGTGGGCGACGCGCTGTACCAGGGCGTGCCCAGAGC 1203	Qy Dp	1518 CCAAATACCGAGGGACACTGGAGGTGCTP
QQ	1141 CTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAGC 1200	i	
Qy	1204 TGAGCCGGCCACCGAGGCCCGGAGACACTATGATGA	λ ⁶	, מ ה
QQ	1201 TGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGTAAGGCCTTGGCAGCCAGC	2 20	
ογ	1240 1239		
QQ	1261 AGCCTGGTGTGGGAGCCGCCCACAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCC 1320	3 :	GCC16C11CCACC1CCACC1CCACCCACCCACCACCACCACCACC
Οy	1240 1239	₹ £	1040 166166166616466116461164611646661646666164666666
QQ	1321 TCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGGATGGACCCCATCTGCATACA 1380	3 ò	10000

λ.	1240		1239
۵	1381	CGGCTTCTCATGGGTGTGGAACATCTCTGCGTTTCAGGAAGGCCTCTGGCTGCTC	1440
>-	1240		1239
Ω	1441	aggagtctgatcagagtcgttgccccagtttgacagaaggaaaggcgg	1500
>	1240		1239
Ω	1501	GTCTAGAGGGAGTGGAGTTAAGGCTGGATTTCAGATCTGCC	1560
>-	1240		1239
Ω	1561	CCCTCTGCTCCCCCAACGACTTTCCAAATAATCTCACCAGGGGCCTTCCAGC	1620
۸.	1240		1239
۵	1621	CCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCC	1680
۸	1240		1239
۵	1681	TCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAG	1740
۸	1240		1239
۵	1741	rgcccacattctctgagggtcagtggaagaacctagactccattgc	1.800
*	1240		1239
Ω	1801	AAGGGGAAGGGTGCTGGGGAGCAGGCTGGTCCACAGCAGGTCTCGTGCAGC	1860
>-	1240		1239
Ω	1861	GFGGTTCCGCCTTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCC	1920
٨	1240		1277
Ω	1921	rescecetereceseses	1980
۸.	1278	GCGCCATCTCCCTGGTCTCTCTGGTCATGACCGGCTGGTGCAGCGATTCGGCACTC	1337
Ω	1981	CGCCATCTCCCTGGTCTTCTCTCGTCATGGACCGGCTGCAGCGATTCGGCACT	2040
× 9	1338	GAGCAGTCTATTTGGCCAGTGTGGCAGTTTCCCTGTGGCTGCCGGTGCCACATGCCTGT 	1397
>-	1398	CCCACAGTGTGGCGTGGTGACAGCTTCAGCCGCCTCACGGGGTTCACCTTCTCAGCCC	1457
۵	2101	CACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGC	2160
^	1458	TGCAGATCCTGCCCTACACACTGGCCTCCCTCACCGGGAGAAGCAGGTGTTCCTGC	1517
۵	2161	CAGATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGAGAAGCAGGTGTTCCTG	2220
>-	1518	CCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCC	1577
۵	2221	CAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTC	2280
>-	1578	TGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGCAGTG	1637
a	2281	GCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGT	2340
5.	1638	GCCTGCTCCCACCTCCACCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTG	1697
c	2341	ccrecreceaceaceaceaceaceaceaceaceaceacaraceracaracerace	2400
> -	869	GGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCC	75.
c	01	GGTGGTGGGTGAGCCCACGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGAO	
>	1758	TCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCT	1817

		qq	3540 CCAAGGTTAGGGTGTTGAAGGAAG
අු	TCGCCATCCTG	λŎ	9
OV O	1818 CCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTC 1877	qa	
Qy	TGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGGGACTTGGCCAAATACT	qa .	. 2956 TCTAGGACTGGGCTGATGAAGGC, 11111111111111111111111111111111111
ପୁପ (IGGICGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACT 2	QY	3016 CCCCCAACTTTCCCCACCAGCTC
da da	1938 CAUCGIAGAAACTICCAGCACTIGGGGTGGAGGCCTGCCTCACTGGGTCCAGCTCC 1997 LILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	qq	3720 CCCCCAACTITCCCCACCAGCTC
δò	CCGCTCCTGTTAGCCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTTCTGTTGCTGCCAAAG	٥y	3076 CAAAGTGCGGTTTCCCAAGCCTT
qa	2701 CCGCTCCTGTTAGCCCCCATGGGGCTGCCGGGCTGGCCGCCATTCTGTTGCTGCCAAAG 2760	අ	
ογ	TAATGTGGCTCTCTGCTGCCCCCCTGTGCTGAGGTGCGTAGCTGCAAAGCTGGGGGC	දු අ	3130 GAATCTCACACAGAAACTCAGGA
යු	TAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTAGCTGCACAGCTGGGGGGC	ò	3196 AGGGGGGTTTAAGTGCCGTTTG
Å i	TGGGGCGTCCCTCTCTCTCTCCCCAGTCTCTAGGGCTGCCTGACGGAGGCCTTCCAAG 217	qa	3900 AGGGGGGTTTAAGTGCCGTTTG
gg	Tegecerce	ò	3256 TTTATACTGTAAGTGAGCAATCA
À t	GGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGCTCCATGCACTGGAATGCGGG 223	g 43	σ
g .	GGGGTTTCAGTCTGGACTTATACAGGGGGCCCAGAAGGGCTCCATGCACTGGAATGCGGG	δλ	3316 TTATATGTTTAAAAA 3330
ογ	2238 GACTCTGCAGGTGGATTACCCCAGGCTCAACGTAACAGCTTCTCTAGTTGAGACACA 2297	qq	4020 TTATATGTTTAAAAA 4034
Dp	2941 GACTCTGCAGGTTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGTTGAGACACA 3000		
Oy Dp	2298 CCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGC 2357	RESULT AAH930 ID	Jr 14 1868 AAH93868 standard: CDNA: 4034 BP
δ	CAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACAC	XX	
q a		XX TQ	04-OCT-2001 (first entry)
δλ	2418 TCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGAGTCCTGAGGGCCAAC 2475	XX DE	P553S CDNA splice variant P553S-
q		XX	; prostate
٥٥	2476 ACACAAGAACCAGGTCCCCTCACAGCCAAGACACACTATTTTGCTAATCCACAACAACCAAGATCAACAAACA	X X X	cytostatic; gene therapy; metast
ු සි	ACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCCTCT 324	s XX	Homo sapiens.
Å	259	N X	WO200151633-A2.
qq		PD XX	19-JUL-2001.
Οy	ACTTATTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTCTGT 265	PF XX	16-JAN-2001; 2001WO-US01574.
q		P.X.	14-JAN-2000; 2000US-0483672.
ò	GTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCCTGAGATAG	PA	(CORI-) CORIXA CORP.
r do		PI PI	MD,
AO	2716 CTGGTCATTGGGCTGATGCCAGAATCTTCTTCTTCTTGGGGTCTGGGCCCCCCAAAAT 2775	PI	Wang A, Meagher MJ;
7 da	CIGGICALTGGGCTGATCALTCTCTTCTCTCGGGGTCTGGCCCCCCAAAAT 347	DR	WPI; 2001-425873/45.
å	COC	F	New polynucleotide encoding a pr
3 A	2770 OCCUPACIONOSACOLIDOS OCCUPACIONIDA OCCUPACIONIDA	Z Z X	diagnosing, monitoring and treat for use in vaccines
l è	, ,	S	Claim 1; Page 460-461; 543pp; En
\$		00 -	The present invention describes

polynucleotide sequences (I) which encode

prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and isolated artibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to exemplification of the present invention.

Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;

ATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGGCTGAGAAG 123 CIGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTGGC 183 63 9 4 AACCAGCCTGCACGCGCTGGCTCCGGGTGACAGCCGCGCGCCCTCGGCCAGGATCTGAGTG Gaps 75.8%; Score 2585.4; DB 22; Length 4034; 82.4%; Pred. No. 0; 1; Indels 709; 0; Mismatches Matches 3325; Conservative Best Local Similarity 64 Query Match 61 124 g 셤 ò g ò

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180 243 303 GAGCCGCCTGCTGCGCCACCGGAAAGCCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGG 363 CCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGGTGGAAGTGGG 423 GGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTG 483 543 CTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGG 603 CTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCT 663 GGGCGTGGGGCTGCTGGTGTGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCT 723 CTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCAT 783 GGCAGCAAGGAGGAGAGGCCGCAGCTTCTGGAGCAGAGCCGAGAAGCAGTTCTGGAG TGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGCC TGCCTGAACGGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGT 121 241 784 181 244 304 301 364 361 424 421 481 544 541 604 601 664 561 724 721 484

123		1240	δ
186	GAAAGGGGAAGGGTGCTGGGGGAGCAGGGCTGGTCCACAGAGGTCTCGTGCAGGTAC	1801	Db
123		1240	δy
180	GGCGTTGCCCACATTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTA	1741	qq
123		1240	Qy
174	GTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGG	1681	QQ
123		1240	Qy
168	CGTCCTAGAAGCGTCTTGAAGCC	1621	qq
123		1240	δy
162	TGTGCCCTCTGCTCCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCCAGG	. 1561	QQ
123		1240	δy
156	AGTCTAGAGGGAGTGGAGGAGTTAAAGGCTGGATTTCAGATCTGCCTGGT	1501	qq
123		1240	Qγ
150	TAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAG	1441	qq
123		1240	ΟŊ
144	CGGCTTCTCATGGGTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCT	1381	qq
123		1240	Óλ
138	TCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGGGATGGACCCCATC	1321	QQ
123		1240	δλ
132	AGGCTGGTGTGGGAGCCGCCCACCAGAGACGACACTCGGGGCTGTGTCTGGG	1261	qq
123		1240	δλ
126		1201	qq
123	TGAGCCGGGCACCGAGGCCCGGAGACACTATGATGA	1204	٥y
120	CTTCACGCTGTTTTACACGGATTTCGTGGGCGGGGGCTGTACCAGGGC	1141	Dβ
120	CTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTTACCAGGGCGTGCCCAG	1144	ΟŸ
114	GCCCCCCACCTGCCCGCCTCTTCGTGGCTGAGCTGTGAGCTGGAGCTGGAGCTGATGAC	1081	qq
114	GCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATG	1084	Qγ
108	CTTGGCTTTCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCAT	1021	qq
108	CTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGC	1024	οy
102	GCCAGCAGCAAGGGCTGTCGCCCCCTCCTTGTCGCCCCCACTGTCGTCGTCGTCCGGGCCCC	961	Dp
102	GCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCC	964	Οy
960	CCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGAGCGCTGGGCCCCACCGA	901	qq
963	CCTCACCTGCGTAGCAGCCACACTGCTGGTGAGGAGGAGGGAG	904	Οy
900		841	qq
0	SGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCAT	844	ò
840		781	Op

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-	CC	3001 CCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTCCCATCTAAAGC 306	OY 2358 CCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGAGTTTCTAGGATGAAACAC 2417	OY 2418 TCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGAGTCCTGAGGGGCAAC 2475	Oy 2476 ACACAAGAACCAGGTCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCTCT 2535	Qy 2536 TACCTTTTATCAGGATGTGGCTGTTGGTCCTTCTGTTGCCATCACAGACACAGGCAT 2595	Qy 2596 TTAAATATTTAACTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGT 2655 1111111111111111111111111111111111	OY 2656 GTTGGTGTCTAATATTGGGTAGGGTGGGGATCCCCAACAACAGGTCCCCTGAGATAG 2715	OY 2716 CIGGLCATIGGGCTGATCATIGCCAGAATCTTCTCCTGGGGTCTGGCCCCCCAAAT 2775	OY 2776 GCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTAC 2835	OY 2836 CCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGCTTCCCT 2895	OY 2896 AACCACCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCACTTCCACTCCCCTTATCTCT 2955	QY 2956 TCTAGGACTGGCTGATGAAGGACTGCCCAAAATTTCCCCTACCCCAACTTTCCCCTA 3015 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	0y 3016 CCCCCAACTTTCCCCACCACCACCACCACACTTTGGAGCTACTGCAGGACCAGAAGCA 3075 Db 3720 CCCCCCAACTTTCCCCACCAGCACCACACCCTGTTTGGAGCTACTGCAGGACCAGAAGCA 3779	Qy 3076 CAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGG 3135	QY 3136 GAAICTCACACAGAAACTCAGGAGCACCCCTGCCTGAGCTAAGGAGGTCTTAICTCTC 3195 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	2y 3196 AGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT	QY 3256 TTTATACTGFAAGTGAACAATCAGACTATAATGTTTATGGTGACAAAATTAAAGGCTTTC 3315	Oy 3316 TTATATGTTTAAAAA 3330
		CGGANGGGGAGCTGTTCCTGCAGT 1277	GCACTC 133 GCACTC 204	GCCTGT 139		TCCTGC 15	GCTTCC 157 -	SCAGTG 163 SCAGTG 234	CTCCGTACGTG 1	FGGACC 175	FGGGCT 181	regerc 187	AATACT 193 	199	CCAAAG 205	36666C 211	CCCAAG 217	GCGGG 22:	ACACA 229 ACACA 300
	1861	OY 1240	QY 1278 GCGCATCTCCCTGGTCTCTCTGGTCATGGACCGGCTGGTGCACCGATTCG	QY 1338 GAGCAGTCTATTGGCCAGTGTGGCAGCTTTCCCTGTGGCTG Db 2041 GAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTG	QY 1398 CCCACAGTGTGGCGTGGTGACAGCTTCAGCCGCCCTCACCGGTTCACCTTCT Db 2101 CCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCAGCCGCCTTCACCGGGTTCACCGGGTTCACCTTCAGCCGCCTTCACCGGGGTTCACCTTCACCGGGGTTCACCTTCACCGGGGTTCACCTTCACCGGGGTTCACCTTCACCGGGGTTCACCTTCACCGGGGTTCACCTTCACCGGGGTTCACCTTCACCGGGGTTCACCTTCACCGGGGTTCACCTTCACCGGGGTTCACCTTCACCTTCACCGGGGTTCACCTTCACCTTCACCGGGGTTCACCTTCACCGGGGTTCACCTTCACTTCACTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTC	Qy 1458 TGCAGATCCTGCCTACACACTGGCCTCCTCTACCACGGGAGAACCAGGTGT Db 2161 TGCAGATCCTGCCTACACTGGCCTCCTCTACCACGGGAGAACCAGGTGT	QY 1518 CCARATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACACCTGATGACCA Db 2221 CCARATACCGAGGGACACTGGAGGTCTAGCATGAGAGCAGCCTGATGACACA	QY 1578 TGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGCAGAG Db 2281 TGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAG	OY 1638 GCCTGCTCCCACCTCCGGGGCTCTGCGGGGCCTCTGCCTGTGATGTC	OY 1698 TGGTGGTGGTGAGCCCACCGAGGCTGGTGGTTCCGGGCCGGGGCATCTGCC Db 2401 TGGTGGTGGGTGAGCCCACCGAGGTGGTTCCGGGCCGGG	Oy 1758 TCGCCATCCTGGATAGTGCCTTCCTGCTGTCCAGGTGGCCCCATCCTGTTTA:	QY 1818 CCATTGTCCAGCTCAGCCAGTCTGTCACTATATGGTGTCTGCGCAGGCC	Qy 1878 TGGTCGCATTTACTTTGCTACACAGGTAC 	Qy 1938 CAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGCCTGCCT	Qy 1998 CCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCGCCAGTTTCTGTTGCTG IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 2058 TAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTAGCTGCACAGCTC	Oy 2118 TGGGGGGTCCCTCCTCCTCCCCAGTC:	Qy 2178 GGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCATGCACTGGAAT L	OY 2238 GACTCTGCAGGTGGATTACCCAGGCTCAGGGTAACAGCTAGCT

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Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                       Human P553S splice variant SEQ ID NO 704.
                  ВР
                 ABL95411 standard; cDNA; 4034
                                                                                                                                                                                                                                                                                          14 - JAN - 2000; 2000US - 0483672.
27 - MAR - 2000; 2000US - 0586100.
12 - MAY - 2000; 2000US - 0568100.
13 - JUN - 2000; 2000US - 0593733.
27 - JUN - 2000; 2000US - 0693793.
27 - JUN - 2000; 2000US - 0693783.
10 - AUG - 2000; 2000US - 0631236.
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990S-0443686.
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9803-0103607.
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9903-0232149.
9903-0238146.
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2000US-0679426.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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DILLON D C.
MITCHAM J L.
HARLOCKER S L
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RETTER M W.
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09-APR-1999;
13-JUL-1999;
12-NOV-1999;
18-NOV-1999;
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09-FEB-1998;
25-FEB-1998;
14-JUL-1998;
23-SEP-1998;
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                     The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention.
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                                                                                                                                   1; Indels 709; Gaps
                                                                                                           75.8%; Score 2585.4; DB 24; Length 4034; 82.4%; Pred. No. 0;
                                                                                    Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;
                                                                                                                                    0; Mismatches
Claim 1; SEQ ID NO 704; 87pp; English.
                                                                                                                       Best Local Similarity 82.4
Matches 3325; Conservative
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1121 TCCTCCATGGGATTTGAACATATGAAAGTTATTTGTAGGGGAAGAGTCCTGAGGGGCAAC 3180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in gene therapy, as a vaccine or in antisense applications.
ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes
                                                            cytostatic;
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                                                           Prostate cancer; prostate tumour tissue; human; mammal;
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                             Prostate cancer-associated DNA sequence #103.
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0; Mismatches
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2001US-276791P.
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2001US-281922P.
2001US-286214P.
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Matches 2499; Conserv
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2428 TICTAGGATGAAACACTCCTCCATGGGATTTGAACATATGAAGTTATTTGTAGGGGAAG 2487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, darithodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer
TTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGT
                                                             2402 TICTAGGATGAAACACTCCTCCATGGGATTTGAACATATG --ACTTATTTGTAGGGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                            AGTCCTGAGGGCAACACACAAGAACCAGGTCCCCTCAGCCC 2501
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A, Day CH, Vedvick TS,
epler WT, Henderson RA;
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                                                                                                                                                                                                                                                                                                                                  Human prosate cDNA P553S splice variant #2
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Fanger GR, Retter MW, Stolk JA, Day CH
Li Sx, Wang A, Skelky YAW, Hepler WT,
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2000US-0570737.
2000US-0593793.
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2000US-0651236.
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10-OCT-2000; 2000US-0685166.
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12-MAY-2000;
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29-AUG-2000;
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                       Indels
 DB 22;
 Score 2196.4;
           Pred. No. 0;
0; Mismatches
 64.4%;
88.2%;
Query Match
Best Local Similarity 88.2
Matches 2560; Conservative
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10	10;	1 TCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTACCACCGGGAGAACCAGG 1080
11	15(9 TGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGA 1568
11.11 CONTROLLED 1.00 1.		I TGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGGACAGGACAGCCTGATGA 1140
16.39 GAGGACATGGGCCTGCTCCACCTCGCGCGCTCCTCCTCTGCTGTTTTTTTT		
1692 CCCRACATORGEOGRAPHICACCOCCACCACCACCACCACCACCACCACCACCACCACC	9 0	GAGGCAGTGGCCTGCTCCCACCTCCACCGCGCTCTGCGGGGCCTCTGCTGTGATGTCT 1688
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1749 GCCTGGACCTCGACATCCTGCATCCCTCCTCCTCCTCCCTC	~ ~	
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1869 GCCTGGGTCTGGTCGCCATTRACTACACAGGTAGTATTTTGCACAGGAGCTTGG 1928 1940 1941 1942	ω ε	9 TTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGCCTATATGGTGTCTGCCGCAG 1868
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2229 GAATGCGGGGACTCTGCAGGTTAACCCAGGTTAACAGCTAGCT	Oy 21 Db 17	69 CCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGAGGCCAGAAGGGCTCCATGCACTG 2228
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2289 TGAGACACCTAGAGAAGGGTTTTTGGGAGCTGAATAACTCAGTCACCTGGTTTCCCA 2348 1861 TGAGACACCCTAGAGAAGGGTTTTTGGGAGCTGAATAACTCAGTCACCTGGTTTCCA 1920 1861 TGAGACACCCTAACCTGCAGTTTTTGGGAGCTGATTACCAGTCACTGGTTTCCA 1920 XX 2349 TCTCTAAGCCCCTTAACCTGCTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG 2408 XX 2409 ATGAAACCCTCATCGGATTTGAACATTTATTGTAGGAGATTTCTAGG 1980 XX 2409 ATGAAACACTCCTCATCGGATTTGAACATTTATTGTAGGGGAAGAGTCCTG 2466 XX 1981 ATGAAACACTCCTCCATGGGATTTGAACATTATTTGTAGGGGAAGAGTCCTG 2466 XX 1981 ATGAAACACTCCTCCATGGGATTTGAACATTATTGTAGGGGAAGAGTCCTG 2466 XX 2467 AGGGGCAACACACACAAGAACCAGCACACACACACTGTTTTTTGTAGGGGAAGATCCTC 1	1	
1861 TGGGACACCCTAGAGGGTTTTGGGAGCTCAGTCACCTGGTTTCCCA 1920 2349 TCTCTAGCCCTTAACCTGCTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG 2408 XX 2349 TCTCTAAGCCCCTTAACCTGCTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG 1980 XX 2409 ATGAAACACTCCTCCATGGGATTTGAACATATG ACTTATTTGTAGGGGAAGAGTCCTG 2466 1981 ATGAAACACTCCTCCATGGGATTTGAACATATG ACTTATTTGTAGGGGAAGAGTCCTG 2466 XX 1981 ATGAAACACTCCTCCATGGGATTTGAACATATGTAGGGGAAGAGTCCTG 2466 XX 2467 AGGGCAACACACACACACACACACACACACACACACTGTTTTTGTAGGGGAAGAGTCCTG 2040 XW 2467 AGGGCAACACACACACACACACACACCACACCACACACA		89 TGAGACACACCTAGAGAGAGTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA 2348
2349 TCTCTAAGCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG 2408 1921 TCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG 1980 2409 ATGAAACCCCTTAACCTGCATTTAATGTAGCTTTTGTAGGGAGTTTCTAGG 1980 2409 ATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTGTAGGGGAAGGTCTG 2466 1981 ATGAAACACTCCTCCATGGGATTTGAACATATGAAAGTTATTTGTAGGGAAACATCTG 2467 2467 AGGGGAAACAACAAGAACCAGGATTCAATGAAAGTTATTTTTTTT		61 TGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA 1920
2409 ATGAAACACTCCTCCATGGGATTTGAACATATG-ACTTATTTGTAGGGAAGGTCCTG 2466	2 1	49 TCTGTAAGCCCCTTAACCTGCAGGTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG 2408
2467 AGGGCAACACAAAAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCA 2526	7 5	09 AIGAAACACICCICCAIGGAITIGAACAIAIGACTIAITIGIAGGGAAGAGICCIG 2466
2527 CCCCCTCTTACCTTTTATCAGGATGTGGCCTCTTGTGGTTGCTTGC	ri r	67 AGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTTGCTGATCCA 2526
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                                            CCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCT
2221 CTTTCCGTGTGTGTGTCTAATATTTGGGTAGGGTGGGGGGATCCCCAACAATCAGGTCCC
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19-JUL-2001. 16-JAN-2001; 2001WO-US01574. 14-JAN-2000; 2000US-0483672. (CORI-) CORIXA CORP. Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG; Wanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW; Wang A, Meagher MJ; WPI; 2001-425873/45. New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines - Claim 1; Page 459-460; 543pp; English. The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and can patient. The cells prepared using (I) or (II) are used treat cancer in a patient. To cells prepared using (I) or (II) are used treat cancer in a patient. The cancer that is diagnosed or treated is particularly patient. The cancer that is diagnosed or treated is particularly prostate cancer (I) and (II) can be used for monitoring the progression of cancer in a patient. The bused for monitoring the progression of cancer in a patient. (I) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to exemplification of the present invention.

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Db	481	GCTCTAGGAGTCTGATCAGAGTCGTTGCCCCCAGTTTGACAGAAGGAAAGGCG
٥y	1241	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db	541	AGGAGTTAAGGCTGGATTTCAGATCTG
Qy	1241	1240
do	601	CCAACGACTTTCCAAATAATCTCACCAGO
٥y	1241	
qq	661	TGAAGCCTATGGCCAGCTGTCTTTGTGTTCC
Oy	1241	1240
QQ	721	CTCCCAGGAAACCTTCAGACTACCTTCCTG
0y		
q	781	GCGTTCGGATGGGCAGCCTGGGGCTGT 8
Qy Db	1269	TCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGTGCAGCGAT 1328
λò	1329	36CACTCGAGCCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTTGCCGTATTTGTTATTTGCTATTTTGCTATTTTGCTTTTTGCTTGC
qq	901	
λa	1389	TGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCAC
qo	961	
λζ	44	TCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGAGAGCAGG 1508
q	05	CTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC
λ'n	0	TGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGA
ą Q	08	GTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGA 1
λά	9	CCAGCTICCTGCCAGCCCTAAGCCTGGAGCTCCCTTCCCT
qc	4	SCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCT
λ		68
g.	0.1	3GCAGTGGCCTGCTCCCACCTCCACCGGCTCTGCGGGGCCTCTGCCTGTGATGTCT 126
λ.	689	74
g Q	61	37ACGTGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGCATCT 132
λy		0
q	1321	CCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTG
·λζ	1809	TTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAG 1868
q	1381	SGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCA
λ	6	GCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGG 1928
q	41	STCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGGGACTTG
λλ	1929	CCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT
ą	1	ACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT
λλ	1989	CCCAGCTCCCCGCTCCTGTTAGCCCCCATGGGGCTGCCGGGCTGCCCGCCAGTTTCTGTTG 2048

οp		Db 2641 CCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCT 2700
		Qy 3127 GTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCTGCCTG
	GCTGGGGGCTGGGGGGTCTCTCTCTCCCCAGTCTAGGGCTGCCTGC	QY 3187 TTATCTCCAGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT
	CCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGAGGCCAGAAGGGCTCCATGCACGAGGGCTCCCCCCCC	Oy 3247 GGTGAATATTTATACTGTAAGTGAGCAATCAGAGTATAATGGTGACAAAATTA 3306
	GAATGCGGGGACTCTGCAGGACTACCCAGGCTCAGGCTTAACAGCTAGCT	QY 3307 AAGGCTTTCTTATAAAAA 3330
	2289 TGAGACACCTAGAGAAGGTTTTGGGAGCTGATAAACTCAGTCACCTGGTTTCCCA 2348 	RESULT 19 ABL95410 ID ABL95410 standard; cDNA; 2904 BP.
	2349 TCTCTAAGCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG 2408 111111111111111111111111111111111111	XX AC ABL95410; XX DT 19-JUL-2002 (first entry)
	2409 ATGAAACACTCCTCCATGGGATTTGAACAFATGACTTATTTGTAGGGGAAGAGTCCTG 2466 	Human P553S sp Human; cancer;
	2467 AGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCA 2526	gene th Homo sa
	2527 CCCCCTCTTACCTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGA 2586	PN US2002022248-A1. XX PD 21-FEB-2002. XX
	2587 CACAGGCATTTAAATATTTAACTTATTTAACAAAGTAGAAGGGAATCCATTGCTAG 2646 	12-JAN-2001; 25-FEB-1997; 01-AUG-1997;
	2647 CTTTCTGTGTTGGTGTCTAATATTTGGGTGGGGGGATCCCCAACAATCAGGTCCC 2706	09-FEB-1998; 25-FEB-1998; 14-JUL-1998; 23-SEP-1998;
	2707 CTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTCCTGGGGTCTGGCC 2766	15-JAN-1999; 09-APR-1999; 13-JUL-1999; 12-NOV-1999;
	2767 CCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCCTCATCCAAATGATAATTCCAAA 2826 	18-NOV-1999; 14-JAN-2000; 27-MAR-2000; 09-MAY-2000;
	2827 TGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTGGGGGTGGGGCTTCAGGTCTCAAC 2886	12-MAY-2000; 13-JUN-2000; 27-JUN-2000; 10-AUG-2000;
	2887 GGCTTCCCTAACCACCCTCTTCTTGGCCCAGCCTGGTTCCCCCACTTCCACTCCCC 2946	PR 29-AUG-2000; 2000US-0651236. PR 06-SEP-2000; 2000US-0657279. PR 02-OCT-2000; 2000US-0679426. PR 10-OCT-2000; 2000US-0685166.
	2947 TCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCAAC 3006 	(XUJJ/) XU J (DILL/) DILL (MITC/) MITC
	3007 TITCCCCTACCCCCAACTITCCCCACCAGGTCCAAACCCTGTITGGAGGTACTGCAGGA 3066 	(HARL/) (JIAN/) (KALO/) (FANG/)
	3067 CCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCT 3126 '	PA (RETL/) RETTER M W. PA (STOL/) STOLK J A. PA (DAYC/) DAY C H.

	(VEDV/) VEDVICK T S.	qq	601 CCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTT 660
	LI S X.	Oy	1241 1240
		qq	661 CCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTC 720
	HENDERSON	Qy	1241 1240
	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD; Fancer CP Batter MW Ctolk IA Day, CH Vodyick TC Cartor D.	qa	721 TCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTGCC 780
	1. SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA; PI; 2002-255649/30.	Qy Dp	1241
XX FT FT	New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer .	Qy	
XX	Claim 1; SEQ ID NO 703; 87pp; English.	Qy	1329 TCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCA 1388
		qq	
		Qy Dp	1389 CATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCT 1448
one One	tch 64.48; So	Qy	1449 TCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTACCACGGGAGAAAGCAGG 1508
Bes	Similarity 88.2%; Pred. No. 0;); Conservative 0; Mismatches 1; Indels 343;	qa	1 TCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGAGAAGCAGG 1
. Yo	82	Oy Op	1509 TGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGA 1568
i & i	TGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTG	oy Db	1569 CCAGCTTCCTGCCAGGCCCTAAGCCTGCAGCTCCCTTCCCTAATGGACACGTGGGTG 1628
9 & 1	regeacaccagrecceregeccerecereses accesses against the contraction of t	QY	1629 GAGGCAGTGGCCTGCTCCACCTCCACGCGCTCTGCGGGGCCTCTGCCTGTGATGTCT 1688 [
3 &	CIGGGCCCCACCGAGCCAGCAGAGGGCTGCCCCCCTCCTTGTGCCCCCCCC	Qy	1689 CCGTACGTGTGGTGGTGAGCCCACCGAGGCCAGGTGGTTCCGGGCCGGGGCATCT 1748
oy Oy	181 CTGGGCCCCACCAGCAGCAGCAGAAGGGCTGTCGGCCCCTTGTCGCCCCCTGTT 240 1010 CCATGCCGGGCCCGTTGGCTTTCCGGAACCTGGCGCCCTGCTTCCCCGGCTGCACCAG 1069	QY	GCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTGT
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. yo. ag	1070 CTGTGCTGCCGCATGCCCGCACCCTGCGCCGCCTCTTCGTGGCTGAGCTGTGCAGCTGG 1129	λ q	09 TTATOGECICCATTOTCCAGCICAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAG I TTATGGGCTCCATTGTCCAGCTCAGCCAGCTGTCTGTCACTGCCTATATGGGTGTCTGCCGCAG I
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g &	ATGGCACTCATGACCTTCACGCTGTTTTACACGCATTTCGTGGCCGAGGGGCTGTACCAG GGCGTGCCCAGAGCTGAGCCGGGCACCGAGACACTATGATGAA	QY	1929 CCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT
g &	421 GGCGFGCCCAAAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGAGGCCT 480	ζζ	CCCAGCTCCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTTCTGTTG 2
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οy		OY .	2049 CTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGGTGGTGGTGCGTAGCTGCACA 2108 11
අ දි	541 GCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTT 600	Qy	2109 GCTGGGGGCTGGGGCGTCCCTCCTCCTCCCCAGTCTCTAGGGCTGCCTGACTGGAGG 2168
Š		qq	1681 GCTGGGGGCTGGGGGCTCCTCTCTCTCTCTCCCAGTCTCTAGGGCTGCCTCACTGGAGG 1740

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AAGGCTTTCTTATATGTTTAAAAA
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Best Local Similarity 80.1%;
Matches 2872; Conservative
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        CCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCATGCACTG 2228
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                                                  GAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCTAGT
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The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of encer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding reals specific for a tumour protein, and for inhibiting the development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human prostate-specific polypeptides and polynucleotides useful diagnosis and treatment of cancer, especially prostate cancer -
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Carter D;
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                                                                                                                                                                                                                               Human; prostate cancer; ss; cytostatic; immunostimulant; tumour
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dvick TS,
erson RA;
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I, Henderson
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Pred. No. 0;
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Skeiky YAW, Hepler WT,
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BP
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AAS64038 standard; cDNA; 4894
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2000US-0636215.
2000US-0651236.
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q q		qq	2391 ATTICAGATCIGCIGGITCCAGCCGCAGIGIGCCCICIGGICCCCCCAAC
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λ. q.	575 CTGAGCCTCTTTCTCATCCCAAGGCCGGCTGCTAGCAGGCTGCTGTGCCCGGATCCC 634	da .	1240
Σ Ω	635 AGGCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGGACTTCTGTGGCCAG 694 [Qy Db	12402571 CAGACTACCTTCTCCTTCAGCAAGGGGGCGTTGCCCACATTCTCTGAG
λ; q;	754	Qy	1240201 AAGAACCTAGACTTCCTAGAGGTAGAAÂGGGGAAGGTGCTGGGG
λ; q,	755 GGCCAGGCCTACTCTGTCTATGCCTTCAGATCAGTCTTGGGGGGTGCCTGGGGTACCTC 814	QY	1240
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ž g	GCGTAGCAGCCACACTGCTGGTG	oy Op	1249 GATGGCCACCTGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGTCTTCTCTGTCTTTTTTTT
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γ q	CCCCGGCTGCACCAGTGTGCTGCCATGCCCCACCCTGCGCCGGCTCTTCGTGGCTT 1 1 1 1 1 1 1 1 1 1	oy Op	1429 CGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACGT
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λ. q	GAGGGCTGTACCAGGCGTGCCCAGAGCTGAGCGGCACCGAGGCCGGGAACTAT 1	Qy	1549 CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGG
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α Σ	2151 ACACTCGGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGCCCCGACTTCTTGTCAGG 2210 .1240 1239	δy	,
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۵	2451	TAATCTCACCAGGGCCTTCCAGGCGTCCTAGAAGCGTCTTGAA
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	2571	ACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGT
	.1240	
0	2631	aacctagactcccattgctagaggtagaaaggggaaggg
_	1240	
0	2691	CAGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCCTTCTCA
_	24	
0	L)	GCTCCGA&CCTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGGCGTTC
~ 0	1249	GATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCAT 1308
	0	
. 0	87	SACCECTEGETGCAGCCATTCCCATTCCACCACTTTTTGCCCAGTGTGCACCACTTT 1368 GGACCGCTGGTGCAGCGATTCGCAGCAGCAGCAGTTTGCCCAGTGTGCCAGTGTGCAGCAGTTT 2930
_	m	CCCTGTGGCTGCCGGTGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGC 1428
^	2931	ccrerescrecestreceacarscerstreceacastrescestrescrestrescress
	42	CGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCT 1488
•	2991	rcacceegrrcaccricrcaeccriscaearccreccracacacacrec
	1489 3051	CTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAG 1548
	1549	CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCC 1608
_	3111	SAGGACAGCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCC
	1609	TAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCTCGCGC 1668
	3171	YTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGCTCT
	99	72
_	23	JTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCCACCGAGGCCAGGGT 329
	1729	78
_	7	.coooccooocaiciocciooaccicoccaicciooaragioccificciorigic 335
	1789 3351	CCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGC 1848
	1849	ATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGT 190
	3411	
	1909	ATTTGACAAGAGGACTTGGCCAAATACTCAGGGTAGAAAACTTCCAGGACATTGGGGTG 1968

Db 4551 AAATTTCCCCTACCCCCAACTTCCCCCAACTTCCCCACCA	RESULT 21 AAH93866 ID AAH93866 standard; cDNA; 4894 BP. XX AC	XX	XX XX XX XX XX XX XX XX Cand can be used invention describes polynucleotide sequences (I) which encode CC prostate-specific proteins (II). (I) and (II) have cytostatic activity, CC and can be used in vaccine production and gene therapy. (I), (II), CC antibodies to (II), fusion proteins comprising (II), and isolated CC T cells prepared using (I) or (II) are used treat cancer in a patient. CC (I) and the antibodies are also used in the detection of cancer in a CC patient. The cancer that is diagnosed or treated is particularly CC (I) and (II) can be used in vaccines. The antibodies or CC (I) and (II) can be used for monitoring the progression of cancer in a patient. CC (I) and (II) can also be used to improve diagnostic and therapeutic CC (I) and (II) can also be used to improve diagnostic and therapeutic CC as well as the prostate cancer. They can indicate the level of metastasis CC AAM01318 represent polynucleotide and amino acid sequences used in the
	1111	ACTGTCTTTTGCTGATCCACCCCCTCTTACTTTATCAGGATGTGGCCTGTTGGTCC TTCTGTTGCTGATCCACCCCCCTCTTACTTTATCAGGATGTGGCCTGTTGGTCC TTCTGTTGCCACCAGAGACACAGGCATTTAAATATTTAATTATTAATTA	2807 TCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTGTTGAAGGAAG
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6	40 A A A A A A A A A A A A A A A A A A A	64 65 64 65 .

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3226
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ACCCCCAACTITCCCCTACCCCCAACTITCCCCACCAGCTCCACAACCC 4610
                                                                                                                AGGGAGGTCTTATCTCTCAGGGGGGTTTAAGTGCCGTTTGCAATAATG
                                                                                                  AGTATATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding a prostate-specific protein, for ing and treating prostate cancer in a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cer; prostate-specific; diagnosis; vaccine; erapy; metastasis; ss.
                                                                                                                                                                                                                                                                                                      ACAAAATTAAAGGCTTTCTATATGTTTAAAAA 3330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               riant P553S-14.
                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 4894 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitcham JL,
R, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US01574.
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the present invention. 28 A; 1448 C; 1354 G; 1163 62.8%; Score 2142.8; DB 80.1%; Pred. No. 0;	qa .	2271 TGCGGTTTCAGGAAGGCCTCTGGCTGCTC
928 A; 1448 C; 1354 G; 1163 T; 1 other; 62.8%; Score 2142.8; DB 22; Length 4 80.1%; Pred. No. 0;		1 TGCGGTTTCAGGAAGGCCTCTGGCT
62.8%; Score 2142.8; DB 22; Length 4 80.1%; Pred. No. 0;		THE RESERVE OF THE PROPERTY OF THE PARTY OF
	i 2	1740
vative	3 8	
14	G QQ	2391 ATTTCAGATCTGCCTGGTTCCAGCCGCAG
GGCTTGGTTCCAGTGCTGGTCTGGTCTGTTGTCCCGCTCCTAGGCTCAGCCAGTGACCAC	QY	1240
JI I PEGCETGACCATATGCCCCCCCCCCCCCCCCCTCTCGCCATCCTTGGCCATCCTC 571 TGCCCTGGACCCTATGCCCCCCCCCCCCCTCATCTCTCGCCATTCTTTTTTTT	qq	2451 ATAATCTCACCAGCGCCTTCCAGCTCAGG
TCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCC 634	Οy	1240
4	qa	_
635 AGGCCCTGGAGCTGGCACTGCTCGTGGGGTGGGGCTGGTGGACTTCTGTGGCCAG 694	yo q	1240
AGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGCTGCTGGACTTCTGTGGCCAG 1	ò	
695 GIGTGCTTCACTCCACTGCAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGT 754 11	qa	2631 AAGAACCTAGACTCCCATTGCTAGAGGTA
CGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGGCTGCCTTGGGCTACCTC 814	Qy	1240
	qq	· 2691 GTCCACAGCAGGTCTCGTGCAGCAGGTAC
GGGACACCAGTGCCCTGGCCCTGGGCACCCAGGAGGAG 874	Qy	40
	qa	Н
875 IGCCICTITGGCCIGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCACACTGCTGGTG 934 	Qy Dp	1249 GATGGGCAGCCTGGGGCTGTTCCTGCAGT
GCTGAGGAGGCAGCGCTGGGCCCCACCGACCAGCAGAAAGGGCTGTCGGCCCCCTCCTTG 994	Qy	1309 GGACCGGCTGGTGCAGCGATTCGGCACTC
	qq ·	
TCGCCCACTGCTGTCCATGCCGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 105	oy G	1369 CCCTGTGGCTGCCGGTGCCACATGCCTGT
CCCCGGCTGCACCTGTGCTGCCGCATGCCCCGCACCTGCGCGGCTCTTCGTGGCT	Oy OD	1429 CGCCCTCACCGGGTTCACCTTCTCAGCCC
1 ccccgcrgcaccag	2 AO	
5 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC 1	ද අධ	3051 CTACCACCGGGAGAAGCAGGTGTTCCTGC
5 GAGGGGCTGTACCAGGCGTGCCCAGAGCTGAGCCGGGGACCGAGGCCCGGAGACACTAT 123	QY	1549 CAGTGAGGACAGCCTGATGACCAGCTTCC
GAGGGCTGTACCAG	qα ·	
GATGA	oy D	1609 TAATGGACACGTGGGTGCTGGAGGCAGTG
GATGAAGGTAAGGCCTTGGCAGCCAGCAGAGGCTGGTGTGGGGAGCCGCCCACCAGAGACG 215	Oy	
123	qq	3231 GGCCTCTGCCTGTGATGTCTCCGTACGTG
ACACICAGGGGTGTCTGGGCTGGTGCCTCTCCATCCTGGCCCCGGACTTCTCTGTCAGG Z21	Qγ	1729 GGTTCCGGGCCGGGGCATCTGCCTGGACC
1 AAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCT 2270	Dp	91
0	δō.	1789 CCAGGTGCCCCATCCCTGTTTATGGGCT
26 27 20 11 11 12 12 13 14 15 15 15 15 15 15 15 15 15 15 15 15 15	GCTGGGGGGGGGGGCCCCCCCGCGGGGGGGGGCGCCCCCC	GCTGAGGAGGCCCCACCAGGAGCAGGAGGCCCCCCCCCTCCTTG GCTGAGGAGGCCCCCCCCCC

Dβ	2271	GCGGTT
οy	1240	1239
QQ	2331	TGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGCTGG 2390
Οy	1240	1239
ΟĎ	2391	GATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCT
Qy	1240	- 1
qq	2451	CTCACCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCG
Qy	1240	1239
Db	2511	TGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCAC
δÿ	1240	1239
Db	2571	CAGACTACCTTCCTCTGCCTTCAGCAAGGGGGGTTGCCCACATTCTCTGAGGGTCAGTGG 2630
δy	1240	1239
q _Q	2631	CCCATTGCTAG
Qy	1240	1239
. qa	2691	GCAGCAGGTACCTGTGGTT
ΟY	1240	GGCGTTC
Db	2751	TGCTCCGACCCTTCCCTCCCAGGCTCTGTCATGGCCCCTCTCCCTCTGCAGGCGTTCG 2810
Qy	1249	GATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCAT 1308
qq	2811	ATGGCCAGCCTGGTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTC
Qy	1309	GACCGGCTGGTGCGGTTCGGCACTCGAGCAGTCTATTTGGCCAGTGT
qa	2871	CGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCTT
Qy	1369	CCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGGGCCGTGGTGACAGCTTCAGC 1428
QQ	2931	CCTGTGGCTGCCGGCGACATGCCTGTCCCACAGTGTGGGCCGTGGTGACAGCTTCAG
Oy	1429	TCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCC
Db	2991	GCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACAC
Qy	1489	CACTGGAGGTGCTA
qq	3051	TACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAG
Qy	1549	
άα	3111	AGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCC
Qy	1609	TCCCACCTCCACCCGCGCTCTGCG
Ор	3171	AATGGACACGTGGTGTTGTGGAGGCAGTGGCCTCCTCCTCTCTCT
Qy	1669	GCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGGTGGG
qq	3231	CCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGGTGAGCCCAGGCCAGG
Qy	72	78
ga	ω.	GITCUGGGCCTCCTGCCTGGACCTCCCCATCCTGGATAGTGCCTTCCTGCTGTC 335
δō.	1789	CCAGGTGGCCCCATCCTGTTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGC 1848

CONGUEGOCCCCATCCCTGTTATGGGCTCCATTGTTCACCCCACTCGCTGCAGTACT CINITALICAL INITIALITY IN INITIALITY IN INITIALITY IN INITIALITY IN INITIALITY INCOCACACACTGGGGTACT CANAGGCCACTCGCCCCGCGGGCTCGGGTCTCACACACTTCACTCCACCCAC	QY 2927 TCCCCCCACTTCCACTCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCA 2986 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ULT 22 ABL95409 standard; CDN ABL95409; 19-JUL-2002 (first en Human P553S splice var Human; cancer; prostat gene therapy; gene; ss Homo sapiens. US2002022248-Al. 21-FEB-2002.	PR 25-FEB 1997; 97US-0806099. PR 01-AMG-1997; 97US-0806099. PR 02-FEB 1997; 97US-0806099. PR 10-FEB 1998; 98US-0030607. PR 14-ULL 1998; 98US-0115453. PR 14-ULL 1998; 98US-0115453. PR 15-JAN-1999; 99US-0123149. PR 15-JAN-1999; 99US-0232149. PR 13-JUL-1999; 99US-0233149. PR 13-JUL-1999; 99US-038946. PR 13-JUL-1999; 99US-043318. PR 13-JUL-1999; 99US-043318. PR 13-JUL-1999; 99US-043318. PR 14-MAY-2000; 2000US-0568100. PR 13-JUN-2000; 2000US-0568100. PR 13-JUN-2000; 2000US-0568157. PR 13-JUN-2000; 2000US-0568157. PR 13-JUN-2000; 2000US-056815. PR 10-AUG-2000; 2000US-056813. PR 10-AUG-2000; 2000US-056813.
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	3351 CCAGGTGGCCCCATCCTGTTATGGGCTCCAGCTCAGCTC	2269 TTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAA	2567 TTCTGTTGCCATCACAGACACAGGCATTTAAATTTTAACTTATTTAACAAAGT 4131 TTCTGTTGCCATCACAGACACAGGCATTTAAATTTTAACTTATTTTATTTTAACAAAGT 2627 AGAAGGGAATCCATTGCTTGTTGTTGTTGTTTAACTTATTTAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGGTCTTGGGGGCTGCCTGGGCTACCTC 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGTGCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAG 874
                                                                                                                                                                                                                                                                                                                                                                                The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 515 TGGCGTGGACGCTATGGCCGCCGCCGTTCATCTGGGCACTGTCCTTGGGCATCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                575 CTGAGCCTCTTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                       Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                        New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.8%; Score 2142.8; DB 24; Length 4894;
llarity 80.1%; Pred. No. 0;
Conservative 1; Mismatches 3; Indels 708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;
                                                                                                                                                                                                                                  nn DC, Mitcham JL, Harlocker SL, Jiang Y, Retter MW, Stolk JA, Day CH, Vedvick TS, A, Skeiky YAW, Hepler WT, Henderson RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 702; 87pp; English.
                                                                                                                                                          LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                     DILLON D C.
MITCHAM J L.
HARLOCKER S I
                                                                                                                                   VEDVICK T S.
CARTER D.
                                                         JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                 WPI; 2002-255649/30
                                                                                                           STOLK J A.
DAY C H.
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Matches 2872; Conserv
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1175 GAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTAT 1234
                                                                            1235 GATGA----- 1239
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                                                            TCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 1054
                                                                                                                         CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCT 1114
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1971 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGC
 GCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCTCCTTG
                                                                                                                                                        1911 CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGGCTCTTCGTGGCT
                                                                                                                                                                                     GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC
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Human secreted protein-e	CITGCATGGGAGITICIAGGATGAAACACICCICCATGGGATTTGAACAIATGACTTA 244	à Č
AC AAD05230; XX X 18-JUL-2001 (first entry)	2329 CTCAGICACCIGGITICCCAICICTAAGCCCCTTAACCIGCAGCTTCGITTAAIGTAGCT 2388	ර් දි
ND0523	3831 TTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTGGGAGCTGAATAAA 3890	qa
RESULT 23	2269 TTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAA 2328	Qy
4	2209 CAGAAGGCTCCATGCACTGGAATGCGGGACTCTGCAGGTGGATTACCCAGGCTCAGGG 2268 11111111111111111111111111111111111	oy do
Db 4791 TCGTCTTATTTATTAGCGGGGGGAATAT Ov 3287 TGTTTATGGTGACAAAATTAAAGGCTTTC		g qq
32	TAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGGGGG 220	g ko
4731	2089 CTGAGGTGCGTAGCTGCACAGCTGGGGGCTGCGTCCCTCCTCCTCCTCCCCAGTCTC 2148	δ á
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3107	GAGGCCTGCCTCATGGTCCCAGCTCCCTGCTCCTGTTAGCCCCATGGGGCTGCCGGG 359	qa
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4551	1909 ATTIGACAAGAGCGACTIGGCCAAATACTCAGCGTAGAAAACTTCCAGCACAITGGGGTG 1968 	۲۵ و
4491	1849 CTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGT 1908	S S
Db 4431 GTGGGCTTCAGGTCTCAACGGCTTCCCTP	1789 CCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGC 1848 11	oy D
Db 4371 TCCCAAATGATAATTCCAAATGCTGTTACC OV 2867 GTGGGGCTTCAGGTCTCAACGGCTTCCCTP	1729 GGTTCCGGGCCGGGCATCTGCCTCGCCATCCTGGATAGTGCCTTCCTGCTGTC 1/88	OY Db
Db 4311 TCTTCTCGGGGTCTGGCCCCCCAAATG OV 2807 TCCCAAATGATAATTCCAAATGCTGTTACC	1669 GGCCTCTGCCTGTGATGTCTCCGTAGGTGTGGTGGTGGCTGAGCCCACCGAGGCCTGGGGT 1/28 	ර් පි
DB 4251 ATCCCCAACAATCAGGTCCCCTGAGATAGG Qy 2747 TCTTCTCCTGGGGGTCTGGCCCCCCAAAATC		qq
26	TAATGGACACGTGGGTGCTGGAGGCAGTGCCTGCTCCCACCTCCACCTCCGCGCTTGCGG 166	a k
Db 4191 AGAAGGGAATCCATTGCTAGCTTTCTGTG	1549 CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCC 1608 3111 CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCTGGAGGTCCCTTCCC 3170	oy .
4131	1489 CTACCACCGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGGTGCTAG 1548 	oy Op
4071 ACTGICTTTTG	1429 CGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCT 1488 111111111111111111111111111111111	oy og
4011 TITGIAGGGAAGACICCICAGGGGCA	1369 CCCTGTGCCGCTGCCGCTGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGC 1428	oy Og
Db 3951 CTTGCATGGGAGTTTCTAGGATGAACACT	1309 GGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTT 1368 	oy Db

ACCCCCAACTTTCCCCACCAGCTCCACAACCC 3046 CAGGGGGGTTTAAGTGCCGTTTGCAATAATG 3226 4730 3CTGGTCATTGGGCTGATCATTGCCAGAATCT 2746 TGCCTAACCCAGGACCTTGGAAATTCTACTCA 2806 2866 CCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGG 4430 2926 4490 ACAAAGTGCGGTTTCCCAAGCCTTTGTCCATC 3106 GGAATCTCACACAGAAACTCAGGAGCACCCCC 3166 TTTTATACTGTAAGTGAGCAATCAGAGTATAA 3286 ACACAAGAACCAGGTCCCTCAGCCCACAGC 2506 TACCTTTTATCAGGATGTGGCCTGTTGGTCC 2566 4130 2626 4190 2686 11 cDNA clone HWBAR14, SEQ ID NO:21. TAACCACCCTCTTCTTGGCCCAGCCTGGT CCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGG

foetal abnormality; developmental abnormality; haematopoietic disorder; mumune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psortasis; sepais; dispetes; arberosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; anglogenic disorder; disorder; asstrointestinal disorder; allergy, pregnancy related disorder; andocrine disorder; allergy, pregnancy related disorder; undocrine disorder; allergy, cell culture; chemotaxis; vulnerary; binding partner identification; tumour; cancer: Human; secreted protein; proliferative disorder; therapy; ss gene (

Homo sapiens.

/product= "Human secreted protein" /transl_except= (pos:209..211, aa:Xaa) /note= "Xaa corresponds to any of the naturally occurring /*tag= b 296.1264 /*tag: c /roduct= "Mature human secreted protein" Location/Qualifiers L-amino acids" 152..1267 152..295 /*tag= sig_peptide mat_peptide Key

WO200134629-A1

17-MAY-2001

08-NOV-2000; 2000WO-US30654.

99US-0164835 12-NOV-1999;

27-JUL-2000; 2000US-0221142

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Komatsoulis GA, Wei P, Fiscella M, Baker KP;

WPI; 2001-308779/32. P-PSDB; AAE01362 New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autoimmune disease and cancer, and used as a food additive or preservative

Claim 1; Page 388-389; 490pp; English.

AAD05220-AAD05282 represent cDNAs corresponding to 21 human secreted ARD1415-AAB01431 represent human secreted protein fragments or variants. The secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 21 genes, developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetenl and developmental abnormalities, hemantopoletic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, autoimmunt neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, echizophrenia, stind disorders (e.g., and storders, and infections represented alsorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proteins to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or

1085 ACACTCGGGGCTGTGTCTGGGCTGGTGCTCCCATCCTGGCCCCGACTTCTCTGTCAGG 1144

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preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or.enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of
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                                                                                                                                                             710; Gaps
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                                                                                                 Sequence 3878 BP; 709 A; 1164 C; 1044 G; 951 T; 10 other;
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Matches 2885; Conserv
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Qy	1789	CAGGTGGCCCCATCCTGTTATGGGCTCCATTGTCCAGCTC
qa	2285	ATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTG
0у	1849	90
qq	2345	TATATGGTGTCTGCCGCAGGCCTGGGTCGGTCGCCATTTACTTTGCTACACAGGTAG
QY	1909	CAAGAGCGACTTGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTG 196
QQ	2405	TTGNCAAGAGCGACTTGG-CAAATACTCAGCGTAG-AAACTTCCAGCMCATTGGGGTG 246
Qy	1969	AGGCCTGCCTCACTGGGTCCCAGCTCCCGGTCTGTAGCCCCATGGGGCTGCGGG 202
qq	2463	GGCCTGCCTCACTGGGTCCCAGCTCCTGTTAGCCCCATGGGGCTGCCGG
QY	2029	CTGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCCCCTGTGCTG 2088
qq	2523	TGGCCGCCAGTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCT
٥y	08	14
qq	2583	TGAGGTGCGTAGCTGCACAGCTGGGGGCTGGGGGGTCCCTCTCTCT
Qy	2149	20
. qa	2643	aggetecetgaetgeaggeettecaagggggttteagtetggaettataeagggagg
Qy	2209	CAGAAGGCTCCAIGCACIGGAAIGCGGGGACTCTGCAGGIGGATTACCCAGGCTCAGGG 2268
QQ	2703	SAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGG
Qy	2269	32
qq	2763	TAACAGCTAGCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAAT
Qy .	2329	38
QQ	2823	CAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCT 288
QY	2389	CTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTA 244
qq	2883	CTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGAAGT
Qy	2447	TITGIAGGGAAGAGTCCIGAGGGGAACACACAGAACCAGGTCCCCTCAGCCCACAGC 2506
qq	2943	TTTGTAGGGGAAGAGTCCTGAGGGGCAACACACAGAACCAGGTCCCCTCAGCCCACAG
QY	2507	ACTGICITITICGGACCCCCCCCCCCTCTAACCACAGAIGGCCTGTIGGCC 256
Ор	3003	ACTGTCTTTTTGCTGATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCC 306
Qy	2567	TICTGTTGCCATCACAGAGACACAGGCATTAAATATTAACTTATTATTAACAAAGT 262
qq	3063	TICTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAATTAA
Οy	2627	AGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGG 268
qa	3123	AGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGG
Qy	2687	ATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCT 274
οp	3183	ATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAAT
Qy	2747	TCTTCTCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCA 280
qq	3243	TCTTCTCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCA 330
QY	2807	TCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAG

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 3047 IGTITGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATC 3106
                                                                                                                                                        TCAGCCCCCAGAGIAIAICIGIGCIIGGGGAAICTCACACAGAAACICAGGAGCACCCCC 3166
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                                                                                                     Consensus sequence of the PS108 gene derived from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS108 gene; prostate disease; benign prostatic hyperplasia; BPH; prostatitis; prostatic intraepithelial neoplasia; PIN; cancer; drug screening; gene therapy; ss.
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Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Stroupe SD;
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                                                                                                                                                                       The present sequence represents the consensus sequence for a PS108 gene. The sequences are PS108 gene-specific. They are used in the method of the invention. The specification describes a method for detecting the presence of a target PS108 polynucleotide in a test sample. The method presence of a target PS108 polynucleotide in a test sample. The method polynucleotide or complement, and detecting the presence of the target PS108 polynucleotide. The products can be used for detecting, polynucleotide. The products can be used for detecting, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as benign prostatic hyperplasia (BPH), prostatitis, prostatic intraeplithelial neoplasia (PIN) and cancer. In particular the products can be used in drug screening and gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                 New isolated prostate-specific polynucleotides - used to develop products for the diagnosis and treatment of prostate diseases, e.g. benign hyperplasia, prostatic or prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2136.4; DB 20; Length 2152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2152 BP; 419 A; 622 C; 569 G; 542 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0;
0; Mismatches
                                                                                                                                         Claim 1; Fig 1A-E; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.7%;
Best Local Similarity 99.9%;
Matches 2149; Conservative
               WPI; 1999-034731/03.
                                 P-PSDB; AAW85068
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                                                                                                                                                                                                                                                                                                                                                                                                                    1981 AGGACCACCCCTGCCTGAGCTAAGGGAGGTTTAATCTCTCAGGGGGGTTTAAGTGCCG
                                                                                              2975 AGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCCAACTTTCCCCAACA
2915 GCCCAGCCTGGTTCCCCCCCACTTCCACTCCCCTCTACTCTTAGGACTGGGCTGATGA
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don J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
erts-Rapp L, Russell JC, Stroupe SD;
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contacting the test sample with at least 1 PS108-specific polynucleo or complement, and detecting the presence of the target PS108 polynucleotide. The products can be used for detecting, diagnosting, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as benign prostatic hyperplasia (BPH), prostatitis prostatic intraepithelial neoplasia (PIN) and cancer. In particular products can be used in drug screening and gene therapy.	Sequence 2145 Br; 410 A; 021 C; 303 G; 341 T; U OLDEF;	Query macun Best Local Similarity 99.8%; Pred. No. 0; Matches 2139; Conservative 0; Mismatches 2; Indels 3; Gaps	1185 ACCAGGGGTGCCCAGAGCTGAGCCGGGCACCGAGGCCGGGAGACACTATGATGAGGC	1 ACCAGGGCGCGGGCACCGGGCACCGGGCCCGGGGAGACACGGGGGAAGGC	61	. 1305 TCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAG 	1365 CTTTCCTGTGGCTGCCGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACACTT	1425 CAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCT	1485 CCCTCTACCACCGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGG 	TITCTGCCAGGCCCTAAGCCTGGAGCTCCC	1605 TCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCACCTCCACCTCCACGCGCGCTCT	1665 GCGGGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGGTG	1725 GGTGGTTCCGGGCGGGGGATCTGCCTGGACTCGCCATCCTGGATAGTGCCTTCCTGC	1785 IGTCCCAGGTGGCCCATCCCTGTTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGTCA	1845 CTGCCTATATGGTGTCTGCCGCAGCCCTGGGTCTGGCCATTACTTTGCTACACAGG	1905 TAGTATTTGACAAGGGGCTTGGCCAAATACTCAGGGTAGAAACTTCCAGCACATTGG 	1965 GGTGGAGGGCTGCGTCACTGGGTCCCCGGTCCCGGTCGTTAGCCCCATGGGGCTGC	2025 CGGGCTGCCCCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCTGT
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CGGGCTGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTTCTGCTGCCACCCTGT 900
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                                                                     AGGCCAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTC
                                                                                                                                      2265 AGGGTTAACAGCTAGCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAA
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The present sequence is derived from a prostate cancer-associated gene, and is represented by Incyte clone number 186463. The sequence is used in the method of the invention. The specification describes a method for identifying biomolecules for the diagnosis or treatment of diseases associated with cell proliferation. The method comprises examining polymolecules, consisting of prostate cancerspecific genes, and genes of unknown function, expressed in cDNA libraries. The patterns of both gene sets are compared to identify genes of unknown function with similar expression patterns to the prostate cancer-specific genes. The biomolecules identified by the method form pharmaceutical compositions useful for the diagnosis and treatment of diseases associated with cell proliferation. Such diseases include cancer of the adrenal gland, bladder and bone, but especially prostate cancer. The method may also be applied using other diseasers specific genes. The prostate cancer-specific genes facilitate the diagnosis and treatment of cell proliferation disorders.
   AATGTCGTCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying biomolecules for the diagnosis and treatment of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer-associated gene; Incyte clone 1864683; bone cancer; cell proliferation; cancer; adrenal gland cancer; bladder cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "prostate cancer-associated protein"
                                                                                                                                                                                                                                                                   ATAATGTTTATGGTGACAAATTAAAGGCTTTCTTATATGTTTA 3326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequence of a novel prostate cancer-associated gene.
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                                                                                                                                             783 CGCGCTCTGCGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGAGCCCCAC
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                                                                                 1237 TGAAGGCGTTCGGAIGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCTGGTCTT
                                                                                                         363 TGCAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCTGGTCTT
                                                                                                                                   CTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAG
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                                                           Gaps
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                                                          3;
           Sequence 2462 BP; 483 A; 726 C; 632 G; 621 T; 0 other;
                                                          9
                                  Score 2065.4; DB 2
Pred. No. 7.6e-314;
                                                          0; Mismatches
                                 Query Match 60.6%;
Best Local Similarity 99.6%;
Matches 2092; Conservative
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GATTAC 1381 TTTTG 2316 TTTTG 1441	SCTTCG 2376 SCTTCG 1501	FTGAAC 2436 FGAAC 1561	STCCCC 2494 STCCC 1621	3TG 25	rratt 2614 	ATTTGG 2674 ATTTGG 1801	GATCA 2734 GATCA 1861	SCTTGG 2794 CTTGG 1921	GTTGAA 2854 GTTGAA 1981	CTTCTCTG 2914 	SCTGATGA 2974 CTGATGA 2101	CCACCA 3034 CACCA 2161	CCCAAG 3094 	AACTC 3154 AACTC 2281	3TGCCG 3214 3TGCCG 2341	GAGCA 3274	AAAAA 3334 AAAAA 2461
GGAATIGCGGGGACTCTGCAGGTG TTGAGACACCTAGAGAAGGT 	CCATCTCTAAGCCCCTTAACCTGCAG(TCTAGGATGAAACACTCCTCCATGGGATTTC 	CTGAGGGGCAACACAGAAGAACCAGGTC 	CACCCCCTTTACCTTTATCAGGATC	GCCATCACAGAGACACAGGCATTTAAATATTTAACT" 	CTAGCTTTTCTGTGTTGGTGTCTAATATTG 	CCCTGAGATAGCTGGTCATTGGGCT 	GGTCTGGCCCCCCAAAATGCCTAACCCAGGAC 	198	ACGCTTCCCTAACCACCCCTCTT(CCCCTCTACTCTCTTAGGACTGGGC; 	CCCTACCCCAACTTTCCCCTACCCCAACTTTCCCCACA 	3ACCAGAAGCACAAAGTGCGGTTT 	CTGTGCTTGGGGAATCTCACACAGAAACTC 	TCTTATCTCTCAGGGGGGGTTTAAGT 	CTTATTTATTTAGCGGGTGAATATTTTATATACTGTAAGT(TAAAGGCTTTCTTATATGTTTAAAAAAAAA
ACAGGGGCTCCATGCACT AGGCTCAGGGTTAACAGCTAGCCTCCTAG 	CTGAATAAACTCAGTCACCTGGTTTC 	TAATGTAGCTCTTGCATGGGAGTTTCTA 	ATATGACTTATTTGTAGGGGAAGAGTCC 	CAGCCCACAGCACTGTCTTTTGCTGATCCACC 	CTGTTGGTCCTTCTGTTGCCATCACAGA 	ATTTAACAAAGTAGAAGGGAATCCATTGCI 	GTAGGGTGGGGGATCCCCAACAATCAGGTC 	GCCAGAATCTTCTTCCTGGGGTCTGG 	aaattctactcatcccaatgataattccaatgctgttacccaaggttag 	GGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCT(CAGCCTGGTTCCCCCCACTTCCACT	GCACTGCCCAAAATTCCCCTACCCCA 	rccacaaccctgtttggagctactgcag 	TTGTCCATCTCAGCCCCAGAGTATATCTGTGCTTGGG 	GGAGCACCCCTGCCTGAGCTAAGGAGGTCTTATV 	TGCAATAATGTCGTCTTATTTATTTAGC 	COGOGTATAATGTTTATGGTGACAAAATTAAAGGCTTTV
2257 CCAC 1382 CCAC	2317 GAGG 142 GAGG	2377 TT 1502 TT	2437 AT 1562 AT	2495 TC 1 1622 TC	2555 GC(1682 GC(2615 AT 1742 AT	2675 GT 1802 GT	2735 TT 1862 TT	2795 AA 1922 AA	2855 GG 1982 GG	2915 GCC 2042 GCC	2975 AG 2102 AG	3035 GCT 2162 GCT	3095 CCT	3155 AG 2282 AG	3215 TT	3275 ATO 11 2402 ATO
Qy Dp	Qy Db	Qy Db	Qy	cy an	Qy Db	Qy Db	Qy	Qy	Qy	Qy	Qy	Qy	Qy	Qy Dp	Qy	Qy	Qy Db

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1177 GGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGA 1236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention is related to a number of partial coding and protein sequences for the human prostate tissue protein PS108. These sequences can be used in the diagnosis and prognosis of prostate diseases, particularly prostate cancer. They can also be used to produce antibodies which can be used in treatment. The present sequence is one of the PS108 partial coding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGCCTGTACCAGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGAGACACTATGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methods for detecting target prostate-specific polynucleotides or diseases of the prostate (e.g. prostate cancer), comprising detecting the presence of any of PS108 nucleic acid sequences in a test sample
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                                                                                                                                                                                                                         Human; prostate cancer; PS108; antibody; tumour; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Cohen M. Colpitts TL, Friedman PN, Gordon J, Granados E
Billing-Medel PA, Klass MR, Roberts-Rapp L, Stroupe SD,
Kratochvil JD, Russell JC, Hodges SC;
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                                                                                                       BP.
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                                                                                                       DNA;
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                                                                                                     AAC64928 standard;
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3335 A 3335
                          2462 A 2462
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qa	241 GACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACAC 300	ė	y
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g ;	AUTGECTECTECTECTACCACGGGAGAGAGCAGTGTTCCTGCCCAAATACCGAGGGGACAC 360	Qy	2616 TTTAACAAAGTAGAAGGGAATCCATTGC
දි සි	153/ TRANSFICETRACRAFIGAGARCACCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGG 1596	qа ,	
ōy	GGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACC	δλ	9
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ογ	CCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGAGC	ολ	36
qa	481 CGCGCTCTGCGGGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGGGTG	qq °	C) (
٥y	1717 CGAGGCCAGGGTGCTTCCGGGCCAGCATCTGCCTGGACCTCGCCATCCTGGATAGTGC 1776	oy de	2/96 AATTCTACTCATCCCAAATGATAATTCC 2/96 AATTCTACTCATCCCAAATGATAATTCC 1611 AATTCTTAATTCCAAAATGATAATTATTCT
Ωþ	541 CGAGGCCAGGGTGCTGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGC 600	3 3	
οy	1777 CITCIGCTGICCCAGGIGGCCCCATCCTGITTAIGGGCTCCAITGICCAGCTCAGCCA 1836	, E	ט פ
QQ	601 CTTCCTGCTGTCCCAGGTGGCCCCCATCCTTATGGGCTCCATTGTCCAGCTCAGCCA 660	3 8	
ογ	1837 GICTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGC 1896	3 5	7,
ορ	661 GTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGCTCGCTC	an d	
ογ	1897 TACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAG 1956	Oy	2976 GGCACTGCCCAAAATTTCCCCTACCCCC
qq	721 TACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAG 780	qq	m
Oy	1957 CACATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCGGTTCGTTAGCCCCAT 2016	ΟŊ	3036 CICCACAACCCIGITIGGAGCIACIGCA
qq	781 CACATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCCGCTCTTAGCCCCAT 840	QO	847
δλ	2017 GGGGCTGCCGGCCTGCCGCCAGTTCTGTTGCTCCCAAAGTAATGTGGCTCTCTGCTGC	δŏ	3096 CTTTGTCCATCTCAGCCCCCAGAGTATA
QQ	841 GGGCTGCCGGGCTGCCGCCAGTTTCTGTTGCTCCCAAAGTAATGTGGCTCTCTGCTGC 900	q a	90
Qy	2077 CACCCTGTGCTGCTGAGGTGCGTAGCTGGACAGCTGGGGGCCTGCGGCGTCCCTCTCTCT	ΟŸ	LO.
QQ	901 CACCCTGTGCTGCTGAGGTGCGTAGCTGGGGGCTGGGGCCTGCGCGTCCCTCTCTCT	QQ	'n
Qy	2137 CTCCCCAGTCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTCGACTT 2196	0y	3216 TTGCAATAATGTCGTCTTATTTATTTAG
QQ	961 CTCCCCAGTCTCTAGGGCTGCCTGCACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGAC-T 1019	QO	024
 ογ	2197 ATACAGGAGGCCAGAAGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTAC 2256	Oy	، ص
q	1020 ATACAGGGAGGCCAAAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTA- 1078	2	2003 ICAGAGIAIAATGITAIGGIGACAAAA
Qy	2257 CCAGGCTCAGGGTTAACAGCTAGCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGG 2316	RESI	RESULT 28
qq	1079 CCAGGCTCAGGGTTAACAGCTAGCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTT-G-1137	í n	AAS07155 standard; cDNA; 2133 BP.
Qy	2317 GAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCG 2376	AC X	AAS07155;
QQ	1138 GAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCCTTAACCTGCAGCTTC- 1196	VY LO	23-OCT-2001 (first entry)
οy	2377 TITAATGTAGCTCTTGCATGGGGGTTTCTAGGATGAAACACTCCTCCATGGGATTTG-AA 2435	A D	Prostate gene PS108-specific cDNA (ES
Dp	1197 TITAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAAA 1256	KW	PS108; immunogen; drug
Qy	2436 CATATGACTTATTTGTAGGGGAAGAGTCCTGAGGGCAACACACAAGAACCAGGTCCCCT 2495	XX XX	prostate ti EST; ss.
QQ	1257 TATGAAAGTTATTTGTAGGGGAAGAGTCCTGAGGGCCAACACACAC	S S	Homo sapiens.
δλ	2496 CAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCCTCTTACCTTTTATCAGGATGTGG 2555	YH.	Key Location/Qualifiers
QQ	1316 CAGCCCACAGCACTGTTTTTGCTGATCCACCCCCTCTTACCTTTTATCAGGATGT-G 1374	I.i.	CDS 1799 /*tag= a

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2675
                                                                                                                                                                          3GTCTCAAGGCTTCCCTAACCACCCTCTTCTTGG 2915
                                                                                                                                                                                                                                                                                                                                                       AGGAGGTCTTATCTCAGGGGGGTTTAAGTGCCGT 3215
                                                                                     GECTGGCCCCCCAAAATGCCTAACCCAGGACCTT-GA 1610
                                                                                                                                                                                                                                                                                                                         ACCCCCAACTTTCCCCTACCCCCAACTTTCCCCACC-G 1846
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                                                                                                                                                                                                                                                                   CCACTCCCCTCTACTCTCTAGGACTGGGCTGATGAA 2975
                                                                                                                                                                                                                                                                             ACCCCCAACTTTCCCCTACCCCCAACTTTCCCCACCAG 3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTTAGCGGGGGGAATATTTTATACTGTAAGTGAGCAA 3275
CACAGAGACACAGGCATTTAAATATTTAACTTATTA 2615
                                         g screening; image localisation;
te tissue disease; cancer; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAAAATTAAAGGCTTTCTTATATGTTTA 3326
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2017
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Klass MR, Kratochvil JD, Roberts-Rapp I
Yu H;
                                                                                                                                                                                                                                                                                                                  Novel PS108 polypeptide useful in assays for detecting antibodies prostate tissue, and as immunogens to produce \rm PS108 antibodies -
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larity 98.9%; Pred. No. 2.3e-290;
Conservative 0; Mismatches 5; Indels 19;
 /product- "Prostate-specific protein PS108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2133 BP; 414 A; 618 C; 561 G; 540 T; 0 other;
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97US-0850713.
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Russell JC, Stroupe SD,
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Matches 2127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 CTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCCAGAGAACACTATGATGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGGCCGTGGTGACAGCTT
                                                                                                    diseases of the prostate (e.g. prostate cancer), comprising detecting the presence of any of PS108 nucleic acid sequences in a test sample
                                                                                                                                                                                                                                                                                                                                                   1185 ACCAGGGCGTGCCCAGAGCTGAGCCGGGCCCGGAGGCCGGAGACACTATGATGAAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                           1245 TTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGG
                                                                                                                                                                   The present invention is related to a number of partial coding and protein sequences for the human prostate tissue protein PS108. These sequences can be used in the diagnosis and prognosis of prostate diseases, particularly prostate cancer. They can also be used to prod antibodies which can be used in treatment. The present sequence is on of the PS108 partial coding sequences.
                                                                                                                                                                                                                                                                                                                          Gaps
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                      Ή;
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                                                                                         for detecting target prostate-specific polynucleotides
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                                                                                                                                                                                                                                                                                               21; Length
                      Stroupe SD,
           Granados
                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                     Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other
                                                                                                                                                                                                                                                                                            Score 1899.8; DB 21
Pred. No. 5.5e-288;
0; Mismatches 2;
           Friedman PN, Gordon J,
                        A, Klass MR, Roberts-Rapp L, Russell JC, Hodges SC;
                                                                                                                                               Claim 1; Column 75-78; 55pp; English.
                                                                                                                                                                                                                                                                                               55.7%;
99.0%;
                                                                                                                                                                                                                                                                                                               Best Local Similarity 99.0
Matches 2121; Conservative
           Colpitts TL,
                                                                WPI; 2000-655655/63.
                                                                                                                                                                                                                                                                                                             Local Similarity
                         Billing-Medel PA,
                                      Kratochvil JD,
                                                                                                        diseases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1785
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           Cohen M,
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QQ DP	Qy Dp	Qy Db	Qy	QY Db	Oy Db	RES AAS ID	X AC X	XX DE XX	KW XX OS	X Y X X Q Q	X P X P X P X	PR X X X X	PI PI XX	DX XX PT	XX P XX	8888	88888)
905 TAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGG	7	025 CGGGCTGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGT 2084	085 GCTGCTGAGGTGCGTACACACTGGGGGCTGGGCGTCCCTCTCCTCTCTCCCCAG 2144	145 TCTCTAGGGCTGCCTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGG 2204	205 AGGCCAGAAGGCTCCATGCACTGGAATGCGGGACTCTGCAGGTGGATTACCCAGGTC 2264	265 AGGGTTAACAGCTAGCTCCTAGTTGAGACACACCTAGAGAGGTTTTTGGGAGCTGAA 2324	325 TAAACTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGT 2384	385 AGCICTIGCAIGGGAGTHICIAGGAACACICCICCAIGGGAITIGAACATAIG-AC 2443 11111111111111111111111111111111111	444 TTATTTGTAGGGAAGAGTCCTGAGGGGAACACAAGAACCAGGTCCCCTCAGCCCAC 2503 11111111111111111111111111111111111	504 AGCACTGTCTTTTGCTGATCCACCCCCTCTTAACCTTTAACAGGATGTGGCCTGTTGG 2563	564 TCCTTCTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAATTAA	624 AGTAGAAGGGAATCCATTGCTAGCTTTTTCTGTGTGTGTAATATTTGGGTAGGGTG 2683 X	84 GGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAA 2743 	44 TCTTCTTCTCCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTAC 2803 	04 TCATCCCAAATGATAATTCCAAATGCTGTTACCCCAAGGTTAGGGTGTTGAAGGAAG	64 AGGGTGGGGCTTCAACGCCTTCCCTAACCCCCTCTTCTCTTGGCCCAGCCT 2923 	24 GGTTCCCCCACTTCCACTCCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGC 2983 	,
Oy 1 Db	Oy 1 Db	Qy 2 Db	Qy 2 Db	Oy 2 Db	Qy 2 Db 1	Oy 2 Db 1	Qy 2 Db 1.	Oy 2.	Oy 2.	Oy 2: Db 13	Oy 2:	Qy 26	Qy 26	Qy 27 Db 15	Qy 28 Db 16	Oy 28 Db 16	Oy 29 Db 17	

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1787 CCAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCCAACTTTCCCCACAGCTCCACA 1845
                                                                                             3104 ATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACC 3163
                                                                                                                                                                                                                       3164 CCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGTTTAAGTGCCGTTTGCAATA 3223
                                                                                                                                                                                                                                                                                                                     3224 ATGTCGTCTTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTA 3283
                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents the coding sequence of prostate gene PS108-specific expressed sequence tag (EST) cDNA clone 171146IH. The sequence was used along with other overlapping cDNA clones to produce a full length consensus sequence (see AASO7155). This sequence could then be used to produce PS108 polypeptides which are useful in assays for detecting antibodies to prostate tissue, and as immunogens to produce antibodies. The polypeptide and for screening compounds which specifically bind to the polypeptide and for screening for drugs, compounds, or any other agent which can be used to treat diseases associated with PS108. The antibody is useful to detect, or for image
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prostate; PS108; Immunogen; drug screening; image localisation; diagnostic; therapeutic; prostate tissue disease; cancer; metastasis; expressed sequence tag; EST; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cohen M, Colpitts TL, Friedman PN, Gordon J;
ges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
upe SD, Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel PS108 polypeptide useful in assays for detecting antibodies to prostate tissue, and as immunogens to produce PS108 antibodies - .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate gene PS108-specific cDNA clone 1711346IH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS07601 standard; cDNA; 2124 BP.
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97US-0850713.
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Stroupe SD,
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localisation of PSIOB antigen in a patient, for detecting or diagnosing a disease or condition, as delivery agents for therapeutic agents as well as for diagnostic tests and for screening for diseases or conditions as sociated with PSIOB, especially cancer. The antibody is also useful for generating chimeric antibodies for therapeutic use, for inhibiting the biological activity of PSIOB, in therapy (for e.g. to treat prostate tissue disease including prostate cancer and its metastases), and to detect the presence of any polypeptide in a test sample which shares one or more antigenic determinants with the PSIOB polypeptide. 88888888888888

1964 1664 1784 GGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCGCTCCTGTTAGCCCCCATGGGGCTGC 2024 1364 1424 1484 1544 CTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCT 1604 540 TGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCA 1844 099 CTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGG 1904 840 480 420 20; 240 300 120 09 GGTGGAGGCCTGCCTCACTGGGTCCCAGCTCCCCGCTCTTAGCCCCCATGGGCTGC CCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTG TCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGCGCGCTCT GCGGGGCCTCTGCCTGTGTCTCCGTACGTGTGGTGGTGGTGAGCCCACCGAGGCCA GGGTGGTTCCGGGCCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGC GGGTGGTTCCGGGCCGGGCCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGC CTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGG TAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGG TCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAG CAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCT 1185 ACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCG CTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTT ACCAGGGCGTGCCCAGAGCTGAGCCGGGCCACCGAGGCCCGGAGACACTATGATGAAGGCG TTCGGATGGGCAGCCTGTGCTGCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGG Gaps DB 22; Length 2124; 20; 2; Indels Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other; Score 1899.8; DB 2: Pred. No. 5.5e-288; Mismatches o; 55.7%; Matches 2121; Conservative Similarity 541 1605 1665 481 1725 1785 1845 661 1905 721 1965 781 241 1545 1425 1485 301 421 1245 1305 121 181 361 Н 61 1365 Query Match

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2863 2983 CCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCC 3103 ATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACC 3163 1491 CCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGT-C 1904 1078 1019 2204 096 GGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAG-A -GCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGAAA AGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGT-G GGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAA TCTTCTTCTTCTCGGGGTCTGGCCCCCCCAAAATGCCTAACCCCAGGACCTTGGAAATTCTAC GGTTCCCCCCACTTCCACTCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGC -AAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGT TTATTTGTAGGGGAAGAGTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCAC TCCTTCTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAATAACAA AGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGG AGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCTCTTGGCCCAGCCT 1079 -GGGTTAACAGCTAGCTCCTAGTTGAGACACCTAGAGAGGGTTTTTGGGAGCTGAA AGCACTGTCTTTTTGCTGATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGG TCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGGTTTCAGTCTGGACTTATACAGG AGGCCAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTC 2265 AGGGTTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAA TAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAAACCTGCAGCTTCGTTTAATGT AGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATG-AC CGGGCTGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCTGCACCCTGT 1610 1669 1728 1846 3104 1551 2804 2864 2924 1787 1020 2385 2444 2504 1315 2564 1374 2624 1433 2684 1492 2744 2984 2325 1197 1256 2085 841 901 셤 g Qγ qq ŏλ qq Qγ q οy g ò Op Qy δy qq Q òγ g QY δŽ g δ Ω οy οy οy g g δ q οy Op δy g

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1964 CCCTGCCTGAGCTAAAGGAGGTCTTATCTCTCAGGGGGGGTTTAAGTGCCCTTTGCAAT- 2022
1905 ATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCA-C 1963
                                  CCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGTTTAAGTGCCGTTTGCAATA 3223
                                                                                               3224 AIGTCGTCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTA 3283
                                                                                                                    2023 ATGTCGTCTTATTTTTTAGCGGGGGAAATTTTATACTGTAAGTGAGCAATCAGAGF- 2081
                                                                                                                                                                                                                                                                                                                                                                                                               Human; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
vasctropic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corresponding to genes differentially expressed in mast cells following activation or in patients with allergic hypersensitivity disease, (I) that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of (II) if at least 6 amino acids. (II) is useful for identifying binding partners. (I) or (II) is useful for diagnosing or treating a disease state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma, urticaria or atopic dermatitis or mastocytosis) in a subject which involves determining the level of expression of (I) or (II). A computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated nucleic acid (ABN81319-ABN81324),
                                                                                                                                                                 3284 TAATGTTTATGGTGACAAAATTAAAGGCTTTCTTATATGTTTA 3326
                                                                                                                                                                                  2082 TAATGTTTATGGTGACAAAATTAAAGGCTTTCTTATATGTTTA 2124
                                                                                                                                                                                                                                                                                                                                                                                 Human mast cell related gene MC14 SEQ ID NO 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/product= "MC14-1"
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                                                                                                                                                                                                                                                                                ABN81320 standard; cDNA; 3663 BP
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28-MAR-2001, 2001US-279115P.
02-APR-2001, 2001US-280143P.
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expression level in a tissue or at least one mast cell of (I), is useful for presenting information to identify the relative expression level of (I). (II) is used as a marker to detect, disgnose or identify an allergic response in a patient. The protein can also serve as a target that modulate gene expression or activity and as an antigen to raise polyclonal or monoclonal antibodies. (II) is useful for identifying agents that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as modulating biological activity and function of (II) and thus are useful for identifying a light and a such as allergic hypersensitivity,
                                                                                                                                                                                                                                                                                                                                                                                                   62 TGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTG 181
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                                                                                                                                                                                         seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis
                                                                                                                                                                                                                                                                                                                                 242 AGTGCCTGAACGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGG
                                                                                                                                                                                                                                                               Score 1854.8; DB 24; Length 3663;
Pred. No. 6.2e-281;
0; Mismatches 682; Indels 303; Gaps
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qa	972 ACAGAAGGCAAGTAGCATTGTGTGACAACCCCTCACCCCCAGGAAGAGGGGCCCCT 1031	3 8	
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qa	1032 GTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTGAAACGCTGCCTCTTACCCTCCT 1091	3 8	
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ò	986 CCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGC 1045	δy	2041 TTCTGTTGCTG
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, o	TGTTTTACACGGATTTCGTGGGCGAAGGGGCTGTACCAGGGCCTGTACCAGGGCGGG	Qy	2221 ATGCACTGGAP
. q	TGAGCCTCTTTCTCATCCCAAGGCCGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCA	qq	2532 ATGCACTGGAA
δò	GCACCGAGGCCCGGAGACACTATGATGATGAGGCGTTCGGATGGGCAGCCTGGGGGCTGTTCC	Qy	2281 CTCCTAGTTGA
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2000US-0605783.
2000US-0636215.
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10-AUG-2000; 2
29-AUG-2000; 2
06-SEP-2000; 2
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                                                                                                                                                                                                                                                                           The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding of cancer especially prostate cancer. The polypeptides, polynucleotides and polynucleotide and/or polypeptide are useful for stimulating the development polynucleotide and/or polypeptide are useful for stimulating an immune response, and for transling cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1470 CCTACACACTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAG
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Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;
                                                                              Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                              Claim 1; Page 484-486; 579pp; English.
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98.7%;
02-OCT-2000; 2000US-0679426
10-OCT-2000; 2000US-0685166
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Best Local Similarity 98.7%
Matches 1841; Conservative
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P-PSDB; AAU69873.
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                                                  CTCCTCTCTCCCCAGICTCTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGGTTTCAGTC
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                                       CTGCTGCCACCCTGTGCTGCTGAGGTGCGTAGCTGCACAGCTGGGGGGCTGGGGCGTCCCT.
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The present invention describes polynucleotide sequences (I) which encode
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                                                                                                                                                                                                                                                            SG;
YAW;
                                                                                                                                                                                                                                                          SL, Jiang Y, Reed, Stolk JA, Skeiky
                                                                                                                      Human; prostate cancer; prostate-specific; diagnosis; vaccine;
                                                                                                                                                                                                                                                          Harlocker S
Retter MW,
                                                                                                                               cytostatic; gene therapy; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 461-463; 543pp; English.
                                                                                                    P553S cDNA splice variant P553S-6.
                                              BP.
                                                                                                                                                                                                                                                          J.F.
                                            AAH93869 standard; cDNA; 6976
                                                                                                                                                                                                   .6-JAN-2001; 2001WO-US01574.
                                                                                                                                                                                                                     14-JAN-2000; 2000US-0483672
                                                                                                                                                                                                                                                         Dillon DC, Mitcham
MD, Fanger GR, Day
                                                                                  (first entry)
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6972 AAAAA 6976
                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
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                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                         Xu J, Dil
Kalos MD,
                                                               AAH93869;
                                                                                                                                                                                                                                                                             Wang A,
                             RESULT 33
                                     AAH93869
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prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and tibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies of (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used to improve diagnostic and therapeutic mathods for can also be used to improve diagnostic and therapeutic.

methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.

Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;

Pace Pace	2488 G 6132 G	2548 GGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGACACAG	2608 CTTATTTAACAAAGIAGAAGGGAATCCATTGCTAGCTTTT	2668	2728 6372	2788 A 	2848 T 6492 T	2908 TCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCACTCCCTCTAC	2968	3028 6672	3088 T 1 6732 T	3148 GAAACTCAGGAGCACCCCTGCCTGAGCTAAGGGAGGTCTTATC	3208 AGTGCCGTTTGCAATAATGTCGTCTTATTATTTAGCGGGGTGA	3268 GTGAGCAAT 6912 GTGAGCAAT	7 3328 AAAA 3332 11111 5 6972 AAAA 6976	RESULT 34 ABL95412 ID ABL95412 standard; cDNA; 6976 BP.	A BBL95412; X 19-JUL-2002 (first entry)	K Human P553S splice variant SEQ ID NO 705. M Human; cancer; prostate cancer; vaccine; cytostatic; gene therapy; gene; ss.
S3.28; Score 1815, 8; DB 22; Length 6976;	QY	Qy	QY	Qy	Qy Db	40 do	QQ QQ	Qy Dp	Qy	QQ Dp	da √o∵	ଦୁଧ ପୁ	Qy Dp	da Op	QQ Dp	REIS	2 2 2 2 3	~
	<pre>; Score 1815.8; DB 22; Length 6976; ; Pred. No. 8.2e-275; 0; Mismatches 22; Indels 2; Gaps</pre>	1470 CCTACACACTGGCCTCCCTCTACCGGGGGGAGAGCAGGTCTTCCTGCCCAAATACCGAG 152	1530 GGGACACTGCAGCTGAGCACAGCAGCCTGATGACCAGCTTCCTGCCAGGCCTTA 158 1530 GGGACACTGCAGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTA 158 5172 GGGACACTGCAGGAGGAGGAGGACAGCAGCATGACTAGACTAGCAGCCCTA 533	1590 AGCCTGGAGCTCCCTTCCCTAATGGACACGTGGTGCTGGTGCTGCTCCCCCACTGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	1650 CTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGGTG	1710 AGCCCACGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGG 	1770 ATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCGGG 1	1830 TCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTT 188 11111111111111111111111111111111	1890 ACTITCCTACACAGGTAGTATITGACAAGAGGGACTIGGCCAAATACTCAGGGTAGAAAA 19 	1950 CTTCCAGCACATIGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGGTCCCGGTCCCGGTA 20	2010 GCCCCAFGGGGCTGCCGGCGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCT 2	2070 CIGCIGCCACCCIGIGCIGCIGAGGIGGTAGCIGCACAGCIGGGGGCIGGGGCGICCCT 2	2130 CTCTCTCTCCCAGTCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGTTTCAGTC 2	2190 TGGACTTATACAGGGAGGCCAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGT 224	2250 GGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGG 230:	2310 TTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGC 236	2370 AGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGA 24	2430 TTTGAACATATGACTTATTTGTAGGGAAGAGTCCTGAGGGGAACACACAGAACCA 24

CCCTCTTACCTTTTATCA 2547 AGATAGCTGGTCATTGGG 2727 CAAAATGCCTAACCCAGG 2787 IGTTACCCAAGGTTAGGG 2847 TTCCCTAACCACCCCTCT 2907 ACTCTCTCTAGGACTGGG 2967 CCCTACCCCAACTTTC 6671 SCCCTACCCCAACTTTC 3027 ;; immunostimulant; us-09-759-143-110.rng

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5472 TCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGTTT
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5172 GGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTA
                                                                               AGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCAC
                                                                                         CTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.2%; Score 1815.8; DB 24; Length 6976; 98.7%; Pred. No. 8.2e-275; arive 0; Mismatches 22; Indels 2; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r diagnosing and tre
and as markers for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New prostate-specific polynucleotides for diseases, in particular prostate cancer, a progression of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 705; 87pp; English.
                                                                                                                                                                                         99US-0443686.
2000US-0483672.
2000US-0538857.
2000US-0538857.
2000US-0570737.
2000US-0570737.
2000US-0636218.
2000US-0651236.
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98US-0020605.
98US-0030607.
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99US-0232149.
                                                                      2001US-0759143
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Matches 1841; Conservative
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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MITCHAM J L.
HARLOCKER S I
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DAY C H.
VEDVICK T S.
CARTER D.
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KALOS M D.
FANGER G R.
RETTER M W.
                               US2002022248-A1
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29-AUG-2000; 2
06-SEP-2000; 2
02-OCT-2000; 2
10-OCT-2000; 2
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27-JUN-2000;
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
                                                                 CTTATTTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTTGGTGTCTAA
                                                                                                        CTGATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGG
                                                                                                                                              ACCTTGGAAATTCTACTCCATCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGG
                                                                                                                                                                                   TGTTGAAGGAAGGTAGAGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCT
                                                                                                                                                                                             TCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCACTCCCTCTACTCTCTAGGACTGGG
                                                                                                                                                                                                                                 CTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCCAACTTTC
                                                                                                                                                                                                                                                                                6612 CTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCCAACTTTC
                                                                                                                                                                                                                                                                                                  3028 CCCACCAGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human mast cell related splice variant gene MC14 SEQ ID NO 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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The invention relates to isolated nucleic acid (ABNB1319-ABNB1324),

corresponding to genes differentially expressed in mast cells following
activation or in patients with allergic hypersensitivity disease, (I)
that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of

(II) if at least 6 amino acids. (II) is useful for identifying binding

comparison of (II) is useful for diagnosing or treating a disease

state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma,

utticaria or atopic dermatitis or mastocytosis) in a subject which
involves determining the level of expression of (I) or (II). A computer

comprising a database containing information identifying the
expression level in a tissue or at least one mast cell of (I), is useful

compresenting information to identify the relative expression level of

comparison as marker to detect, diagnose or identify an allergic

comparison a patient. The protein can also serve as a target that

modulate gene expression a cattudyty and as an antigen to raise

contained.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agents that modulate expression of the protein or agents, such as agonists or antagonists. The agonists or antagonists are useful for modulating biological activity and function of (II) and thus are for alleviating disease conditions such as allergic hypersensitivity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTG
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                                          variant"
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                                      "MC14 alternatively spliced
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100.0%; Pred. No. 7.5e-251;
iive 0; Mismatches 0;
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28-MAR-2001; 2001US-279115P.
02-APR-2001; 2001US-280143P.
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Matches 1662; Conservative
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٥y	TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGCTGCCTGC	Oy P	1844 AC
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oy G	944 GCAGCGCTGGGCCCCACCGAGCAGAGGGCTGTCGGCCCCCTCCTTGTCGCCCCAC 1003	XX A XX	ABA91283; 08-APR-2002
oy B	1004 TGCTGTCCATGCCGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCGGGTG 1063	XX DEX XX	Thioredoxin
ογ	CACCAGGTGTGCTGCCGCATGCCCCGCACCTGCGCCGGCTCTTCGTGGCTGAGCTGTGC 1	XX OS	cancer; vac
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oy Op	1124 AGCTGGATGGCACTCATGACGTTTTACACGGATTTCGTGGGCGAGGGCTG 1183 	N X Q	WO200200892
Qy Dp	1184 TACCAGGGCGTGCCCAGAGCTGAGCCGGGCAGGCCCGGAGACACTATGATGATGAAGGC 1243 	XX PF PR	19-JUN-2001 26-JUN-2000
å å	GITCGGATGGCCAGCCTGGGCTGTTCCTGCAGTGGGCCATCTCCTGGTCTTCTCTG 1	PR XX PA	30-OCT-2000 (SMIK) SMI
oy S	GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA 1	PI XX DR	Cabezon Sil WPI; 2002-1
a 8	1021 GTCAIGGACCGGCIGGIGCAGCGAITCGGCACTCGAGCAGTCTAITIGGCCAGIGIGGCA 1080 1364 GTTTTCCTGTGGCTGCCGGTGCCACATGCCTACAGAGAGAG	XX P	P-PSDB; AAM
G 8	GCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACATGTGGCCGTGGTGACACGCT	# E E E	betw ing
å da	1424 TCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483	TY XX PX XX	use - Example 5;
oy Dp	1484 TCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGT 1543 	2222	The present from the 5' the human u
λ _o δ	1544 GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603	2225	tail. The which inclu yeast alpha
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                                                                                                                                                                                                                                                                                                           CTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903
                                                                                                                                                                                                                                                                                                                                                                                                       sequence encoding triple fusion protein comprising ubiguitin ween thioredoxin and polypeptide of interest, useful for recombinant polypeptide of interest suitable for medicinal
                                                                                                 nt sequence is that of a triple gene fusion comprising, 5' end, the trxA thioredoxin gene from Escherichia coli, ubiquitin coding sequence, the prostate antigen P501S ids 55-553) coding sequence, and DNA encoding a histidine etriple fusion was constructed in plasmid pATT15063, luded the Saccharomyces cerevisiae CUP1 promoter and ha prepro signal sequence. The triple fusion protein 0661) was produced in E. coli G1724 transformants. This mple of the production of triple fusion proteins of the comprising ubiquitin fused between thioredoxin and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n; trxA; ubiquitin; P501S; tumour; prostate; antigen; ccine; therapy; human; gene; ds.
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       A claimed method
protein of interest, in this case P501S(aa55-553). A claimed metho of producing a recombinant protein of interest involves: culturing a host cell (preferably E. col1) under conditions which allow for co-expression of the triple fusion and a ubiquitin-specific endoprotease (especially UBPI from Saccharomyces cerevisiae); and recovering the recombinant protein directly from the bacterial cells after it has been subjected to the action of the ubiquitin-specific endoprotease in vivo. In the present case, a p501-like protein of 509 amino acids is generated. The recombinant protein can used as a vaccine for cancer therapy.
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                                                                                                                                                                                        Query Match 44.1%; Score 1503; DB 24; Length 2133; Best Local Similarity 100.0%; Pred. No. 5.3e-226; Matches 1503; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                             Sequence 2133 BP; 384 A; 656 C; 614 G; 479 T; 0 other;
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          CACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTG
                                                                                                                                                                 AAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTG
                                         GCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCC
                                                                                           1580 CCAGGCCCTAAGCCTGGAGCTCCCTTAATGGACACGTGGGTGCTGGAGGCAGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P501S; tumour; prostate; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Xaa not given in amino acid sequence of Figure 12b (AAM50662), which has a Val residue at amino acid position 20B not not encoded by the present sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thioredoxin-ubiquitin-P501S(aa1-320)His triple gene fusion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thioredoxin; trxA; ubiquitin; P501S; tu cancer; vaccine; therapy; human; gene;
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Escherichia coli
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2104 GCG 2106
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1203 TGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACTGCTGGTGGCTGAGGA 1262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; pastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein-encoding gene 11 cDNA clone HWBAR14, SEQ ID NO:55.
                     883 TGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCACCCCACACTGCTGGTGGCTGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           943 GGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1323 CTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCGGCT
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                                                                                                                   1023 CACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGC
                                                                                                                                                                                                                                                                           823 CATTGACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTT
GGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGCACTTCTGTGGCCCAGGTGTGCTT
                                                                                           CACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGC
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complement (528..139)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a triple gene fusion comprising, from the 5' end, the trxA thioredoxin gene from Escherichia coli, from the 5' end, the trxA thioredoxin gene from Escherichia coli, canno acids 1-320) coding sequence, and plan encoding a histidine tail. The triple fusion was constructed in plasmid pRITI5115, cail. The triple fusion mas constructed in plasmid pRITI5115, conder the control of the lambda pL promoter. Triple fusion proteins of protein (see AAM50662) was produced in E. coli G1724 transformants. This is an example of the production of triple fusion proteins of the invention comprising ubiquitin fused between thioredoxin and a protein of interest, in this case F5015(aal-320). A claimed method of protein of interest involves: culturing a host cell (preferably E. coli) under conditions which allow a host cell (preferably E. coli) under conditions which allow condoprotease (especially UBPL from Saccharomyces cerevisiae); and recovering the recombinant protein directly from the bacterial cells after it has been subjected to the action of the cubiquitin-specific endoprotease in vivo. In the present case, expression was controlled by addition of tryptophan. The expression was controlled by addition of tryptophan. The combinant protein can used as a vaccine for cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                       Novel DNA sequence encoding triple fusion protein comprising ubiquitin fused between thioredoxin and polypeptide of interest, useful for producing recombinant polypeptide of interest suitable for medicinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 TATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1593 BP; 308 A; 472 C; 461 G; 352 T; 0 other;
                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; Fig 12b; 87pp; English.
                                                                                                                                                                                                                                                               Delisse AEF;
                                                                                                  19-JUN-2001; 2001WO-EP06952.
                                                                                                                                                26-JUN-2000; 2000GB-0015619
                                                                                                                                                                      30-OCT-2000; 2000GB-0026484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               963; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                               Cabezon Silva TEV,
                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAM50662
                                                       03-JAN-2002
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Ambo5220-Aabo5282 represent CDNAs corresponding to 21 human secreted protein genes, and AAE01352-AAE0143 represent the proteins they encode. AAE01413-FAAE0143 represent human secreted proteins they encode. The secreted proteins and their genes are useful for preventing. Treating or ameliorating medical conditions, e.g., by protein or gene therapy. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the passed on the tissues in which they are most highly expressed, and include the new genes. Specific uses are described for each of the 21 genes, cancer, tumours, foetal and developmental abnormalities. Cancer, tumours, foetal and developmental abnormalities, haematopoletic disorders, diseases of the immune system, AIDS, autoimmung calesases (e.g., rheumatoid arthritis), inflammation, allergies, conditive disorders, disbates, atherosclerosis, cardovascular disorders, copnitive disorders, alabates, atherosclerosis, cardovascular disorders, and progenic disorders, and conditive disorders, independent disorders, and infections. The progenic disorders, independent disorders, and infections. The projection of also before transplantation, for supporting cell culture of primary tissues, correspondent tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or protein of the invention can be used as a food additive or protein of the invention can be used in allevating specific for a protein of the invention can be used in allevating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., the present sequence represents a human secreted protein-encoding cDNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autoimmune disease and cancer, and used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            989 AIGGGAGITICIAGGAIGAAGCGACTCNICCAIGGGAITIGAACAIATAAAGITATIIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM, Komatsoulis GA, Wei P, Fiscella M, Baker KP;
                                                                                                                                                                                                                                           /product= "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1019 BP; 276 A; 227 C; 257 G; 255 T; 4 other;
/note= "Does not include start codon"
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                                  /partial complement (528..526)
                                                                                                                                                                  complement (525..142)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1999; 99US-0164835.
27-JUL-2000; 2000US-0221142.
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                                                                            sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                             3053 GAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCC 3112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3233 TATTTATTTAGCGGGGGGGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTA 3292
                                                                                                                                   069
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929 AGGGAAGAGTCCTGAGGGGCAACACACAAAAAGACCAGGTCCCCTSAGCCCACAGCACTGTC 870
                                                                           630
                                                                                                                                                                                                                                                                                            149 TATTTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2513 ITTTTGCTGATCCACCCCCTTTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGT
                                                               2573 IGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAATTTAACAAAGTAGAAGG
                                                                                                         2633 GAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCC
                                                                                                                     629 CCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAA
                                                                                                                                                                                                                                                    2693 AACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCT
                                                                                                                                                               Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human /M. tuberculosis fusion protein RA12-P501S-E2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Homo sapiens.
Chimeric - Microbacterium tuberculosis.
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                                                                                                                        799 CTGCCTGGCCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTACCT
                                                                                                                                                                                                 859 GGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGC
                                                                                                                                                                                                                                                                    919 AGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCT
                                                     GGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L, Jiang Y, Reed SG;
Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis; ss.
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Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ral2-P501S-E2 construct cDNA sequence.
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Kalos MD, Fanger GR, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH93917 standard; cDNA; 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding rells specific for a tumour protein, and for inhibiting the development polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for esponse, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 GGCCGCAGGCATCACCTATGTGCCCCCTCTGCTGGAAGTGGGGGGTAGAGGAAGTT
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.3%; Score 794.6; DB 22; Length 1203; 99.5%; Pred. No. 2.2e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky XAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 17; Page 542-543; 579pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention.
                                                                                                                                                                         20000S-0593793.
20000S-0605783.
20000S-0636215.
20000S-0651236.
20000S-0657279.
                                                                                     2001WO-US09919
                                                                                                                                         2000US-0568100
2000US-0570737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 797; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAU69907
                WO200173032-A2
                                                                                                                                                                                                                                                                02-OCT-2000;
10-OCT-2000;
                                                                                     27-MAR-2001;
                                                                                                                                                                           13-JUN-2000;
27-JUN-2000;
                                                                                                                                                                                                                10-AUG-2000;
                                                                                                                                                                                                                               29-AUG-2000;
                                                                                                                                                                                                                                                 06-SEP-2000;
                                                                                                                       27-MAR-2000;
                                                                                                                                         09-MAY-2000;
12-MAY-2000;
                                                  04-0CT-2001
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I). (II), to antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. To calls prepared using (I) or (II) are used treat cancer in a patient. To patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used in vaccines. The antibodies or (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGGAAGTGGGGGGTAGAGGAGGTA 438
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0; Mismatches 4: 7-2
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                                                                                                                                                                                                                                                                                                                                                                         tch 23.3%; Score 794.6; al Similarity 99.5%; Pred. No. 2.2 797; Conservative 0; Mismatches
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cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
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Carter D;
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A, Day CH, Vedvick TS,
epler WT, Henderson RA;
                                                                                                         Ral2-P501S-E2 construct cDNA sequence SEQ ID NO 851
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Retter MW, Stolk JA, Day CH
J A, Skeiky YAW, Hepler WT,
                                                                                                                                                  Chimeric - Mycobacterium tuberculosis.
Chimeric - Homo sapiens.
1159 CACGGATTTCGTGGGCGAGGG 1179
         1182 CACGGATTTCGTGGGCGAGTG 1202
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990S-0232149.
990S-0288946.
990S-0352616.
990S-0439313.
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HEPLER W T.
HENDERSON R A.
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HARLOCKER S L.
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FANGER G R.
RETTER M W.
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CARTER D.
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DAY C H.
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WANG A.
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12-MAY-2000;
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                                                                                                     The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
         New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the
                                                                                                                                                                                                                Query Match 23.3%; Score 794.6; DB 24; Length 1203; Best Local Similarity 99.5%; Pred. No. 2.2e-115; Matches 797; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                               Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;
                                                                           Example 17; SEQ ID NO 851; 87pp; English.
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                                            progression of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a new DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1341 CAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                               Polypeptides comprising immunogenic portions of prostate proteins used in a vaccine for the treatment of prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 673.4; DB 19; Length 789; Pred. No. 1.8e-96; 0; Mismatches 40; Indels 6;
                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
                                                                                                               Prostate; cancer; tumour; vaccine; immunogen; clone;
                                                                                         tumour clone
                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 38-39; 130pp; English
                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.78;
94.28;
                                                                                       CDNA sequence of prostate
                                                                                                                                                                                                                            98US-0020956.
97US-0806099.
97US-0904804.
                                                                                                                                                                                                          98WO-US03492.
                                                                  (first entry)
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                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP
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                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent
CCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCCATCCCTGTTTATGGGCTCCA
                                                                                                                TCGCCATTTACTTTGCTACACGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAG
                                                                                                                                                     CGTAGAAAACTTCCAGCA - - CATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCC
                                                                                                                                                                                                                              AATGTGGCTCTCTGCTGCCACCCTGTGCT-GCTGAGGTGCGTAGCTGCACAGCTGGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                          Prostate tumour specific gene; human; prostate cancer; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human prostate specific tumour protein and fragments for detecting and treating prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                          prostate tumour specific gene L1-12.
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                                                                                                                                                                                                                                                                                                                                    BP
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bind an immunogenic portion of a prostate protein (such as by this sequence). An antibody which binds to an immunogenic of the prostate protein, and the method can be used to detect, progression of, or treat prostate cancers. The antibody may conjugated to a therapeutic agent for use in therapy of prostate
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                                                                                                    19.7%; Score 673.4; DB 19; Length 789; 94.2%; Pred. No. 1.8e-96; tive 0; Mismatches 40; Indels 6;
                                                                                 C; 221 G; 182 T; 14 other;
                                                                                 Sequence 789 BP; 122 A; 250
                                                                                                                             Conservative
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AAA06250 standard; cDNA; 789 BP

RESULT 44 AAA06250 ID AAA0

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1998

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1821 TTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGG 1880
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                                                       TGCTCCCACCTCCACCCGCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTG 1700
                                                                                                              1701 TGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCG 1760
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                                                                      301 TGCTCCCACCTCCACCCGCGCTCTGCGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGG
1581 CAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCC
                241 CAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCC
                                                                                                                              421 CCATCCTGGATAGTG-CTTCCTGCTGTCCCANGTGGCCCCATCCTGTTTATGGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate cDNA sequence #10
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2000US-0657279.
2000US-0679426.
2000US-0685166.
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2000US-0568100.
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10-AUG-2000;
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06-SEP-2000;
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10-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polypeptides can be used as a probe or to modulate the expression of the polypeptides or an be used as a probe or to modulate the expression of the polypeptides. AAA06541 to AAA06691 and AAV82000 to AAX82000 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                          SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes isolated polypeptides, comprising an
                                                                                                       Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide useful for treating and diagnosing prostate cancer comprises an immunogenic portion of prostate tumor protein \,
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                                                                             Human immunogenic prostate tumour protein cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                             Mitcham JL;
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                                                                                                                                                                                                                                                                                                                                                                                                             Хu J,
                                                                                                                         immunogenic; cytostatic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                             Dillon DC, Harlocker SL, Yuqiu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 99; 263pp; English.
                                                                                                                                                                                                                                                             98US-0115453.
98US-0116134.
98US-0159812.
98US-0159822.
99US-0232149.
99US-0232880.
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                                                 13-JUN-2000 (first entry)
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23-SEP-1998,
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polynucleotides, polypeptides, fusion proteins of the polypeptides, darkbodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antigenic epitopes cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for attimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development polynucleotide and/or polypeptide are useful for stimulating an immune response, and for transing cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
                                                                                                                                                    New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer
                            Kalos MD;
Carter D;
                  Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y,
Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                    invention relates to isolated prostate-specific
                                                                                                                                                                                                                     Claim 1; Page 232-233; 579pp; English.
                                                                                                            WPI; 2001-639232/73
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Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;

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1341 CAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCC 1400 1401 ACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGC 1460 1461 AGAICCIGCCCTACACACTGGCCTCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCA 1520 AATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGC 1580 CAGGCCCTAAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCC 1640 TGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCG 1760 1641 TGCTCCCACCTCCACCGGGGGTCTGGGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGG 1700 241 CAGGCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCC 300 301 TGCTCCCACCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGG 360 1 CAGTCTAINTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCAGTGCTGTCCC 60 Gaps Query Match 19.7%; Score 673.4; DB 22; Length 789; Best Local Similarity 94.2%; Pred. No. 1.8e-96; Matches 745; Conservative 0; Mismatches 40; Indels 6; 1521 1581 181 1701

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1881 TCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAG 1940

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1941 CGTAGAAAACTTCCAGCA--CATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCC 1998

1999 CGCTCCTGTTAGCCCCATGGGGCTGCCGGCTGGCCGCCAGTTTCTGTTGCTGCCAAAGT 2058 2059 AATGTGGCTCTCTGCGCACCCTGTGCT-GCTGAGGTGCGTAGCTGCACAGCTGGGGGGC 2117 completed: June 9, 2003, 16:13:19 ne : 816 secs 2118 TGGGGGGTCCC 2128 778 TNGGGNGTTCC 788 Search com Job time : δý QQ qq δ ŏ q

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

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ALIGNMENTS

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linear				•		Vertebrata;	; Hominidae;	•	r, M.A.	diagnosis o	
bp DNA	25272.					Craniata; '	Catarrhini		and Cheeve	therapy and	
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329	Sequence 110 from Patent WO0125272. AX106329	AX106329.1 GI:13922014		•	Homo sapiens	yota; Metazo	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 3410)	Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.	Compositions and methods for therapy and diagnosis of prostate	٠
AX106329	Seguence AX106329	AX106		human.	Ношо	Eukar	Mamma	1 (b	Xu,J.	Compo	cancer
RESULT 1 AX106329 LOCUS	DEFINITION ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	

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atent: WO 0125272-A 110 12-APR-2001; ORIXA CORPORATION (US) 1. 3410 /organism="Homo sapiens" //db_xref="taxon:9606" 667 a 1014 c 945 g 783 t 1 others	th 100.0%; Score 3409.6; DB 6; Length 3410; Similarity 100.0%; Pred. No. 0; 10; Conservative 0; Mismatches 0; Indels 0; Gaps	GGGAACCAGCCTGCACGCGCTGGCTCCGGGTGACAGCCGCGCGCG	GTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGGTGAGCATGGGCTG 	AAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTT	GGCGGCAGCAAGGAGAGAGACCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTG 	GAGIGCCIGAACGGCCCCTGAGCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG	GGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTT -	TGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT 	GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGCCATTGGTCCAGTGCTGGCCTGGT 	CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCGCGCTTTTTTTT	GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGC	CGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCAT	CCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT	GCTCTCTGACCTCTTCCGGGACCCGGACCAGTGTCGCCAGGCCTACTCTGTCTATGCCTT	CATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG	
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2061 GCAGGACCAGAAGCACAAAGTGCGGT 3121 ATATCTGTCCTTGGGGAATCTCACACACACACACACACAC	RESULT 2 AX140620 LOCUS DEFINITION Sequence 110 from Patent WOG ACCESSION AX140620 VERSION KEYWORDS SOURCE Numan. ORGANISM EUKARYOLS; Metazoa; Chordata Mammalia; Butheria; Primateas Mammalia; Butheria; Primateas Homo sapiens EUKARYOLS; Motorata Mammalia; Butheria; Primateas Mammalia; Butheria; Primateas Nu, J. Dillon, D.C., Mitcham, Reed, S.G., Kalos, M.D., Retter Skeed, S.G., Compositions and methods for Compositions and Mang.A. BASE COUNT GORDATION (US) FEATURES SOURCE AND	y Ma Loc hes	Db 241 GAGTGCCTGAACGGCCCCTGAGCC
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1 (bases 1 to 3410)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
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Compositions and methods for the therapy and diagnosis of prostate

Patent: WO 0151633-A 110 19-JUL-2001;

CORIXA CORPORATION

cancer

JOURNAL TITLE

Location/Qualifiers

.3410

source

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS

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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sequence 110 from Patent W00151633. AX200480 GI:15390293 AX200480.1 human. AX200480 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 3

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120 180 180 240 240 300 300 360 360 420 420 480 480 540 540 900 900 999 999 720 720 780 780 9 9 181 GCCGCCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTG GGGAACCAGCCTGCTGGCTCCGGGTGACAGCGGCGCGCCTCGGCCAGGATCTGA GTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG AAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTT GAGTGCCTGAACGGCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG GGTGAGCCGCCTGCTGCGCCACCGGAAAGCCCCAGCTCTTGCTGGTCAACCTGCTAACCTT TGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCG CGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCCAGGCCCCTGGAGCTGGCACTGCTCAT CCTGGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT 541 GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGC 0; Gaps 6; Length 3410; 0; Indels; 1 others DB ¥ 100.0%; Score 3409.6; 100.0%; Pred. No. 0; 0; Mismatches /organism="Homo sapiens" /db_xref="taxon:9606" a 1014 c 945 g 78: Matches 3410; Conservative Similarity ø 667 361 61 61 121 241 361 Query Match 421 601 301 481 601 199 199 721 781 421 721 Best Local BASE COUNT ORIGIN g QΥ g qq ò οy а Ω q δ Ob οy q δ qq οy g ٥y qq Qγ Q ò qq Qγ QQ δλ PAT 29-AUG-2001

1861 TGCCGCAGGCCTGGGTCTG	1921 CGACTTGGCCAAATAC 	1981 CACTGGGTCCCAGCTC 1981 CACTGGGTCCCAGCTC 2041 HTCTGTTGCTGACTABB	2041 TTCTGTTGCTGCCAAAGI	ZIOI GCIGCACAGCIGGGGCCZ 	2161 ACTGGAGGCCTTC	2221	2281	2341 GTTTC	2401 TTTCTAGGA	2461 GTCCTGAGGGGC	2521 GATCCACCCC	2581 CAGAGACACAGGCA.	2641 TGCTAGCTTTCTGTGT	2701	Oy 2761 CTGGCCCCCCAAAATGCCTAACC Db 2761 CTGGCCCCCCAAAATGCCTAACC	2821	2881 CTCAACG	Qy 2941 CTCCCTCTACTCTCTAGAN
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	841 TGCCTGGCCCCTACCTGGGCACCCAGGGGGTGCCTCTTTGGCCTGCTCACCCTCAT 900	901 CTICCICACCIGCIGIAGCACACIGCIGGIGGAGGAGGAGCAGCGCTGGGCCCAC 960	961 CGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCCACTGCTGCTCGTCCAGGCCGGC 1020	1021 CCGCTTGGGTTTCGGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGCTGCCG 1080	CATGCCCGGACCCTGCGCGCGCTCTTCGTGCCTGACTGGTGCAGTGGATGCACTCTT114 [1141 GACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTGTACCAGGGCGTGCCCAG 1200	1201 AGCTGAGCCGGGCACCGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT 1260 	1261 GGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCAGTGGACCGGCTGGT 1320	1321 GCAGCGATTCGGCACTCGAGCACTCTATTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGC 1380 	1381 CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGG 1440	1441 GTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGA 1500	1501 GAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAG 1560 	1561 CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTACCTAATGGACACGT 1620 11111111111111111111111111111111111	1621 GGGTGCTGGAGGCAGTGGCTGCCACCTCCACCCGCGCTTGCGGGGCCTCTGCCTG 1680 1621 GGGTGCTGGAGGCAGTGGCTGCTCCACCTCCACCTCGCGGGGCCTCTGCCTG 1680	TGATGTCTCCGTACGTGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCG 17	GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGCCCCCCCC	1801 ATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 1860 1801 ATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGTCACTATATGGTGTC 1860	1861 TGCCGCAGGCCTGGGTCGCCATTTACTTTGCTACAGGTAGTATTTGACAAGAG 1920
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1861	TGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 1	920
1921	CGACTTGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGTGGAGGGCCTGCCT	086
1981	CACTGGGTCCCAGCTCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGT 2	040
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2401	1 TITCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA 2	2460
2461	1 GTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCCAGCACTGTCTTTTGCT 2	2520
2521	APCCACCCCCTCTTACCTTTATCAGGATGIGGCCTGTTGGTCCTTCTGTTGCCATCA 	2580
2581 2581	1 CAGAGACACAGGCATTTAAATTTTAACTTATTTATTTAACAAAGTAGAAGGGAATCCAT 2 	2640
2641	1 IGCTAGCTTITCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCA	2700
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2947	1 CTCCCCTCTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACC 3	3000

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CCCCACTGCTGTCCATGCCGGGC 1020 AGAGCCGAGACGAAGCAGTTCTG 240 540 TGTGCAGCTGGATGGCACTCAT 1140 TGTGCAGCTGGATGCCACTCAT 1140 GGCTGTACCAGGGCGTGCCCAG 1200 300 CCACTATGGTCÇAGAGGCTGTG 300 TTGCTGGTCAACCTGCTAACCTT 360 ATTGGTCCAGTGCTGGGCCTGGT 480 099 AAGGCGTTCGGATGGGCAGCCT 1260 SAAGGCGTTCGGATGGGCAGCCT 1260 1261 GGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGT 1320 540 rGCTTCACTCCACTGGAGGCCCT 720 900 AGCCTCTTTCTCATCCCAAGGC 600 099 780 CAGGCCTACTCTGTCTATGCCTT 780 CTGCCATTGACTGGGACACCAG 840 CICTITGCCTGCTCACCCTCAT 900 096 CTGCCATTGACTGGGACACCAG 840 STCTTTGGCCTGCTCACCTCAT 900 AGGAGGCAGCGCTGGGCCCCAC 960 CCACTATGGTCCAGAGGCTGTG GTGGACGCTATGGCCGCCGCCG AGCCTCTTTCTCATCCCAAGGGC CCCTGGAGCTGGCACTGCTCAT CCCTGGAGCTGGCACTGCTCAT BAGGAGCACCTGGCCCCAC AGGCCTACTCTGTCTATGCCTT

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1261	1321	1381	1441	1501	1561	1621 1621	1681	1741	1801	1861	1921 1921	1981	2041	2101	2161	2221	2281	2341
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100 from Patent W0019339. 1 GI:21541123 ans and methods for the therapy and diagnosis of breast to cost and methods for the therapy and diagnosis of breast to 0198339-A 100.27-DEC-2001; Mominidae, Homo. A. X. J. Dillon, D. C., Retter, M. W. and Harlocker, S. L. Coction/Qualifiers 1. :310 'Holling for the therapy and diagnosis of breast to 0198339-A 100.27-DEC-2001; Coction/Qualifiers 1. :310 'Holling for the therapy and diagnosis of breast to 0198339-A 100.27-DEC-2001; Coction/Qualifiers 1. :310 'Holling for the therapy and diagnosis of breast to 0198339-A 100.27-DEC-2001; Coccognosis of breast to 0198339-A 100.27-DEC-2001; Coccognosis of breast to 0198339-A 100.27-DEC-2001; Coccognosis of breast to 01980-A 100.08; Proceeding for 100.08; Proceeding for 100.08; Proceeding for 100.08; Procedure of 100.08; Procedu	Qy 721 GCTCTCTGACCTCTTCCGGGACCCGGACCAGGACCACGGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACTGTCCCAGACCACTGTCCCAGACCACTGTCCCAGACACCTGTCCCAGACACTCTTCCGGACCCCGGACCACTGTCCCAGACCACCTGCCTG	901 901 961	0y 1021 CCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCGGG	OY 1141 GACCTTCACGCTGTTTACACGGATTCGTGGGCGAGGGG	Oy 1261 GGGGTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCT	OY 1381 CGGTGCCACAFGCCTGTCCCACAGTGTGGCCGTGGTGACA	QY 1501 GAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGA DD	Oy 1621 GGGTGCTGGAGCCGTGCTCCCACCTCCACCGCGGGGGGGG
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	11 (1) 100 from Patent W00198339. 12 (1) 11 (2) 12 15 14 11 23 13 (1) 12 (1) 12 15 14 11 23 14 (1) 12 (1	WO 0198339-A 100.27-DEC-2001; CORPORATION (US) Location/Qualifiers 13410 /organism="Homo sapiens" //db_xref="taxon:9606" a 1014 c 945 g 783 t 1 others	100.0%; Score 3409.6; DB 6; Length 3410; Similarity 100.0%; Pred. No. 0; O; Conservative 0; Mismatches 0; Indels 0; Gaps GGGAACCAGCTGCACGCTGCTCCGGGTGACAGCCGCGCGCTGCTCGGCTAGATCTGA	GTGATGAGACGTGTCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG	GCCGCAGCAGGAGGAGGCCGCAGCTTCTGGAGCCGCGCGCG	GGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCACTGCTGCTGGTCAGAGGCTGTG [GGGGGTAGAGGAGATCATGACCATGGTCCTGGCCATTGGTCCAGTGCTGGGCCTGGT	GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGGGGCGCGCGC

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Xu,J., Kalos,M., Stolk,J.A., Zasloff,E.J., Zhang,X., Houghton,R.L., Filho,A.M., Nolasco,M., Badaro,R. and Reed,S.G. Direct Submission
Submitted (27-APR-2001) Antigen Discovery, Corixa Corporation, 1124
Columbia Street, Seattle, WA 98104, USA
Location/Qualifiers
                                                                                         3001 CCCAACTITCCCCTACCCCCAACTITCCCCACCAGCTCCACAACCCTGTTTGGAGCTACT 3060
                                                                                                                                                                                                          3241 TAGCGGGGTGAATATTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACA 3300
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CTCCCCTCTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCCCAAAATTTCCCCTACC
                                                    GCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGT
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/organism="Homo sapiens"
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IPRAGMILACEDPREDELALLIGYGLLOBYCGOVCPTPLEALLSDLFREDPHCROBY
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1014 c 945 9 783 t 1 others ö 099 120 180 240 240 300 300 360 360 420 420 480 480 540 540 900 900 099 720 780 780 720 9 9 GGGAACCAGCCTGCACGCCTCGCGTAACAGCCGCGCGCCCTCGGCCAGGATCTGA GTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG AAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTGCTAGGCAGTT GCCGCCAGCAAGGAGGAGAGGCCGCAGCTTCTGGAGCAGAGGCGAAGCAGTTCTG GAGTGCCTGAACGGCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG GGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTGGTCAACCTGCTAACCTT TGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT CTGTGTCCCGCTCCTAGGCTCAGCGAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCG GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGC CGGCTGGCTAGCAGGGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCAT CCTGGGCGTGGGGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT Gaps 9; Length 3410; ; 0 0; Indels DB ;; Score 3409.6; ;; Pred. No. 0; 0; Mismatches 100.0%; 100.0%; Conservative Query Match Best Local Similarity Matches 3410; Conserv æ 667 61 61 121 121 181 181 241 241 301 541 721 301 361 361 421 421 481 481 541 601 601 661 661 721 BASE COUNT ORIGIN

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Birect Submission
Direct Submission
Direct Submission
Direct Submission
Enfectious Diseases, Division of Genetic Resources; 23-1, Toyama I-chome, Shinjuku-ku, Tokyo 162-8640, Japan
CE-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5288-1111(ex.2120), Fax:81-3-5285-1181)
                                                                       PRI 13-JUN-2001
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R. Site2: DraIII (CACATGTG)

Description: 1st strand cDNA was primed with an oligo(dT) primer large strands of the strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5 and 3 primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to product was digested with Sfil and size selection was performed to arclude fragments <1.5kb.The Sfil-digested PCR product was cloned into distinct DraIII sites of pME185-FL3. AhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method
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RVOVERKRMTWLGIGPVLGLVSVPLINGSASDHWRGRYGRRFPFNMSEGIGILSEFU
IPRAGWLAGLLCPPREFLEILLIGVGLLDFCGOVCFTPLEALLSDLFRDPHCROA
XSVYAFWISLGGCLGYLLPAIDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVA
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AELCSWMALMTFTLFYTDFVGEGLYQGVPRAELGTEARRHYDEGVRMGSLGLFLQCAI
SLVFSLVMDRLVQREGTRAVYLASVAAFPVAAGATCLSHSVAVVTASAALTGFTFSAL
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SGLLPPPPALCGASACDVSVRVVVGEPTEARVVPGRGICLDLAILDSAFLLSQVAPSL
FMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQVVFDKSDLAKYSV"
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                     to mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Osada.N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
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                                                                                             clone:QtrA-11310, full insert
                                                                                                                                                                                                      oligo capping; fis (full insert sequence).
Macaca fascicularis adult male temporal lobe right cDNA to clone_lib:macaque brain cDNA library QtrA clone:QtrA-11310.
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/clone_lib="macaque brain cDNA library QtrA"
/dev_stage="adult"
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/protein_id="BAB46871.1"
/db_xref="GI:13874497"
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/db_xref="taxon:9541"
/clone="QtrA-11310"
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itch 85.0%; Score 2900.2; DB 9; Length 3514; al Similarity 94.8%; Pred. No. 0; 3155; Conservative 0; Mismatches 118; Indels 54; Gaps 13;	51 CAGGATCTGAGTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGC 110 221 CAGGATCTGAGTGATGAGATGTGTCCCCACTGAGGTGCCCCACAGCAGCAGCAGCAGGTTTGAGC 280	111 ATGGGCTGAGAAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTC 170	171 CTAGGCAGTTGGCGGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGA 230	231 AGCAGTICTGGAGTGCCTGAACGGCCCCTGACCCCTGGCCCACTATGGTCC 290	291 AGAGGCIGIGGGTGAGCCGCCTGCTGCGGCACCGGAAGCCCAGCTCTTGCTGGTCAACC 350	351 TGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCGCGCCTCTGC 410	411 TGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGC 470	471 TGGGCCTGGTCTGTCCCCGCTCCTAGGCTCAGCGAGACCACTGGCGTGGACGCTATG 530	531 GCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCA 590	591 TCCCAAGGGCCGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGG 650	651 CACTGCTCATCCTGGGCGTGGGGCTGCTGCTTCTGTGGCCAGGTGTGCTTCACTCCAC 710 	711 TGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGGCCACTGTCGCCGGCCTACTCTG 770	771 TCTATGCCTTCATGATCAGCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG	831 GGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGC 890	891 TCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGC 950 	951 TGGGCCCCACCGAGCCAGCAGAGGGCTGTCGCCCCTCCTTGTCGCCCCCTGCTGCT 1010	1011 CATGCCGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGC 1070
Query Match Best Local Matches 315	Qy Dp	Qy Db	Qy Db	oy Db	Qy Db	Qy Db	Qy Db	QY Db	Qy Db	Qy Db	Oy Db	Oy Dp	çy Dp	oy Db	Qy Db	Qy Dp	Qy Db

Qy	1071	TGTGCTGCCGCATGCCCCGCACCCTGCGCCGCTCTTCGTGGCTGAGCTGTGCAGCTGGAG	1130
QQ	1241	GTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCTGG	1300
Qy	1131	GCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGG	1190
qa	1301	GGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTATACCAG	1360
Qy	1191	CTGCCCAGAGCTGAGCCGGCACCGAGGCCCGGAGACACTATGATGA	20
Dp	1361	GTGCCCAGAGCTGAGCTGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCG	4
δ	1251	TGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGCTCATGG	-
Db		GGGCAGTCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTTGGT	1480
QY	1311	ACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCAGCTTTCC	1370
Db	1481	GGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATCTGGCCAGTGTGGCAGCTTT	1540
Qy	1371	CTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCG	1430
qq	1541	<u>erescreccestaccacereccierccacagistescretesisaces successives de la constanta </u>	1600
Qy	1431	CCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACAC	149
Dp	1601	CTCACTGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC	1660
Οy	1491	CCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAG	1550
Db	1661	CGGGGGGGGGGGGGGGTGTTCCTGCCCAAATACCGAGGGGACGCTGGAGGCACTAGC	1720
οy	1551	GTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTA	1610
qq	1721		1780
οy	1611	ATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGCTCTGCGGG	1670
QQ	1781	ACACGIGGGIGCIGGAGGCAGIGGCCIGCTICCACCICCACCGCGCTCTGCGGG	1840
Qγ	1671	CTCTGCCT	1730
qq	1841	TICCTGCGATGTCTCTGTACGTGGTGGTGGTGGTGAGCCCACCGAGGCCAGGGTG	1900
Qy	1731	TCCGGGCGCGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGT	1790
Dp		SGATAGTGCCTTCCTGCTGTCC	1960
Qy	1791	(7) -	1850
qq		GGCCCCGTCCTGTTCATGGGCTCCATCGTCCAGCTCAGCCAGTCTGTCACTGCC	2020
Qy	1851	TATEGRETCTGCCGCAGGCCTGGGT	1910
qa	2021	SCTGCAGGCCTGGGTCTGGTTGCTTTACTTTGCTACACAGGTAGTA	2080
Qy	1911	SACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGG	1970
qq	2081	GGGTGG	214
QY	1971	CCTGCCTCACTGGGTCCCCAGCTCCCCTC-CTGTTAGCCCCATGGGGCTGCC	2029
ρp	2141	CTCACTGGGTCCCAGCTCCCCACTCTTGTTAGCCCCCATGGGCTGCTGGG	220
Qy	2030	TGGCCGCCAGTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGC	2089
ОÞ	2201	GCCGCCAGTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTG	226
Qy	2090	TGAGGTGCGTAGCTGCACAGCTGGGGGCGTCCTCTCTCTC	2149
Dp	2261	SGTGCGTAGCTGCACAGCTGGGGGCTGGGGGCATCCCTCTCCTCCTCCTCCCAGTC	2320
Qy	2150	AGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCC	2209

233 MACCAMOGRAMOGRAMOGRAMOGRAMOGRAMOGRAMOGRAMOGR	d y		Dp 3	3373 TGCCGTT
2354 TROCCOGGCTCAGGCTTAMACACCTACCTGGCTCAGACATACCTAGACAGGCGTTT 200 2411 TROCCAGGCTCAGGGTTAMACACCTACCTGGCTCAGACACCTAGACAGGGGTTT 200 2411 TROCCAGGCTCAGGGTTAMACACCTACCTGGCTCAGACACCTAGACAGGGGTTT 200 2412 TROCCAGGCTCAGGGTTAMACACCTACCTGGCTCAGACACCTCAGACGGGTTT 200 2413 TGCGCTCAGCCGTTAGACGTCAGCTCAGCTCAGACCCCCTCAGACGGCTTT 213 251 TGCGCTCAGTCAGCTCAGCTCAGCTCAGACGCTCAAAACTCCTCGCGGGATT 213 251 TGCGCTCAGCCCAGACTTCATTTGTAGGGAACTTCAAAACTTACTCAGGGATTTAACTTACAGACGTTTAACTTACAGACGTTTAACTTACAGGGAACTTAAAATTTAACTAGGGAACTTAAAATTTAACTACAGGGAACTTAAAATTTAACTAGGGAACTTAAAATTTAACTACAGGGAACTTAAAATTTAACTAGGGAACTTAAAATTTAACTAGGGAACTTAAAATTTAACTACAGGGAACTACAAAATTTTAACTAGGGAACTACACCTCTCGTTTAAATTTAAACTAAAGTTATTAACAAAGTTATTAACAAAGTTAATTTAACAAAGTTAAACTACACAGGGCAACACCCCTTAAAATTTAAACTAAAAGTTAAACTACACACAC		AGAAGGCAAGGCATTGATTGATTGCTCCATGCAATTGGGGAATCTGCAAGTGGAT		
2314 TGGGAGCTGARTAMCTCAGTCACTCGAGTTCCCACTCATAGCCCCTTAACCTCCACC 2377	> 0	TACCCAGGCTCAGGGTTAACAGCTAGCTCCTAGTTGAGACACACCTAGAGAAGGGTTTT		3330 AAAAAA 3488 AAAAAA
2333 TICGITTANTICH COUNTING CANGOG ACTIVICTA GOAT CAAAACACTCCTCCATCCATCCATCCATCCATCCATC		TGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAG-CCCCTTAACCTGCAGC	RESULT 9 AX200995 LOCUS	
2433 GAACATATG—ACTATATGGAGGAAGGCCGGCAACACACACACAGGGT 2490 2621 GAACGTGAGCCCCCCGCGCGCGCGCGCGCCCCCCCCCCC	~ 0	TTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAACACTCCTCCATGGGATTT 	DEFINITION ACCESSION VERSION KEYWORDS	Sequence AX200995 AX200995.
2491 CCCCTGAGCCCACAGCACTGTTTTTGCTGATCCACCCCCCTGTTACCAGGA 2550 2673 CITITITITITITITITITITITITITITITITITITIT	~ 0	GAACATATGACTTATTTGTAGGGAAGAGTCCTGAGGGGAACACACACAAGAACCAGGT 	SOURCE ORGANISM	
2551 TGTGGGCTGTTGGTCCTTCTTGCATCAAGACACAGGCATTTAAATTTTAACTT 2610 2734 GGGGCTGTTGGTTCCTTGTTGCATCAAGACACAGGCATTTAAATTTTAACTT 2793 2611 ATTATTTAACAAAGTACAAGGGAATCCATTGCTGTTGTTGTTTGT	> 0	CCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCCTCTTACCTTTACAGGA	REFERENCE AUTHORS	1 (bases Xu,J., Di Reed,S.G. Stolk,J.A
2611 ATTATTTAACAAGTAGAAGGCAATCCATTGCTAGCTTTTCTGTGTTGTTGTTATATTA 2794 ATTTATTAACAAGTAGAAGGCAATCCATTGCTAGTTTGTTT	> 0	TGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAACTT	TITLE JOURNAL	Compositicancer Patent: W
2671 TTGGGTAGGGTGGGGAATCCCCAACAATCAGGTCCCTGAGATAGCTGGTCATTGGGCTG 2730 2854 TTGGGTAGGGT-GCGATCCCCAACAATCAGGTCCCTGAGATCATTGGGCTG 2911 2731 ATCATTGCCAGAATCTTCTTCTCTCGGGTCCACTGAGATCATTGGGTC 2911 2731 ATCATTGCCAGAATCTTCTTCTCTCTGGGGTCCACCCCCCAAAATGCCTAACCCAGGAC 2971 2912 ATCATTGCCAGAATCTTCTTCTTCTTGGGTCCACCCCCCAAAATGCCTTAACCCAGGAC 2971 2913 ATCATTGCCAGAATCTTCTTCTTCTGGGGTCTGGGCTCTAACCCCAGGAC 2971 2914 TTGGAATCTTCTTCTTCTTCTTGGGTTGGCTTCAAACCCCTAACCCAGGAC 2971 2915 TTGGAATTTTAATCTCATCCCAGGTTCAACCCCTAACCCCAGGTT 2850 2917 TGGAATTTTAATCTCATCCCAATGGTTTACCCAAGGTTAGGGGTT 2850 2918 TGAAGGAAGTTGGAGGGGGGTTCAACGGTTCAAACGCCTATTCTT 2910 3019 TTGGAATTTTAATCTCATCCCAATTCCAAATGGTTTACCCAAGGTTAGGGGTT 2910 3019 TTGGAATTTTAATTCATCAAGGTTCAAATGGTTTACCCAAGGTTAGGGGTT 2910 3011 CTTGGCCCAGCTCGACTTCAACTCCCAATGGTTAACCCCTTTTTCT 3091 3011 CTTGGCCCAGCTTCAACTTCCAACAGGTTCCCCTAACCCCCTTTTTCT 3091 3012 TTGGAAGGAAGTTGCACCCAATTTTACTCCAAACGGTTGGGTTG 2970 3013 TAGAAGGAAGTTGCACCCCCACTTCAACCCCCCTTTTTCT 3091 3014 TTGGAAGGAAGTTCCCCCAAATTTTCCCCTAACCCCCCTTTTTCT 3091 3015 ATGAAGGAACTTTCACACCCCCCAAATTTTCCCC 3194 3016 TTTGGCCCAAACTTTGCACATTTTAACTTCTCACACACAC	~ 0	ATTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATAT	FEATURES	ø)
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2791 TYGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGGT 2850 11111111111111111111111111111111111		ATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGGCCCCCAAAATGCCTAACCCAGGACC	Bes Mat	t Local Similari ches 3325; Cons 4 AACCAGO
2851 TGAAGGAAGGTGGGGCTTCAACCCAAGGTTACCCAAGGTTAGGGGGT 3031 2851 TGAAGGAAGGTGGGGCTTCAGGTCTCAACGCTTCCTTCT 2910 3032 TGAAGGAAGGTGGGGCTTCAGGTCTCAACACCCCTTTTCT 3091 2911 CTTGGCCCAGCTGGTTCCCCCCACTTCCACTCTCTCTCTTTTCT 3091 2912 CTTGGCCCAGCTGGTTCCCCCCACTTCACCTCTCTCTAGGACTGGGCTG 2970 1		TTGGAAATTCTACTCACCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGT	. qq	
2911 CTTGGCCCAGCTGGTTCCCCACTTCCACTCCCTAACCACCCCTTTTCT 3091 2912 CTTGGCCCAGCTGGTTCCCCCACTTCCACTCCTTCTCTAGGCTGGGCTG 2970 3092 CTTGGCCCAGCTTGGTTCCCCCCACTTCTACTCTCTCTAGGACTGGGCTG 2970 3092 CTTGGCCCAGCTTGGTTCCCCCCACTTCTACTCTCTCTAGGACTGGGCTG 3151 2971 ATGAAGGCACTGCCCCAAAATTTCCCCTACTCCCTACTCCCCACTTTCCCC 3030 1111111111111111111111111111111111		TGAAGGAAGGTGGGGGTTCAAATTCCAAATGCTGTTACCCAAGGTTAGGGGGT TGAAGGAAGGTAGAGGGGTTCAGGTCTCAACGGCTTCCCTAACGACGTCTTCT		
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3152 ATGANGGCCCCGAAATTTCCTCACCCCCACTTTCCC 3194 3031 ACCAGCTCCACAAATTT		CTTGGCCCAGCCTGGTTCCCCCCATTCTACTCCCCTCTACTGTCTCTCTAGGGCTG ATGAAGGCACTGCCCAAAAATTTGCCCTACCCCCAACTTTCCCCTACCCCAACTTTCCCC		184 GGCAGCA 181 GGCAGCA
3031 ACCAGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCACAAAGTGCGGTTTCC 3090		ATGAAGGCACTGCCTGAAATTTCCCTCACCCCCAACTTCCCC		244 TGCCTGA
3091 CAAGCCTTTGTCCATCTCGG-CCCCCAGAGTATATCTGTGCGGAATCTCACACAGA 3149		ACCAGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCC		241 TGCCTGA 304 GAGCCGC
3150 AACTCAGGAGCACCCCTGCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGG		CAAGCCTTTGTCCATCTCAG-CCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGA		301 GAGCCGC
3210 TGCCGTTTGCAATAATGTCGTCTTATTTAGCGGGGGAATATTTATATTTATT		0 AACTCAGGAGCACCCCTGCCTGAGCTAAAGGGAGGTCTTATCTCTCAGGGGGGGTTTAAG 		
	.~	TGCCGTTTGCAATAATGTCGTCTTATTTAGCGGGGTGAATATTTATACTGTAAGT		

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TTGCAATAAT --- GTCTTATTTATTTAGCGGGGCAAATATTTTATACTGTAAGT 3429
                                 CAGAGTATAATGTTATGGTGACAAAATTAAAGGCTTTCTTATATGTTTAAAA 3329
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3., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
A., Skeiky, Y.A., Wang, A. and Meagher, M.J.
Ions and methods for the therapy and diagnosis of prostate
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CAGCGTAGAAAACTTCC CCGCTCCTGTTAGCCCC	TAATGTGGCTCTCTGC TAATGTGGCTCTCTGC GGGCGTCCTCTCCC	(n —	CTA	CCCTTAACCTGCAGCT	TCCTCCATGGGATTTGAACATATG	ACACAAGAACCAGGTC	TACCTTTTATCAGGAT(TTAAATATTTAACTTATT 	GTTGGTGTCTAATATT 	CTGGTCATTGGGCTGATC	8=8	CCAAGG CCAAGG	AACCACCCTCTTCT	TCTAGGACTGGG TCTAGGACTGGG	0000
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedyick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A., Hepler,W.T. and Henderson,R.A. Compositions and methods for the therapy and diagnosis of prostate
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3840 GAATCTCACACACAGAAACTCAGGAGCACCCCCTGCCTGAGCTAAGGGAGGTCTTATCTCTC 3899
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo
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Description: 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.5kb.nhe Sfil-digested PCR product was cloned into distinct Draili sites of PME18S-FL3. XhoI sites just outside the Draili sites can be used to isolate the CDNA insert. Libraries
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Macaca fascicularis brain cDNA clone:QmoA-10594, full insert
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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2 (bases 1 to 2917)
Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S. Direct Submission
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                                                                                            /tissue_type="medulla oblogata"
/clone_lib="macaque brain cDNA library QmoA"
/dev_stage="adult"
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oligo-capping method
nstitute of Medical Science,
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/protein_id="BAB60745.1"
/db_xref="GI:14388391"
                                                              /organism="Macaca fascicularis'
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FIGGGGCTGGGGCTCCCTCCTCTC FIGGGGCTGGGGCTCCCTCCTCTC FIGGGGCTGGGGCATTCCAGGGGCATTA FIGGGGTTTCAGTCTGGACTTC GCTCCAGGGGCTTTCAGTCTGGACTTC GCTCCAGGGGGCTTTCGAGTGTGGACTTC GCTCCAGGGGATTTCAGCTTGGACTTC GCTCCAGGGGATTTCAGGATGTGGGGGACT GTTGTTTTCTGGGTTTCCAGGTGAACCTCTAG GCGAGGATTTCTAGGATGAGCACCTA GTTGTTTTCTAGGATGAGCACCTAG GTTTTTCTGGGTTTCTAGGATGAACACTC GTTTTTTGTTTTTTTTTT	CCAGTCTCTAGGGCT 2155 	PACAGGGAGGCCAGAAGG 2215 	CTGCAGGTGGATTACCCA 2259 	GAGACACCTAGAGAAGGGTTTTGGGAG 2319 	ACCTGCAGCTTCGTT 2378 	ATGGGATTTGAACAT 2438 CTGGGATTTGAACGT 2040	NGAACCAGTCCCCTC 2496 	CTTACCTTTTATCAGGATGTGGC 2556	ATTTAACTTATTAT 2616 	GTCTAATATTGGGT 2676 	ATTGGGCTGATCATT 2736 	ACCCAGGACCTTGGAA 2796 ACCCAGGACCTTGGAA 2391	TTTAGGGTGTTGAAGG 2856 	CTCTTGGC 2916 CTCTTGGC 2511	TCTCTAGGACTGGCTGATGAAG 2976 	AACTTTCC AACTTTCC	TGCGGTTTCCCAAGC 3096 	CTCACACAGAAACTCA 3155
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                                                                                                                                                                                                                                                                                                                        human.

Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 2904)

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,

Stolk,J.A., Skelky,Y.X.A., Wang,A. and Meagher,M.J.

Compositions and methods for the therapy and diagnosis of prostate
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3216 TTGCAATAATGTCGTCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAA
                                                                  2793 TIGCAATAAT---GTCTTATTTAGCGGGGCAAATATTTATACTGTAAGTGAGCAA
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88.2%; Pred. No. 0;
Live 0; Mismatches 1; Indels 343;
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Matches 2560; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2703 ACCTGATTGTTGGGGATCCCCCACCCTACCCAAATATTAGACACCAACACAGA----- 2651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2367 AGGTTAAGGGGCTTAGA-----GATGGGAAACCAGGTGACTTGAGTTTATTCAGCTCCCA 2314
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                                                                                                                                                                                                                           33 ------ProbroGlyPro-ProGlyThrSerGlyHisProGlySe 45
                                                                                                                                                                                                                                                                                                                                                               45 rProGlySerProGlyTyrGlnGlyProProGlyGluProGlyGlnAlaGly---ProSe 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 -----AlalleGlyProSerGlyProAlaGlyLysAspGlyGluSerGlyArgProGl 89
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US-09-759-143-110 (1-3410) x US-08-931-820-4 (1-1057)
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CCTGCAGAGTCCCGCATTCCAGTGCATGGLyAspProGlyProProGlyAlaGlnGly 127 CCTGCAGAGTCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCTATAAGTCCAG 2189	97 111 111 111 111 111 111 111 111 111 1	0-4 & 0-0 0-0 H 0	TGGGCAGGAACACCTGCTTCTCCGGTGGTAGAGGGGGCCACTGTGTAGGGCA 1467 [1]
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. qa	44	 ProGlyAlaGlnGlyProAlaGlyBroGlyGlySerArgGly 460
Qy	1193	CGCCCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTG 1134
qq	461	 AspProGlyProProGlyAlaGlnGlyProAlaGly
Qy	1133	CCATCCAGCTGCACAGCTCAGCCACGAAGAGCCGGCGCAGGGTGCGGGGCATGCGGCAGC 1074
qa	473	ProGlyGlySerArgGlyAspProGlyProProGlyAlaGlnGlyProAlaGly 490
Qy	1073	ACAGCTGGTGCAGCCGGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGC 1014
qa	491	ProGlyGlySerArgGlyAspProGlyProProGlyAlaGlnGlyProAlaGlyFroGly 510
Qy	1013	ATGGACAGCAGTGGGGGGGCGACAAGGAGGGGGCCGACAGCCCTTCTGCTGGCT 963
qa	511	GlySerArgGlyAspProGlyProProGlyAlaHisGlyProAlaGlyProLysGlyAla 530
QY	962	
Db	531	11sG1
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QQ	547	
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Qy	782	GCATAGACAGAGTAG
QQ	589	roGlyAlaGlnGlyProAl
Qy	725	AGTGGAGTGAAGCACACACAGAAGTCCAGCAGCCCCA 66
qq	603	roGlyProfroGlyAlaGlnGlyProAlaGlyProGl
Qy	899	
qq	619	GlySerArgGlyAspProGlyProProGlyAlaGlnGlyProAlaGlyProGlyGlySer 638
Qy	635	TGGGATCCGGCACAGCAGCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGC 579
qq	639	ArgGlyAspProGlyProProGlyAlaGlnGlyProAlaGlyProdlyGlySerArgGly 658
Qy	578	TCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGGGGGCGCCATAGCGTCCAC 519
qq	629	AspproGlyProPro
Οy	518	GCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACCAGGCCCAGCACTGGACCAA 459
qq	670	GlyProGlyGlySerArgGlyAspProGlyProGlyAlaGln 684
Οy	458	TGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAGAGCGGCA 399
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Db 100 GlyAspProGlyProProG Qy 2287 CTAGGAGGCTAGCTGTTAA	639 oGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLe 659 224 CGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCTAGGAATCA 165 ::: ::: :::
QY 2347 GGGAAACCAGGTGACTGAG	281 TGGGCCAGGCGGGTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCT 225
US-09-759-143-110 (1-3410) x US-0	620 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr-Pr 639
	338 AGAGCTGGGCTTTCCGGTGCCGCAGCCAGCGGGTCACCAGCCTCTGGACCATAG 282
Percent Similarity: 32.33% Best Local Similarity: 30.10%	
Pred. No.: 4.82e-19 Score: 353.50	398 CATAGGTGATGCCTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 339
ment Scores:	586 GlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 605
; MOLECULE TYPE: protein US-08-642-255-72	446 IGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGAGAGGGGGGGA 399
TOPOLOGY: linear	572SerProGlyAlaProGlyThrProGlyProGlnGlyLeuPro 585
; TYPE: amino acid	506 TGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCA 447
SEQUENCE CHARACTERISTICS:	562 GlyThrProGlyProGlnGlyLeuProGiy
TELEX: 910 277299 FHT UR THEODMANTION FOR SEC. 72	563 AGGACAGTGCCCAGATGAAGGGCCGGCGGCGCCATAGCGTCCACGCCAGTGGTCAC 507
; TELEPHONE: (415) 494-8700	548 ThrProGly
REGISTRATION NOMBER: 20,0 REFERENCE/DOCKET NUMBER: TELECOMMINICATION INFORMATIO	623 ACAGCAGCCTGCTAGCCAGCCGTCTGGGATGAGAAGAGGCTCAGCAGGATGCCCA 564
- 1	:::
; FILING DATE: ; CLASSIFICATION: 435	683 AGTCCAGCACCCCACGCCCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGC 624
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08	512 SerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGly 529
; OPERATING SISTEM: PC-DOS/ ; SOFTWARE: PatentIn Releas	CCAGTGGAGTGAAGC
COMPUTER: IBM PC COMPATIBLE COMPATIBLE	501 ProGlyThrProGlyProGlnGlyLeuProGly 511
COMPUTER READABLE FORM:	797 CCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGT 741
COUNTRY: USA	484 GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 500
CITY: San Francisco	GGGCCAGGGCAC
; ADDRESSEE: FLEHR, HOHBACH ; STREET: 4 Embarcadero Cen	LeuriosiyserriogiyalariogiyinrriosiyrrosingiyLeurrosiyserrio
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TITLE OF INVENTION: HIGH MO	VECCOMPOS.
; GENERAL INFORMATION: ; APPLICANT: CAPPELLO, Joseph	959 TGGGGCCCAGCGCTGCCTCCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGA 903
; Sequence /z, Application 05/080 ; Patent No. 57/3249	435 ProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro 453
RESULT 41 US-08-642-255-72	1019 CCCGGCATGGACAGTGGGGGGGACAAGGAGGGGGCGACAGCCCTTCTGCTGGCTG
	415 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 434
Qy 59 CAGATCCTGGCCGAGG	1070 GCTGGTGCAGCCGGGAAGCAGGCGCCCCAGGTTCCGGAAAGCCAAGCGGG 1020
693 roGlyAlaProG	395 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 414
105	1124TGCACACCTCAGCCACGAAGAGCCGGCGCGGGGGGGGGG
Db 674 uProGlySerProGlyAla	379 GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGly 394
QY 164 GCCAGGGGCCATTTCTGC	CATGAGTGCCATCCAGC
Db 659 uProGlySerProGlyAla	

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TTTATTCAGCTCCCAAAACCCTTCTCTAGGTGTGTCTCAA 2288
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                  CAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCA- 106
                                                                    TGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACT 60
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Necular Weight Collagen-Like
Polymers
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Ler, Suite 3400
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	qa	74 LeuProGlySerProGlyAlaProGlyThrProGlyProGlnGly 88
105ACACCTGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACT 60	Oy Dp	2167 CTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGAGAGA
CAGATCTGGCCGAGGCGCGCGCTGTCACCCGGAGCC 22 LILLIL :::III	δγ	2107 GTGCAGCTACGCACCTCAGCAGCAGCAGCAGAGAGAGAGA
	Qy	2047 AACAGAAACTGGCGGCCAGCCGGCAGCCCCATGGGGCTAACAGGGGGGGG
JS/0839/033A Joseph	, dg	1987 CCCAGTGAGGCAGCCCTCCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGC 1928
	QY	1927 CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGGCC 1868
AUDRESSE: FLEHK, HOHBACH, TEST, ALBKITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California COUNTRY. IISA	do do	CTGAGCTGGA y
11 FF F	do do	1807 CAGGGATGGGGCCACCTGGGACAGCAGGAGGCAC
SYSTEM: Patent: LICATION	QY	1768 CAGGATGGCGAGGTCCAGGCAGATGCCCGGCCCGGAACCACCTGGC 1721
O \$7.	QQ Dp	1720 CTCGGTGGGCTCACCCACCACCACGACGACGACATCACGGCAG 1674
REGISTRATION NUMBER: 20,015 REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1 TELECOMMUNICATION INFORMATION: TELECHOME: (415) 781-1989	Qy Dp	1673 AGGCCCGCAGAGCGCGGGTGGAGGTGGGAGCCACTGCCTCCAGCACCCAGTGTC 1614 :::
415) 398-3 277299 SEQ ID NO	Qy	1613 CATTAGGAAGGAGCTCCAGGCTTAGGCCTGGCAGAAGCTGGTCATCAGGCTGTCCT 1554
LENGTH: 897 amino acids TYPE: amino acids STRANDEDNES: single TYPOLOGY: linear	Qy Dp	1553 CACTGCTAGCACCTCCAGTGCCCCTCGGTATTTGGGCAGGAACACCTGCTTCT 1500
Ξ.		1499 CCCGGTGGTAGAGGGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACC 1440 :::
Pred. No. 2.67e-19 Length: 897 Score: 356.50 Matches: 263 Percent Similarity: 35.16% Conservative: 32 Best Loral Similarity: 43.45% Mismatches: 37	Qy	1439 CGGTGAGGGCGCTGAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGGCACC 1382
5.73% Indels: 1.73% Gaps: 1.00 v HS-08-307-6338-50 (1-907)	Qy	1381 -GGCAGCCACAGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATGGCT 1323
NACCAGGTGACTTATTCAGCTCC	Qy Db	1322 GCACCAGCCGGTCCATGACCAGAGAAGACCAGGGAGATGGCGCACTGCAGGAACA 1266
CTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCCGCATTCC	ογ Op	1265GCCCCAGGCTGCCCATCCGAACGCCTT 1239 140 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlyBrodLnGlyLeu 359
	δ	1238 CATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCCACGCCCTGGTACAGCC 1179

Db 360 ProGl	Qy 1178 CCTCG	Db 379 GlyAla	Oy 1124	Db 395 AlaPro	-	415	1019	435	959	454	Qy 902 AGATG	Db 464 LeuPro	Oy 857 GGTAGG	Db 484 Gly	Qy 797 CCCCAI	Db 501 Pro	Qy 740CCC	Db 512 SerPro	Qy 683 AGTCC	Db 530 AlaPro	Qy . 623 ACAGC!	Db 548 ThrPro	Qy 563 AGGACA	Db 562 GlyTh	Qy 506 recer	Db 572	Qy 446 TGGTC1	Db 586 GlySer	Qy 398 CATAGO	909 qa	Qy 338 AGAGCI	Db 620 AlaPro	Qy 281 TGGGCC	ŏ	Oy 224 CGGCTC	200
74 LeuProGlySerProGlyAlaProGlyAlaPro	GGAGAGAGAGGAGGACCCCAGCT		2107 GTGCAGCTACGCACCTCAGCACAGGGTGGCAGCAGAGAGAG		2047 AACAGAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAACAGGAGCGGGGGACCTGGGA 1988		1987 CCCAGTGAGGCAGGCCTCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGC 1928		1927 CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCCAGCCA	 145GlyProGlnGlyLeuProGlySerProGlyA 155	1867 TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAA 1808	155 laproGlyThrProGlyProGlnGlyLeuProGlySerPro 168	1807 CAGGGATGGGGCCACCTGGGACAGCAGGAAGGCACTATC 1769		1768 CAGGAIGGCGAGGICCAGGCAGAIGCCCCGGCCCGGAACCACCTGGC 1721		1720 CTCGGTGGGCTCACCACCACCACGTACGGAGACATCACAGGCAG 1674								1499 CCCGGTGGTAGAGGGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACC 1440		1439 CGGTGAGGCGGCTGAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGGCACC 1382		CAAATAGACTGCTCGAGTGCCGAATCGCT		GGAGATGCCGCACTGCAGGAACA	ro	1265GCCCCAGGCTGCCCATCCGAACGCCTT 1239		1238 CATCATAGIGICICCGGGCCTCGGGCTCAGCICIGGGCACGCCCIGGIACAGCC 1179	
අු	Qy	qq	0y	qq	Oy	qq	ογ	qq	Qy	Dp	٥y	Ob	Qy	qq	οy	QQ	ογ	qq	ò	, d	Ολ	QQ	Qy	qq	οy	qq	Οy	qa	οy	qq	Οy	qq	Qy	qq	Qy	

3CCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGC----- 1125 ----GGTGCAGCCGGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGG--- 1020 --TGCACAGCTCAGCCACGAAGAGCCGGCGCGAGGGTGCGGGCATGCGGCAGCACA 1071 roGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 414 lySerProGlyAlaProGlyThrProGlyPro---GlnGlyLeuProGlySerPro 378 laProGlyThrProGlyProGlnGly------LeuProGlySerProGly 394 3CATGGACAGCAGTGGGGCGACAAGGAGGGGGCCCGACAGCCCTTCTGCTGGCTCGG 960 3AGGGTGAGCAGGCCAAAGAGGCACTCCT------CCTGGGTGCCCA 858 SCCCAGCGCTGCCT---CCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGA 903-.--Gly 463 AAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGT 741 529 AGCAGCCCCACGCCCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGC 624 CAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAGAGCCTCAGCAGGATGCCCA 564 oGly-------ProGlnGly---LeuProGlySerProGlyAlaPro 561 IGAGCCTAGGAGCGGGACAGGCCCAGGCCCAGCACTGGACCAATGCCCCAGCACCA 447 ATGAACTICICCICTACCCCCA-------CTICCAGCAGAGGGGGCA 399 GTGATGCCTGCGGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 339 CCGGAAGAGGTCAGAGAGCAGGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGA 684 AGTG---CCCAGATGAAGGGCCGGCGGCGATAGCGTCCACGCCAGTGGTCAC 507 ----- 571 STGGGCTTTCCGGT----GCCGCAGCAGCGGCTCACCCACAGCCTCTGGACCATAG 282 CAGGCGGG---TAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCT 225 CTGCTCCAGAAGCTGCGGCCTCTCCTCCTTGCTGCCGCCAACTGCCTAGGAATCA 165 :::|||||||
roGlyAlaProGlyFroGlyProGlnGlyLeuProGlySerProGly-----|| |hrProGlyProGlnGlyLeuProGly-----||| |aProGlyThrProGlyProGln-----

APPLICANT: Ferrari, Franco A.

959 454 902	TGGGGCCCAGCGCTGCCTCCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGA 9	903
857		798
797	CAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGT 	741
740		684 529
683 530	AGTCCAGCAGCCCACGAGGATGAGCAGTGCCAGGTCCAGGGGCTGGGATCCGGG 	624 547
623	ACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCA	564
563	AGGACAGTGCCCAGATGAAGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCAC	507
562	inglyLeuProGly	571
506 572	TGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCA	447 585
446 586	IGGTCATGAACTTCTCCTCTACCCCCA	399
398	CATAGGTGATGCCTGCGGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTGACCAGCA	339 619
338	AGAGCTGGGCTTTCCGGTGCCGCAGCAGCGGCTCACCCCAGCAGCCTCTGGACCATAG	282
620	AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr-Pr	639
281 639	TGGGCCAGGCGGTAGGGCTCAGGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCT	225 659
224	CGGCTCTGCTCCAGAAGCTGCGGCCTCTTCCTTGCTGCCGCCAACTGCCTAGGAATCA	165
164	GCCAGGCGCCCATTCTGCCAGCCTTTGGTGCCGGTCCAGCTTCTCAGCCATGCTCA	106
674		693
105		60
693	rogiyalarrogiyinrrrosiyrrogingiyLeurrogiyserrrogiyalarrog	7.17
59	CAGATCCTGGCCGAGGCGCGGGTGTCACCCGGAGCC 22 ::: YThrProGlyProGlnGlyLeuProGlySerProGlyAla 725	
7917 105	SULT 39 -09-444-791A-103 Sequence 103, Application US/09444791A Patent No. 6355776 GENERAL INFORMATION:	

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TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2347 GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTCTCAA 2288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 LeuproGly------SerProGlyAlaProGlyThrProGlyProGlnGly 73
                                                                                                                                                                                      NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
STREET: Flehr Hobbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLUM TYPE: FLOPPY GISK
MEDLUM TYPE: FLOPPY GISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/44,791A
FILING DATE: 22-NO: 6355776-1999
APPLICATION NUMBER: US 08/482,085
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 29-APR-1993
APPLICATION NUMBER: US 06/927,258
FILING DATE: 29-APR-1987
APPLICATION NUMBER: US 06/927,258
FILING DATE: MINCRMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Trecertin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
TELECOMMUICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFRAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-759-143-110 (1-3410) x US-09-444-791A-103 (1-837)
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Conservative:
Mismatches:
Indels:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
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Richardson, Charles
Chambers, James
Causey, Stuart
Pollock, Thomas J.
Cappello, Joseph
Crissman, John W.
                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 837 amino acids
TYPE: amino acids
STRANDEDNESS: single
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COMPUTER READABLE FORM:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 ProGln------GlyLeuProGlySerProGlyAlaProGlyThrProGly--P 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 LeuProGly------SerProGlyAlaProGlyThrProGlyProGlnGly 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2107 GIGCAGCTACGCACCTCAGCACCACGGGGGGCAGCAGAGAGCCACATTACTTTGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 LeuProGlySerPro---GlyAlaPro------GlyThrProGlyPro---GlnGly
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                                                  Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                         FILLING DATE: 007-007-1055
CLASSIETCATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/927,258
FILLING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILLING DATE: 29-DEC-1993
ATTORNEY AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,085B
FILING DATE: 07-JUN-1995
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PROTOCOLORY
                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 103: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 Leu---ProGlySerPro---
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356.50
35.16%
31.35%
5.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 837 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 GlySerProGly----
                                                                                                                                                                                                                                                                                                                                                                                              415-398-3249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-482-085B-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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1867 TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGGACTGGACAATGGAGCCCATAAA 1808
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1927 CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCC 1868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1613 CATTAGGGAAGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCT 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1553 CACTGCTAGCACCTCCAGTGTCCCCTCGGTATT-----TGGGCAGGAACACCCTGCTTCT 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1439 CGGTGAGGGCGCTGAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGGCCACC-- 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1381 -GGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCT 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 CATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCC 1179
                                                                                                                                                                                                                                                                                                                                                                                              1768 CAGGATGGCGAGGTCCAGGCAGATGCCCCGGC-------CCGGAACCACCCTGGC 1721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1070 GCT-----GGTGCAGCCGGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGG--- 1020
                                                                                                                                                                      340 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlnGlyLeu 359
                                                                     --GlySerProGlyA 155
                                                                                                                                                                                                                                                                                                                                   -----GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 ProGlySerProGlyAlaProGlyThrProGlyPro---GlnGlyLeuProGlySerPro 378
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                                                              -----GlyProGlnGlyLeuPro-
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W.
018030el Peptides Comprising Repetitive
of Amino Acids and DNA Sequences Encoding the Same
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                                                                                             CCCAGGATGAGCAGCTCCAGGGGCCTGGGATCCGGGC 624
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o Center, Suite 3400
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larles
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398 CATAGGTGATGCCTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 339
                                                                                 338 AGAGCTGGGCTTTCCGGT---GCCGCAGGCGGCTCACCCCACAGCCTCTGGACCATAG 282
                                                                                                               281 TGGGCCAGGCGGG---TAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCT 225
                                                                                                                                                                                                                                                          224 CGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAGGAATCA 165
                                               ----ProGlyThrProGlyProGlnGlyLeuProGlySerProGly 619
                                                                                                                                                                                                                                                                                                   659 uProGlySerProGlyAlaProGlyThrProGly-------ProGlnGlyLe 674
                                                                                                                                                                                                                                                                                                                                              164 GCCAGGCGCCCATTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCA- 106
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674 uProGlySerProGlyAla---ProGlyThrProGlyProGlnGly-LeuProGlySerP 693
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                                                                                                                                                                                                                                                                                                                                                                                                                                    --- ACACCTGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACT 60
                                                                                                                                                                                                   BE: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             712 lyThrProGlyProGlnGlyLeuProGlySerProGlyAla 725
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APPLICANT: Dorman, Mary A.
TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
TITLE OF INVENTION: REPETITIVE DNA
NUMBER OF SEQUENCES: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/707,237A
FILING DATE: 03-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PURDATATION DATA:
PRIOR PAPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
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FILING DATE: 29-OCT-1987
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Capello, Joseph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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FILING DATE: 09-NOV
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2107 GIGCAGCTACGCACCTCAGCACACAGGGTGGCAGCAGAAGCCCACATTACTTTGGCAGC 2048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1927 CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGGCCC1868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1867 TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAA 1808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 GlySerProGly-----GlyProGlyThrPro----GlyProGlnGly 58
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                                                                                                                                                                                                                                                                                                                                                        837
263
32
327
218
57
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 3 -55186-10/WHD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
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                                                                                                           TELEPHONE: (415) 781-1989
TELEFAX: (415) 388-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    2.61e-19
356.50
35.16%
31.35%
5.73%
                                                                                                                                                                                                        837 amino acids
                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                       amino acid
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GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAGC GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAGC		arity: 31.35% Mismatches: 5.73% Indels: 1 Gaps:
	₹ .	110 (1-3410) x US-08-642-255-101 (1-837)
GTAGGAGGCTAGCTGTAAACCCTGGGTAATCCACCTGCAGAGTCCCGCGATTCC Leulrolly	4 4	28. 28.
ACCOCATGGAGCCCTTCGGCCTCCTGTATAAGTCCAGACTGAAACCCCTTGGAAGCC Leubrod1ySerPro	oo Lo	AGCTGTTAACCCTGAGCTGGGTAATCCACCTGCAGAGTCCCCGCATTCC 222
CTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	27	216
GTGCGGCTAGCGCGCGCGCGCGCGGGGGGGGGGGGGGGG	67	210
GUCCAGTACGCACCTCAGCACCACGACACACACACACATACTTTGCACTACCTCACCACTACCTAC	8	prodlySerProGlyAlaProGlyThrProGly 100
AACAGAAACTGGGGCCAGCCCGCAGCCCCATGGGGCTAACAGGAGCGGGGGGGG	101	TACGCACCTCAGCAGCACACAGGTGGCAGCAGAGACCACATTACTTGGCAGC 204
CCCAGTGAGGCAGCCCTCCAATGTGCTGGAAGTTTTCTACGTGATTTTGGC 1ySerProGlyAlaProGlyThrPro	047	198
LyserProdlyAlaProdlyThrPro	116	192
CAGGCCCCCAGACCCAGGCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGACCCAGGCCCAGACCCAGGCCCAGACCCAGCACCAGACCCCAGCACCCAGCACCCAGCACCAGGAAGGCACCCCAGCACCCAGCACCAGCACCAGCACCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCCAGCACCCCACCA	136	1
TGGGGCAGACCATATAGGCAGTGACAGCTGAGCTGGACATGGAGCCCATAAA TGGGGCAGACACCATATAGGCAGTGACAGCTGAGCTG	927	186
TGGGGCAGACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAA	4	12
CAGGGATGGGGCCACCTGGGACAGCAGGAAGGCAC	367	TCCGGCAGACACCATATAGGCAGTGACAGCTGGCTGGGCTGGACAATGGAGCCCATAAA
CAGGAGGCGAGGAGCCCGGC	307	CAGGGATGGGGCCACCTGGGACGCAGGAAGGCACTATC 176
CAGGAGGCGAGCAGGAGCCCGGCCCGGAACCACCCTGGC	69	GlyalaproGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaP
CTCGGTGGGCTCACCCACCACCACGAGACATCACAGGCAG [1:::	981	CAGGATGCCAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCTGGC
rodinglyLeuprodiySerProGlyAlaProGlyThrProGlupProGlnGlyLeuProG AGGCCCGCAGAGCGGGGGGGGGGGGGGGGCAGCCCAGCCCCCC	720	CTCGGTGGGCTCACCACCACCACGACGAGACATCACACGCAG 167
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COTTAGGGAAGGGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTTAGGGGAAGCTGGTCATCAGGCCTGCCAGGCAGG	573	AGCCCCCCAGAGCGCGGGTGGAGGGGAGCACTGCCTCCAGCACCCACGGTGTC 161
roG1yThrProG1pgFroG1nG1yLeuProG1y-SerProG1yAlaproG1yThrPro CACTGCTAGCACCTCCAGTGTCCCTCGGTATTTGGGCAGGAACACCTGCTTCT	613	CATTAGGGAAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCT 155
CACTGCTAGCACTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCT	246	roGlyThrProGlyProGlnGlyLeuProGly-SerProGlyAlaProGlyThrFro
CCCGGTGGTAGAGGGAGGCCAGTGTAGGGCAGGATTGCAGGGCTGAGAAGGTGAACC IIIIII :::!!!	553 265	CACTGCTAGCACCTCCAGTGTCCCCTCGGTAITTGGGCAGGAACACCTGCTTCT
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CGGTGAGGGCGGCTGAAGCTGTCACCACCACACTGTGGGACAGGCATGTGGCACC 138:	275	ProGlyProGlnGlyLeuProGlySerProGlyAla-ProGlyThrPr
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e	340 GlyProGlnGlyLeuProGlySerProGl	(T)	S
12	238 CATCATAGTGTCTCCGGGCCTCGGT	TCAGCTCTGGGCACGCCCTGGTACAGCC 1	1179
e.	360 ProGlySerProGlyAlaProGlyThrProGl	yProGlnGlyLeuProGlySerPro	
11	1178 CCTCGCCCACGAAATCCGTGTAAAACAGC	SAGTGCCATCCAGC	1125
m	379 GlyAlaProGlyThrProGlyProGlnGly	LeuProGlySerProGly	394
11	124T	GCGGGGCATGCGGCAGCACA	1071
E)	roG		414
10	070 GCTGGT	GCAGCCGGGGAAGCAGGGCCCCAGGTTCCGGAAAGCCAAGCGGG 1	1020
4	415 GlyProGlnGlyLeuProGlySerProGl	en	434
10	019	CCCTTCTGCTGGCTCGG	096
4	435 ProGlySerProGlyAlaProGlyThr	lyLeuProGlySerPro	453
Ji	959 TGGGGCCCAGCGCTGCCTCCTCAGCC	CCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGA 9	903
7	454 GlyAlaProGlyThrProGlyProGln	-Gly	463
٥,	902 AGATGAGGGTGAGCAGGCCAAAGAGGCACTCCT	CCTGGGTGCCCA	828
4	464 LeuProGlySerProGlyAlaProGlyTh	GlyProGlnGlyLeuProGlySerPro	483
ω	857 GGTAGGGGCCAGGGCACTGGTGTCCCAC	GTAGCCCAGGCAGC	798
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	740CCCGGAAGAGGTCAGAGAGCAGGGCC		
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	683 AGTCCAGCAGCCCCAGGCTGAGA	AGICCAGCAGCCCCAGGCCCAGGAIGAGCAGIGCCAGCICCAGGGGCCIGGGAICCGGGC (624
	530 AlabroGlyThrProGlyProGlnGlyLe		547
	⋿	GCTAGCCAGCCGCCCTTGGGATGAGAAAGAGCTCAGCAGGATGCCCA	564
	ProGly	InglyLeuproglySerProglyAlaPro	561
	563 AGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGC	STCCACGCCAGTG	507
	562 GlyThrProGlyProGlnGlyLeuProG	1y	571
	9	CTGAGCCTAGGAGGGGACACAGGCCCAGCACTGGACCAATGCCCAGCACCA	
	572SerProdlyAlaProGlyThrP	oglyproginGly	585
	446 IGGICATGAACTICTCTCTCTCACCCCA	CTTCCAGCAGCAGAGGGGGCA	399
	586 GlySerProGlyAlaProGlyThrProG		605

CAGGAACA 1266 CAGGAACA 1266 CAGGAACA 1266 CAGGAACA 1266 CAGGAACA 1266 CAGGAACA 1266 CAGGACTTTCCGGT CAGGACTT 1239 CAGGACTT 1230 CAGGACTT 1230 CAGGACTT 1230 CAGGACTT 1230 CAGGACTT 1230	ACAGCC 1179 OY 224 SerPro 378 Db 659 1125 Db 659 rogly 394 Db 674 OY 105	414 DD 1020 Db 434 RESUI 960 US-06 453 ; Pat 903 ; GH	TITLE OF INVENTION: ORRESPONDENCES: CORRESPONDENCES: CORRESPONDENCE ADDRESSEE: FLEHR, STREET: 4 EMBARCA CITY: San Francis STAFE: 4 EMBARCA COUNTRY: USA STAFE: 4 EMBARCA COUNTRY: USA STAFE: 4 EMBARCA COUNTRY: USA STAFE: 5 EMBARCA COMPUTER: ISA PC (OPERATING SYSTEM: SOFTWARE: PALCALLY COMPUTER: ISA PC (OPERATING SYSTEM: SOFTWARE: PALCALLY COMPUTER: STAFE COMPUTER: STAFE COMPUTER: STAFE COMPUTER: DATE OFTWARE: PALCALLY COMPUTER: PALCALLY COMPUTER: DATE OFTWARE: PALCALLY COMPUTER: PALCA	547 547 564 507 571 585 339 605	Percent Similarity:
132 GCACCAGGCGCTCCATGATAGINSETPRO	OY 1238 CATCATAGTGTCCGGGCCTCGGTGCCCGGCTCGGCCCGGGTACAGCC	995 AlaProGlyThrProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 9y 1070 GCTGGTGCAGCGGGGAAGCAGGGCCCCAGGTTCCGGAAAGCCAAGCGGG 10	QY 902 AGATGAGGGTCAGCGAAGAGGCACTCCT	Qy 683 AGTCCAGCACCCCAGGATGAGCAGTCCAGGGCCTGGGATCCGGGC Db 530 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla	-

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ProGlyThrProGlyProGlnGlyLeuProGlySerProGly 619
                                                                  3GGCTCAGGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCT 225
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|GlySerProGlyAlaProGlyThrProGlyProGlnGlyLe 659
                                                                                                             GCGGCCTCTCCTTGCTGCCGCCAACTGCCTAGGAATCA 165
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|ProGlyThrProGly------ProGlnGlyLe 674
                                                                                                                                                         CAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCA- 106
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Mecular Weight Collagen-Like
n Polymers
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ter, Suite 3400
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Matches:
Conservative:
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DB: 1 Gaps: 57 US-09-759-143-110 (1-3410) x US-08-477-509B-103 (1-837)	Qy 2347 GGGAAACCAGGTGACTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTCTCAA 2288	QY 2287 CTAGGAGGCTAGCTGTTAACCCTGGGGTAATCCACCTGCAGAGTCCCCGCATTCC 2228	Qy 2227 AGTGCATGGAGCCCTTCTGGCCTCCTGTATAAGTCCAGACTGAAACCCCTTGGAAGGC 2168	Qy 2167 CTCCAGTCAGGCAGCCCTAGAGACTGGGGAGGGGAGGGCACGCCCAGCCCCAGCT 2108	QY 2107 GTGCAGCTACGCACCTCAGCAGGAGGGGGGCAGCAGAGCACACTTACTT	Qy 2047 AACAGAAACTGGCGGCCAGCCCGGCAGCCCATGGGGCTAACAGGAGCGGGGAGCTGGGA 1988	QY 1987 CCCAGTGAGGCAGCCTCCACACATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGC 1928	1927	145CLYPIOGLINGLYBEACEC 1867 TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGGACATGGAGCCCATAAA 1867 TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGGACATGGAGCCCATAAA 1	YLeuProGlySerProGlyAlaP	1768	1720	OY 1673 AGGCCCGCAGAGCGCGGGTGGAGGTGGGCCACTGCCACCACCACCACGTGTC 1614 ::	Oy 1613 CATTAGGGAAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCT 1554	OY 1553 CACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCT 1500	Qy 1499 CCCGGTGGTAGAGGGAGGCCAGTGTAGGGCAGGATCTGCAGGCTGAGAAGGTGAACC 1440		QY 1381 -GGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCT 1323
Db 674 uProGlySerProGlyAlaProGlyThrProGlyProGlnGly-LeuProGlySerP 693	Qy 105ACACCTGCTGCTGGGGCACCTCAGTGGGGACACCTCATCACT 60 	Qy 59 CAGATCCTGGCCGAGGCGCGGCTCTCACCCGGAGCC 22	RESULT 35 US-08-477-509B-103 ; Sequence 103, Application US/08477509B : Datent NA 5770697	GENERAL INFORMATION: APPLICANT: Ferrar1, Franco A APPLICANT: Cappello, Joseph AppliCANT: Crissman, John w	APPLICANT: Dorman, Mary A TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same Manage of Engineers: 117.	CORRESPONDENCE ADDRESS: ADDRESSE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400	CITT: Sall Francisco ; STATE: California ; COUNTRY: US ; ZIP: 94111	COMPUTER READABLE FORM: COMPUTER: Floppy disk COMPUTER: IBM PC compatible COMPATER: PC PC COMPATIBLE	COFFACTION DATA: CURRENT APPLICATION NUMBER: US/08/477,509B	CLASSIFICATION: 435 PRIOR APPLICATION DATA: PRIOR DATE: 29-DEC-1993	FRIOR APPLICATION NUMBER: US 08/053,049 FILING DATE: 22-APR-1993 FRIOR APPLICATION DATA:	APPLICATION NUMBER: US 0//114,010 FILING DATE: 29-OCT-1987 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 06/927,258	FILING DATE: 04-NOVIDSO ATTORNEY/AGENT INFORMATION: NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801 ATTORNEY AGENT ATTORNEY AGENT ATTORNEY ATTORNEY ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY.	; FEFERENCATION INOMEARING TELECOMMUNICATION INFORMATION: ; TELEPHONE: 415-781-1989 ; TELEFAX: 415-389-3249 ; TELEFAX: 0.15-389-3249 ;	∵. ₩	STRANDEDWESS: SINGLE ; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-08-477-509B-103	Alignment Scores: 2.61e-19 Length: 837 Pred. No.: 356.50 Matches: 263 Score: Score: 35.16% Conservative: 32	ty: 31.35% Mismatches: 5,73% Indels:

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	1178 CCTCGCCCACGAAATCCGTGAAAACAGCTGAAGGTCATGAGTGCCATCCAGC 1125 11 11 11 11 11 11
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ογ	1106 AGAGCCGGCGCAGGGTGCGGGGCATGCGGCAGCACAGCTGGTGCAGCCGGGGAA 1053	670
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a	CCCCCCCCC To compose of the compose	Qy 38 GGCTGT
λŏ		Db 698 roGlys
QQ	401 ProglyalaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGly 420	RESULT 34
Qy	995 ACAAGGAGGGGCGACACCCTTCTGCTGGCTCGGTGGGGCCCCAGCGCTGCCTCCT 939	US-08-175-155-68 : Sequence 68, Appl
qa	421 ThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro 439	; Patent No. 5641648
٥٨	938 CAGCCACCAGCAGTGGGTGCTACGCAGGTGAGGAAGATCAGGGTGAGCAGGCAAAGA 879	APPLICANT: Fe
7 E		
ł	0H000HJJ	; APPLICANT: DOI ; TITLE OF INVENT
à		TITLE OF INVEN
qq	Julia	CORRESPONDENCE
Oy	833 CCCAGTCAATGGCAGGCAGGCAGGCAGCCCCAAGACTGATCATGAAGGCAT 774	; ADDRESSEE: ; STREET: Fou
qa	467 proGlyProGlnGlyLeuProGlySerProGlyAlaPro	; CITY: San F. STATE: CA
Οy	773 AGACAGAGTAGGCCTGGCGACAGTGGTCCGGGAAGAGGTCAGAGAGA 720	COUNTRY: US
qq		COMPUTER READA
ΛO	CACAGA	COMPUTER: I
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ò	659 TGAGCAGTGCCAGGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCGG 600	APPLICATION ;
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2		ATTORNEY/AGENT NAME: ROWLA
οy	CCCTTGGGATGAGAAGAGCTCAGCAGATGCCCAAGAACAGTG CCCAAGATGAGAGAGTGAGAGTGAGAGAGTGAGAGAGTGAGAGAGTGAGAGAGTGAGAGAGAGTGA	REGIST
. qa		TE
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qa	548 ProGly	INFORMATION E SEQUENCE CE
Qy	482 AGACCAGGCCAGCACTGGACCAATGCCCAGCACGTGGTCATGAACTTCTCCTCTACCC 423	; LENGTH: 837 ; TYPE: amino
qa	G1n	; STRANDEDNESS ; TOPOLOGY: 1
Qy	422 CCA	; MOLECULE TYPE US-08-175-155-68
QQ	G1y	Aliqnment Scores:
Qy	374 ACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCC 318	Pred. No.: Score:
qq	586 ThrproGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGln 605	Percent Similarity Best Local Similar
Qy	317 GCAGCAGGCGCTCACCACAGCCTCTGGACCATAGTGGGCCAGGCGGTAGGGCTC 261	Query Match: DB:
QQ	GlyAlaProGlyThr-ProGlyProGlnGlyLeuProG	US-09-759-143-110
Qy	260 AGGGGGCGTTCAGGCACTCCAGAACTGCTTCGCTCTGCTCTCCAGAAGCTGCGGC 201	Qy 2347 GGGAP
qq	625 rProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGl 645	
δŷ	CAGCC	Qy 2287 CTAGG
qq	uProGlySerProGlyAlaPr	Dp 29 LeuP1
QY		Qy 2227 AGTGG
qq	659 oGlyThrProGlyProGlnGly-LeuProGlySerProGlyAlaProGlyThrProGlyP 679	Db 74 LeuPi

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AAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTTCTAGGTGTGTCTCAA 2288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E ADDRESS:
Flehr, Hohbach, Test, Albritton & Herbert
our Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   837
263
32
327
218
57
                                                                                                                                                                                   orman, Mary A.
NATION: Methods for Preparing Synthetic intron: Repetitive DNA pleness: 69
                                                                                                                                                                                                                                                                                                         ADABLE FORM:
PE: Floppy disk
I IBM PC compatible
S SYSTEM: PC-DOS/MS-DOS
PRACENTIN Release #1.0, Version #1.30
PLICATION DATA:
THE 29-DEC-1993
AMTION: 435
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Mismatches:
Indels:
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Dalland, Bertram I.
TION NUMBER: 20015
EL/DOCKET NUMBER: A-55186-5/BIR
ICATION INFORMATION:
E: 415-781-1989
FOR SEQ ID NO: 68:
ARRACTERISTICS:
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                                              errari, Franco A.
appello, Joseph
rissman, John W.
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----TATCCAGGATGCCGAGGTCCAGGCAGAT 1745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1589 TAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCC 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1529 CTCGGTATT----TGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGGCCAGTG 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1475 TGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGCGGCGGCTGAAGCTGTCA 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1415 CCACGGCCACACTGTGGGACAGGCATGTGGCACC --- GGCAGCCACAGGGAAAGCTGCCA 1359
                                              2083 CAGGGTGGCAGCAGAGGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGG 2024
                                                                                                                                     1963 CAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTAC 1904
                                                                                                                                                                                                                                                                                                                1903 CTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGT 1844
                                                                                                                                                                                                                                                                                                                                                                                                       1843 GACAGACTGGCTGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAG 1784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1744 GCCCCGGC------CCGGAACCACCTGGCCTCGGTG------GGCTCACCA 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1649 GTGGGAGCAGCCACTGCCTCCAGCACCCACGTGTCCATTAGGGAAGGGAGCTCCAGGCT 1590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1154 ACAGCGTGAAGGTCATGAGTGCCATCCAGC------TGCACAGCTCAGCCACGA 1107
                                                                                         83 ProGlySerProGlyAlaProGlyThrProGly--ProGlnGlyLeuProGlySerProG 102
                                                                                                                                                                                                                                                                      122 ro-----GlyProGlnGlyLeuP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 lyLeuProGly------SerPro-----GlyAlaProGlyThrP 152
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       72 ------GlyAlaProGlyThrProGlyProGln------GlyLeu 82
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2263 AGCCTGGGTAATCCACCTGCAGATCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTC 2204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2143 TGGGGAGAGAGGAGGGACGCCCCAGCCCCCAGCTGTGCAGCTACGCACCTCAGCAGCA 2084
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32 AlaProGlyThrProGlyGluGlnGlnHisHisELeuGlyGlyAlaLysGlnAlaGly
                                                                                                                                                                                         Sequence 53, Application US/08397633A
Patent No. 577357
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A-58848-1/BIR PROP-011-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-759-143-110 (1-3410) x US-08-397-633A-53 (1-829)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/397,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: ROWland, Bertram I
REGISTARION NUMBER: 20,015
REFERENCE/POOKET NUMBER: A-58(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARATERISTICS:
                                                                                         38 GGCTGTCACCCGGAGCC 22
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                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
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Best Local Similarit
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                                                                                                                                                                 -08-397-633A-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                 RESULT 33
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208 202 202 202 196 107 107 107 107 107 107 107 107	13 CAGGGTGGCAGCAGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGG 2024 1	3 CAGCCCCATGGGGCTAACAGGAGCGGGGACCTGGGACCCAGTGAGGCAGGC	GAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTAC 1904	CTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCCTGCGGCAG	GACAGACTGGCTGAGCTGGACATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAG 1784	CAGGAAGGCAC	4 2 0 0	m 03	9 GT	0 0	<pre>29 CTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGGCCAGTG 1476</pre>	ro 44	15 CCACGGCCACACTGTGGGACAGGCATGTGGCACCGGCAGCGCACAGGGAAAGCTGCCA 1359	58 CACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCGGCCGG			14 TGCCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCCCCTCGCCACGAAATCCGTGTAAA 1155	4 ACAGCGTGAAGGTC
	083 83	023	963	903		783 C 152 r	744 G 172 e	CC 1y	649 GT 212 rc	589	529	475		58	98	65 26 Pr	14	154

Qy	1106	AGAGCCGGCGCAGGCTGCGGGCATGCGGCAGCTGGTGCAGCCGGGGAA 1053
Db	381	GlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySer 400
Qy	1052	GCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGCATGGACAGCAGTGGGGCG 996
QQ	401	ProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGly 420
Qy	995	ACAAGGAGGGGCCGACAGCCTTCTGCTGGCTCGGTGGGGCCCAGCGCTGCCTCCT 939
Db	421	ThrproGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro 439
Qy	938	CAGCCACCAGCAGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAGA 879
Db	440	GlnGlyLeuProGlySerProGlyAlaPro 449
٥y	878	GGCACTCCT
Db	450	GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr 466
Qy	833	CCCAGICAAIGGCAGGCAGGAGGTAGCCCAGGCACCCCAAGACIGAICAIGAAGGCAI 774
Db	467	ProGlyProGlnGlyLeuProGlySerProGlyAlaPro
٥y	773	AGACAGAGTAGGCCTGGCGACAGTGGTCCCGGAAGAGGTCAGAGAG 720
Db	480	GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 497
Qy Db	719	GGGCCTCCAGTGGAGGACACACCTGGCCACAGAAGTCCAGCAGCAGCAGCAGGA 660
Qy	629	TGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCGG 600
Dp	516	GlyLeuProGlySerProGlyAla528
٥y	599	GAGAAAGAGGCTCAGCAGGATGCCCAAAGGACAGTGCCCAGATGAAGG 5
o qq	529	3lnGlyLeuProGlySerProGlyAlaProGlyThrProGly
Qγ	542	GCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACAC 483
qq	548	ProGlySerProGlyAlaProGly 555
Qy	482	AGACCAGGCCAGCACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTTACCC 423
qq	556	
Qy	422	CCACTTCCAGCAGAGGGGGCACATAGGTGATGCCTGCGGCCAAAC 37
qq	572	ProGlyProGlnGlyLeuProGlySerProGlyAla
QY	374	ACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAAGAGCTGGGCTTTCCGGTGCC 318
Db	586	
Qy	317	GCAGCAGGGGCTCACCCACACACCATGGACCATGGGCCAGGGGGGTAGGGCTC 261
qq	909	
Oy	260	AGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTTCCAGAAGCTGCGGC 201
Db	625	rPr
Qy	200	CICTCCICCIIGC
Db	645	yThrProGlyProGlnGlyLeuProGlySerProGlyAlaPr 6
Oy	140	CTTTGGTGCCGGTC
qq	629	oglyThrProGlyP
Qy	95	CTGTGGGGCACCTCAGTGGGGACACGTCTCATCACTCAGATCCTGGCCGAGGCGCGC 39

|||| | 693 ArgGlyAspProGly 697

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39 CGCTGTCACCCGGA 25

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2320 GCTCCCAAAAACCCTTCTCTAGGTGTGTCT---CAACTAGGAGGCTAGCTGTTAACCCTG 2264
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                                                                                         APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A
APPLICANT: FERRARI, Franco A
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
ADDRESSEE: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                                                               STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              829
256
33
324
219
53
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COMPUTER: IBM PC COMPATIBLE
OPPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPELICATION NUMBER: US/08/642,255
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-759-143-110 (1-3410) x US-08-642-255-132 (1-829)
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 20,015
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A5556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-871
TELEFAX: 910 277299 FFT UR
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 amino acids
TYPE: amino acid
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RESULT 32
US-08-642-255-132
US-08-642-255-132
Sequence 132, Application US/08642255
Patent No. 5773249
GENERAL INFORMATION:
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357.00
34.78%
30.81%
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       COUNTRY: USA ZIP: 94111-4187 COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
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Best Local Similarity:
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us-09-759-143-110.rai

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1181 -GCCCCTCGCCCACGAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTG 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1608 GGGAAGGGAGCTCCAGGCTTA-----GGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCC 1555
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                                                                                                                                    1876 AC-------CCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGA 1830
                                                                                                                                                                                                               1829 GCTGGACCAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGA---AGGCAC 1773
                                                                                                                                                                                                                                                                                             -CCGGAACCACCC 1725
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                                                                                             -------ArgGlyAspPro 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: High Molecular Weight Collagen-Like TITLE OF INVENTION: Protein Polymers NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
                                                                                                              ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
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265
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-759-143-110 (1-3410) x US-08-642-255-62 (1-1064)
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 455556-3/BIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 494-8700
TELERAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 amino acids
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                      FERRARI, Franco A.
  CAPPELLO, Joseph
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                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: Si
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                                                                                                                                                                                                 USA
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  APPLICANT:
                                                                                                                                                                                                 COUNTRY:
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	130 uProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGl	150
ι,		395
1	50 yAlaProGlyThrProGlyGluGlyGlnGlnHisHisLe	163
m ,	5 ATGTGCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGG	455
П	63 uGlyGlyAlaArgGlnAlaGlyAspValGly	173
4	6 GCATTGGTCCAGTGCTGGGCCTGTGTGTCCCGGTCCTAGGCTCAGCCAGTGACCACT	515
[4SerProGlyAlaProGlyThrProGlyProGln	184
וט	516 GGCGTGGACGCTATGGCCGCCGCCCTTCATCTGGGCACTGTCCTGGGCATCCTGC	575
1		191
un.	DODLD	979
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9	27 CGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGG	671
23		229
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23	::: GlnAlaGlyAspValGlySerProGlyAlaPr	249
7	20 recteredaceretreeggacec	755
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7	56 GCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCC	815
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80	reccatteactegeacaccagtecctegecccctacctegecacccage	698
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80	870 AGGAGIGCCTCTTIGGCCIGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGC 9	929
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б	30 TGGTGGCTGAGGAGGCAGCGCTGGGCCCAGCAGCAGGAGGGCTGTCGCCCCT	686
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σ	90 CCTTGTCGCCCCACTGCTGTCCATGCCGGCCCGCTTGGCTTTCCGGAACCTGGGCG	1046
es.	31	349
10	047 CCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTTT 1	1106
34	9 aProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyTh	367
1107	TCGTGGCTGAGCTGTGCAG	155
m	7 rProdlyGluGlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySe	387
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38.	7 rProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPr	406

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1209 CGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCCAGCCTGGGGCT-- 1266
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                        480 oGlyProGlnGlyLeuProGlySerProGly-AlaProGlyThrProGly---ProGlnG 499
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559 SerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlyAlaPro
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                             406 oGlyThrProGlyProGlnGlyLeu-----
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Patent No. 5773249
GENERAL INFORMATION:
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Db 657GlnHisHisLeuGlyGlyAlaArgG Qy 1969GAGGGCTGCCTC ::	RESULT 30 US-08-397-633A-31 Sequence 31, Application US/08397633A Patent No. 577377 GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: 105 CORRESPONDENCE ADDRESS: ADDRESSEE: FLEHR, HOHBACH, TEST, STREET: 4 Embarcadero Center, Sui	COUNTY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-4187 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIOLS OPERATING SYSTEM: PC-DOS/NS-DOS SOFTWARE: Patentin Release #1.0. APPLICATION NUMBER: US/08/397,633 FILING DATE: CLASSIFICATION NUMBER: US/08/397,633	GEN TICA T	TOPOLOGY: linear MOLECULE TYPE: peptide -397-633A-31 ment Scores: 6.7e-20 No.: 364.00 nt Similarity: 33.95% Local Similarity: 29.69% Match: 1	US-09-759-143-110 (1-3410) x US-08-397-63 QY
331 rProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAl 349 1047 cccrGcTrCcccGGCTGCACCAGCTGCCGCATGCCCGCACCCTGCGCGGCTCT 1106 111 :::	G G F - P G C	GTGGCAGCTTTCCCTGTGGCTGCCG 138	1481 GCCTCCTCTACCACGGGAACCAGGTGTTCCT		
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ICACTGGGTCCCAGCTCCCGGTCTGTTAGCCCC 2014
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|yaspvalGlySerProGlyAlaProGlyThrPro 110
GlnAlaGlyAspValGlySerProGlyAlaProG 676
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|aProGlyThrProGlyGluGlyGlnGlnHisHis 91
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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DB: US-09-759-143-110 (1-3410) x US-08-642-255-120 (1-762)	84 GGTGCCCCACAGCAGCAGGTGTTGAGC		OY 138 AAGGCTGGCAGAAATGGGCGCTGGCTGATTC 170	Db 72 GlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHisHis 91	Oy 171 CTAGGCAGTTGGCGGCAGCAAGAAGAGGAGGCGCAGCTTCTGGAGCAGAGCGAGACGA 230		Db 111 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro-GlnGlyLe 130	Oy 289	336 TCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGCATCCTT	Db 150 yAlaProGlyThrProGlyGluGlyGlnGlnHisHisLe 163	396	Db 163 uGlyGlyAlaArgGlnAlaGlyAspValGly173	456 GCATTGGTCCAGTGGTCTGGTCTGTCCCGCTCCTAGGCTCAGCCAGTGACCACT	1/4SELPIOGLYALAPPOGLYThrProGLyProGLyProGLn		Qy 576 TGAGCCTCITTCTCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCC 626		Qy 627 CGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGG 671	672	Db 229 yGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAlaPr 249	Qy 720 TGCTCTCTGACCTCTTCCGGGACCC	CTACT			Db 277 yAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro 291	870 AGGAGTGCCTCTTTGGCCTGCTCACCTTCCTCACTGCGTAGCAGCCACACTGC	292 -GlyAlaProGlyThrProGlyGluGlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAl	QY 930 TGGTGGCTGAGGAGGCAGGGCCCCACCAGCAGAAGGGCTGTCGGCCCCT 989	990	
Oy 269 GTAGGGCTCAGGGGCCGTTCAGGACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCA 212	AAGCTGCGGCCTCTCCTTG	 Db 798 yProLeuGly1leAlaGly1leThrGlyAlaArgGlyLeuAlaGlyProProGlyMetPr 818	182	818	<pre>Qy 122 TTCTCAG</pre>	92 TGGGGCACCTCAGTGGGGACACGTCATCACTCAGATCCTGGC	857 laGlyThrAlaGlyGluProGlyArgAspGlyAsnProGlySerAspGlyLeuProG	Oy 48	RESULT 29	os 00 042-233-120 ; Sequence 120, Application US/08642255 ; Patent No. 577249	GENERAL INFORMATION: APPLICANT: CAPPELLO, Joseph		; TITLE OF INVENTION: Protein Polymers; NUMBER OF SEQUENCES: 135	STREET: 4 Embarcadero Center, Suite 3400	CITY: San Francisco	COUNTRY: USA ZIP: 94111-4187	COMPUTER REMUMBLE FORM: COMPUTER: IBM PC compatible	SYSTEM: PC Patentin F LICATION DAT	** AFFLICATION NUMBER: US/UB/042,255 FILING DATE: CALASTERIAN 435 ** TRANSPORT TO THE TRA	ATTOKNET/AGENT INFORMATION: NAME: ROWLAND, Bertram I.	; REGISTRATION NUMBER: 20,015 ; REFERENCE/DOCKET NUMBER: A55556-3/BIR ; TELECOMMUNICATION INFORMATION:	: IELEFRONE: (#12) 494-0/00 : TELEFAX: (415) 494-0771 : TFI:X: 010 277200 EPH ID	; INFORMATION FOR SEQ ID NO: 120: SEGUIENCE CHRARAFERISTICS.	; LENGTH: 762 amino acids ; TYPE: amino acid	EDNESS:	; WOLECULE TYPE: protein US-08-642-255-120	Scores:	rieu. No.: 6.4e-20 Lengin: 762	ity: 29.69% Mismatches: 5.67% Indels:	

Db			δ	1181
Οy	2129 AGG	AGGGACGCCCCAGCCCAGCTGTGCAGCTACGCACCACAGAGGTGGCAGCAG 2070	: =	513 61
οp	221 gG1	yGluProGlyProGlnGlyHisAlaGlyAlaGlnGlyProProGl 237	}	
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1058	AGCAGGGCGCCCAGGTTCC	
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618		
899	TGAGGGTGAGCAAAAGAGGCACTCCTCGGTGCCCAGGTAGGGGGCCAGGG 843	
629	ProGlyAspLysGlyGluGlyGlyAlaProGlyLeuProGlyIleAlaGlyPro 646	
842	CACTGGTGTCCCAGTCAATGGCAGGCAGGCAGGTAGCCCAGGCAGCCCCCAAGACTGATCA 783	
647		
782	TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGT 729	
653	ArgGlyGluThrGlyProProGlyProAlaGlyPheProGlyAlaProGlyGlnAsn 671	
728	728 CAGAGAGGCCTCCAGTGGAGTGAAGCACATGGCCACAGAAGTCCAGCAGCAGC 669	
672	GlyGluProGlyGlyLysGlyGluArgGlyAlaProGlyGluLysGlyGluGlyGlyPro 691	
668	CGCCCAGGATGAGCAGTGCCAGGTCCAGGGGCCTGGGATCGGGGCACAGCA 618	
692	ProGlyValAlaValProProGlyGlySerGlyProAlaGlyProProGlyProGln 710	
617	GCCCTGCTAGCCAGCCGCCCTTGGGATGAGAAAGGGCTCAGGAGGATGCCCAAGGACA 558	
711	GlyValLysGly 722	
557	GIGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACCCCAGTGGTCACTGGCTGAGC 498	
723	727	
497	CTAGGAGCGGGACACAGACCAGCACTGGACCAATGCCCAGCATGGTCATGA 438	
728	ProGlyAlaArgGlyLeuProGlyPro	
437	ACTICTCCTCTACCCCCACTICCAGCAGAGGGGGGCACAIAGGTGATGCCTGCGGCCA 378	
741	GlyAsnProGlyProProGlyProSerGlySer751	
377	AACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCC 318	
767	CAGGCGG 27 roGlyGl 78	

	spAlaGlyGlnProGlyGl	269 GTAGGGCTCAGGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTCGTCCA 212		YrobeusiyilealadiyileThrGlyAlaArgGlyEeuAlaGlyProProGlyMetPr 81	184 CCAATIGCTAGGAATCAGCCCCCCATTTCTGCCCAGCCCTTTGGTGCCGGTCCAGC 123 818 OGlyProArgGlySerProGlyProGlnGlyValLySGlyGluSerGlyLySProGl 837	122 TTCTCAG	837 yalaasnGlyLeuSerGlyGluargGlyProProGlyProGln-GlyLeuProGlyLeuA 857	92 TGGGCCACCTCAGTGGGGACACGTCTCATCACTCAGATCCTGGC	C	lyArgAspGlySerProGlyGlyLysGlyAs	RESULT 28 Sequence 21, Application Us/09548608 GENERAL INFORMATION: APPLICART: Ponde, Martin TITLE OF INVERTION: A Method for Assaying Collagen Fragments TITLE OF INVERTION: A Method and Use of the Method to Diagnose the Presence of TITLE OF INVERTION: A Method and Use of the Method to Diagnose the Presence of Universe OF Sequences: Disorders Associated with the Metabolism of STATILE OF INVERTION: Disorders Associated with the Metabolism of COMPRESSES: Darby & Darby PC STREET: 805 Third Avenue CITY: New York COMPITER: New Yo
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2939 GGAAGTGGGGGGAACCAGGCTGGGCCAAGAGAAGAGGGGTGGTTAGGGAAGCCGTTGAGA 2880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 ---AlaIleGlyProSerGlyProAlaGlyLysAspGlyGluSerGlyArgProGlyArg 91
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Mismatches:
Indels:
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                                                                   ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                364.50
30.79%
25.73%
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             TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapier
amino acid
                                                                                                                                                                                                                                   Best Local Similarity:
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qq	200 oGlyalaLysGlyGluValGlyProAlaGlySerProGly213	٥	1202 CTCTGGGCACGC
Qy	2189 GACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGGAG 2130	7 f	
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Qy	2129 AGGGACGCCCCACCCCCAGCTGCAGCTACGCACCTCAGCAGCAGCAGGGGCGCCAGCAG 2070	S &	513 GlubroLusglu
qa	221 gGlyGluProGlyProGlnGlyHisAlaGlyAlaGlnGlyProProGl 237	3 6	
0y	2069 AGAGCCACATTAGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGC 2010	Š Š	11/8 CCICGCCCACGA
Db	237 yProProGlyIleAsnGlySer	2 2	
Qy	2009 TAACAGGAGCGGGGAGCTGGGACCCAGTGAGGCAGCCCTCCCACCCA	7 A	
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qq	261GlyLeuMetGlyAlaArgGlyProProGlyProAla 272	δ	1034
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δy		qq	
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δλ	1595 CAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCAC 1542	3 6	
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qq	458 GINGIYProProGlyLysAsnGlyGluffyrGlyProGlnGlyProProGlyProInfGly 477	Qy	377 AACACACCTCC

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ą	513	GlyproLysGlyGlualaGlyAlaProGlyAlaProGlyGlyLysGlyAspAlaGlyAla 532
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λ	6	TGAGGGTGAGCAAAGAGGCACTCCTCGGTGCCCAGGTAGGGGGCCAGGG 843
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λζ	842	ino t
q	647	
. qc	782	TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGGTCCCGGAAGAGGT 729 :::
λy	728	CAGAGAGCAGGGCCTCCAGTGGAGTGAAGCACCTGGCCACAGAAGTCCAGCAGCCCCA 669
q	672	GlyGluProGlyGlyLysGlyGluArgGlyAlaProGlyGluLysGlyGluGlyGlyPro 691
λy	899	CGCCCAGGATGAGCAGTGCCAGCTCCAGGGCCTGGGATCCGGGCACAGCA 618
qc	692	ProGlyValAlaValProProGlyGlySerGlyProAlaGlyProFinGlyProGln 710
λy	617	GCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACA 55
qc	711	GlyvalLysGly
λλ	557	GTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGC 498
qc	723	1
λy	497	CTAGGAGGGGACACAGACCAGCCCAGCACTGGACCAATGCCCAGCACATGGTCATGA 438
qc	728	Δ
λλ	437	ACTTCTCTCTACCCCCACTTCCAGCAGAGGGGGCACATAGGTGATGCCTGCGGCCA 378
qc	741	
>	377	AACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCC 318

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2939 GGAAGTGGGGGGAACCAGGCTGGGCCAAGAAGAGGGGGTGGTTAGGGAAGCCGTTGAGA 2880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2879 CCTGAAGCCCCACCCTCTACCTTCCAACACCCTAACCTTGGGTAACAGCATTTGGAA 2820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2819 TTATCATTTGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGGCATTTTGGGGGGCCAGA 2760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2759 CCCCAGGAGAAGAATTCTGGCAATGATCAGCCCAATGACCAGCTATCTCAGGGGACCT 2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2699 GATTGTTGGGGATCCCCCACCCTACCCAAATATTAGACACCAACACACAGA------ 2651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2543 AAAAGGTAAGAGGGGGTGGATCAGCAAAAAGACAGTGCTGTGGGCTGAGGGGACCTGGT 2484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2423 GGAGGAGTGTTTCATCCTAGAAACTCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2363 TAAGGGGCTTAGA----GATGGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAA 2310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2309 CCCTTCTCTAGGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCC 2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 Ala-----Glylle-ProGlyPheProGlyMetLys---GlyHisArgGlyPheAspGl 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 GlySerProGlyTyrGlnGlyProProGlyGluProGlyGlnAlaGly---ProSerGly 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 ProProGlyProProGly------72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 --- AlaileGlyProSerGlyProAlaGlyLysAspGlyGluSerGlyArgProGlyArg 91
                                                                                                                                                                                                                                                                                                                                                                             1078
290
57
354
426
62
                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39-759-143-110 (1-3410) x US-09-570-573-21 (1-1078)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                            COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 -----
                                                                                                                                                                                                                                                                                                                                                                             6.94e-20
364.50
30.79%
25.73%
5.86%
                                                                                                                                                                                                                                       OKGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                         cent Similarity:
Local Similarity:
ry Match:
                                                                                                                                                                                                                                                                                                                                                            nment Scores:
                                                                                                                                                                                                                                                                                                              19-570-573-21
                                                                                                                                                                                                                                                                                              CLONE:
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Db 4	Oy 13	an	UY 17	Qy 12		Oy 11 Db 5	Oy 11	,	Oy 11 Db 5	Qy 10	Dp 2	Qy 10	ממ מ	o qa	Qy 9	9 qa	δy 8	DD QQ	Oy 8	Qy 7	9 90	Oy 7	op qq	o v	a an		an io	oy o	Qy 4
							_																					()	 .
2363 TAAGGGGCTTAGAGATGGGAAACCAGGTGACTGAGTTATTCAGCTCCCAAAAA 2310 111 111		189 yProProGlyThrAlaGlyPhePro	2249 ACCTGCAGAGTCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCTGTATAAGTCCA 2190	OCLYALDLYSCLYCLUVALCLYFIONLGSTYSCEFFIOGLY	214Glydlaptro-SerAsnGlyAlaptroGlydlaptro-221	2129 AGGACGCCCCAGCTGTGCAGCTACGCACCTCAGCAGCAGGAGGGTGGCAGCAG 2070			2009 TAACAGGAGCGGGGAGCTGGGACCCAGTGAGGCAGGCCCTCCACCCCAATGTGCTGGAAG 1950 248INSGINGINMAFGIVPPAAIAGIVI PPAGIVAIAPPA	TITICIACGCTGAGIAITIGGCCAAGTCGCTCTTGTCAATACIACCTGTGTAGCAAAGT	561	1889 AAATGGCGACCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGA 1830	273 GlyAlaAsnGlyAlaProGlyLeuArg	1829 GCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACACAGGAAGGCAC 1773		GLIAALAGIYILEProGlyValProGlyAlaLysGlyGluAspGlyLysAspGlySerPro	1751 GGCAGATGCCCCGGGCCCGGAACCACCCTGGCCTCGGTGGGCTCACCCACC		CGGAGACATCACAGGCAGAGGCCCGCA	gGlyalaLeuGlySerArgGlyProAlaGlyProAsnGlyIleProGlyGluLyS-GlyP	1652 GAGGTGGGAGCCACTGCCTCCAGCACCCACGTGTCCATTAGGGAAGGAGCTC 1596 111			1541 CTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGG	393	1481 CCAGTGTGTAGGCCAGGATCTGCAGGGCTGAGAGGTGAACCCGGTGAGGGGGGGCTGAAG 1422	404 ProGlyProProGlySer-GlnGlyGluSerGlyArgProGlyProPcoGlyProse 422	TGTCACCACGGCCACACTGTGGGACAGGCATGTGGCACCGGCAGCCAGGGAAAGCTG	٠ ٢
Qy Db	Qy	qa	y g	3 8	<i>t</i> , q ₀	λο d	3 8	ැ අ	Qy	Qy	qa	Qy	qq	oy e		q _Q	ογ	QQ	٥٧	qq ,	Qy Op	δy	qq	QY	Dp	Qy	QQ	٥٠ ١	λo

Db	440	::: AspGlyAlaProGlyLyEysAsnGlyGluArgGlyGlyProGlyGlyProGlyPro 457
٥y	1301	GAGAGAAGACCAGGGAGATGGCGCACTGCAGGAACAGCC 1263
Db	458	::: ::: ::
Qy Db	1262	CCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAG 1203
٥	1202	
qq	49	1yGlyProProGlyGluAsnGluLysProGlyGluPro 512
Qy	1181	920 1179
QQ	513	 GlyProLysGlyGluAlaGlyAlaProGlyAlaProGlyGlyLySGlyAspAlaGlyAla 532
Oy	1178	CCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACA 1119
. da	533	ProglyGluArgGlyPro
Qy	1118	GCTCAGCCACGAAGAGCGGCGCAGGGGGGGGGGGGGGGG
qq	544	AlaProGlyLeuArgGlyGlyAlaGlyProProGlyProGluGlyGlyLySGlyAlaAla 563
Qy do	1058	GGGGAAGCAGGCCCCAGGTTCC
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Qy	1034	
QQ	584	ArgGlyGlyLeuGlySerProGlyProLysGlyAspLysGlyGluProGlyGlyProGly 603
Qy	1013	ATGGACAGCAGTGGGGCGACAAGGAGGGGGCCGACAGCCCTTCTGCTGGCTCGG 960
Db	604	AlaAspGlyValProGlyLysAspGlyProArgGlyProThr617
Qy	959	AGCAGTGTGCTGCTACGCAGGTGAGGAAG
Db	618	GlyProlleGlyProProAlyProAla
Qy	899	ပ္ပ
QQ	629	ProGlyAspLysGlyGluGlyGlyAlaProGlyLeuProGlyIleAlaGlyPro 646
Qy	842	CACTGGTGTCCCAGTCAATGGCAGGCAGGGAGCCAGGCAGCCCCCAAGACTGATCA 783
pp	647	
Qy	782	TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGATCCCGGAAGAGGT 729
qq	653	ArgGlyGluThrGlyProProGlyProAlaGlyPheProGlyAlaProGlyGlnAsn 671
Qy	728	CAGAGAGCAGGCCTCCAGTGGAGGAACACCTGGCCACAGAAGTCCAGCAGCCCCA 669
qq	672	GlyGluProGlyGlyLysGlyGluArgGlyAlaProGlyGluLysGlyGluGlyGlyPro 691
Qy	899	CGCCCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCA 618
Db	692	ProGlyvalAlavalProProGlyGlySerGlyProAlaGlyProGlyProGln 710
Qy	617	GCCCTGCTAGCCAGCCGCCCTTGGGATGAGAAGAGGCTCAGCAGGATGCCCAAGGACA 558
Db	711	GlyValLysGly 722
QY	557	GTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGC 498
DP	723	
Qy	497	CTAGGAGCGGGACAGACAGGCCCAGCACTGGACCAATGCCCAGCACCATGGTCATGA 438

557 GTGCCCAGATGAAGGGCCGGCGGCGATAGCGTCCACGCCAGTGGTCACTGGCTGAGC 498	723 727	497 CTAGGAGCGGGACACAGACCAGCCCAGCACTAGGCCCAGCCAG	728 ProGlyAlaArgGlyLeuProGlyPro	7	AACACATCAGGGCAAAGGTTAGCAGGGCAACAAAAAAGGTTAGAAAAAAAA		ACAGCCTCTGGACCATAGTGGGCCCAGGGG 2	767 PróGlySerProGlyValSerGlyPro-LysGlyAspAlaGlyGlnProGlyGl 784	269 GTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTCCA212	784 uLysGlySerProGlyAlaGlnGLyProProGlyAlaProGl 798	211GAAGCTGCGGCCTCTCCTTGCTGCG 183	798 yProLeuGlyIleAlaGlyIleThrGlyAlaArgGlyLeuAlaGlyProProGlyMetPr 818	182 CCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCAGC 123	818 oGlyProArgGlySerProGlyProGlnGlyValLysGlyGluSerGlyLysProGl 837	122 TTCTCAG		TGGGGCA	857 laGlyThrAlaGlyGluProGlyArgAspGlyAsnProGlySerAspGlyLeuProG 876		lyGluAsnGly	SULT 26
Oy	Ор	ò	QQ	Oy Dp	ογ	· 8	Qy	qq	٥y	qq	QY	qq	Qy	qq	Qy	qq	Qy	Dp	ΟÝ	ДQ	RESULT 26 US-09-500-6 Sequence Sequence Sequence Tack TITLE

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2939 GGAAGTGGGGGGAACCAGGCTGGCCAAGAGAGAGGGGTGGTTAGGGAAGCCGTTGAGA 2880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2819 TTATCATTIGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGGCATTTTGGGGGGCCAGA 2760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2759 CCCCAGGAGAAGAAGATTCTGGCAATGATCAGCCCAATGACCAGCTATCTCAGGGGACCT 2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2603 ATATTTAAATGCCTGTGTCTCTGTGATGGCAACAGAAGGACCAACAGGCCACATCCTGAT 2544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 Ala-----Glylle-ProGlyPheProGlyMetLys---GlyHisArgGlyPheAspGl 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 sGlyGluAsnGlyLeuProGlyGluAsnGlyAlaProGlyProMetGlyProArgGlyAl 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 GlySerProGlyTyrGlnGlyProProGlyGluProGlyGlnAlaGly---ProSerGly 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-759-143-110 (1-3410) x US-09-500-811-21 (1-1078)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                    NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                  CLONE: COLLAGEN ALPHA 1 (III) US-09-500-811-21
                                                                                                                                                                   TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.94e-20
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30.79%
25.73%
5.86%
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
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		QC D	404 ProGLY
qq	175 175	ò	1421 CTGTCACCA
δò	2423 GGAGGAGTGTTCATCCTAGAAACTCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGT 2364	7	
qq	175 175	gg ,	
ò	2363 TAAGGGGCTTAGACATGGGAAACCAGGTGACTTTATTCAGCTCCCAAAAA 2310	δλ	
5 E	-Asp6]yAlaArd6]ySerAsp6]v61nproGlyProProGl	qa	
}		δλ	1301 GAGAGAAGA
δλ	2309 CCCTTCTCTAGGTGTCTCTCAACTAGGAGGCTGTGAACCCTGAGCCTGGAGACTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTGTTGAGC	qq	458 GinglyPro
a a	YPIOPIOGLYINLAGGLYPINEPIO	οy	1262 ccaggcrgc
δλ	ACCTGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCCTGTATAAGTCCA	qa	478 ProGlyGly
qo		Oy	1202 CTCTGGGCA
Qy	agagactggggagagaggag :::	qq	
ф		Oy	1181
ογ	TGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAG :::	qa	513 GlyProLys
qq	221 gGlyGluProGlyProGlnGlyHisAlaGlyAlaGlnGlyProProGl 237	δδ	1178 CCTCGCCCA
, oy	AACAGAAACTGGGGGCCAGCCGGCAGCCCCATGGGGC	qa	 533 ProGlyGlu
q	237 yProProGly1leAsnGlySer	ÓÀ	1118 GCTCAGCCA
δy	2009 TAACAGGAGGGGGAGCTGGGACCCAGTGAGGCCGCCTCCACCCCAATGTGCTGGAAG 1950	- da	
qa	248LysGlyGluMetGlyProAlaGlyIleProGlyAlaPro 260	3 8	
ογ	1949 ITTICTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGT 1890	ζ, <i>t</i>	
qa	::: ::: ::: ::: ::: ::: ::: ::: ::	an o	264 GLYFIOFIC
è	1889 AAATGGCCAACTAGACTTAGGCTTGCAGACACATATAGGCAGTGACAGACTGACT	QY	1034
à â	V [5) (5	qq	584 ArgGlyGly
g G	olyniansiiolyniariosiy Leuniy	δλ	1013 ATGGACAGO
δy		qa	604 AlaAspGly
Q	284 AlaGlyGluProGlyLysAsnGlyAlaLysGlyGluProGlyProArgGlyGluArgGly 303	٥٨	959 TGGGGCCCA
οy	1772	qd	
qa	304 GluAlaGlyIleProGlyValProGlyAlaLysGlyGluAspGlyLysAspGlySerPro 323	à	
δλ	1751 GGCAGATGCCCCGGCACCGGAACCACCTGGCCTCGGTGGGCTCACCCACC	7 d	
g		g G	
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ga	gelyAlabedolysetAtgelyFloataclyFloashelyticerioclystery ory.	٥y	782 TGAAGGCA1
Qy		qq	653ArgGl)
qq		OV	728 CAGAGAGC
Oy	CAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCAC	qa	672 GlyGluPro
qa	377 roGlyArgAspGlyValProGly-GlyProGlyMetArgGlyMetPro 392	0y	668 CGCCCAGG
Qy	1541 CTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGGAGG 1482	qa	 692ProGly
qa	393	Qy	617 GCCCTGCT
Qy	1481 CCAGTGTGTAGGGAGCAGGATCTGCAGGGGGGGGAAGGTGAACCCGGTGAGGGGGGGCTGAAG 1422	qa —	::: 711 GlyValLy:

404	ProGlyProProGlySer-GlnGlyGluSerGlyArgProGlyProProGlyProSe
	CTGTCACCACGCCACACTGTGGGACAGGCATGTGGCACCGGCAGCCAGGGAAAGCTG 13:
422	GlyProArgGlyGlnProGlyValMetGlyPheProGlyProLysGlyAsn 439
1361	CCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCACCAGGTCCATGACCA 13
440	ysasnGlyGluargGlyGlyBroGlyGlyProGl
0	GAGAGAGACCAGGGAGATGGCGCACTGCAGGA
458	lnGlyProProGlyLysAsnGlyGluTyrGLyProGlnGlyProProUlyProTnrGly 477
9 1	CCAGGCTGCCCATCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGG
_	Proclyclydspurys
1202	GlvProProGlvGluAsnG
8	11 200 -1600 11
513	G1n/
	CTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACA 11
533	31yGluArgGlyPro
1118	
1058	3GAAGCAGGGCGCCAGGTTCC
56	
103,	GAAAGCCAAG
28,	yProLysGlyAspLysGlyGluProGlyGlyProGl
	3 ATGGACAGCAGTGGGGCGACAAGGAGGGGCCGACAGCCCTTCTGCTGGCTCGG 96
09	4 AlaAspGlyValProGlyLysAspGlyProArgGlyProThr
95	9 TGGGCCCAGCGCTGCCTCAA
- 0	5GIJPELOLIBEGLIJFLUFLOGIJFLUGALG SGIJPELOGIJFLUFLOGIJFLUGALG SGIJPELOGIJFLUFLUFLUGALG SGIJFLUFLUFLUFLUFLUFLUFLUFLUFLUFLUFLUFLUFLUF
62	9 ProGlyAspLysGlyGlyGlyGlyAlaProGlyLeuProGlyIleAlaGlyPro 64
84	2 CACTGGTGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCC
64	7ArgGlySerProGlyGlu
78	2 TGAAGGCATAGACAGAGTAGGCCTGGCGA
9 · qa	3ArgGlyGluThrGlyProProGlyProAlaGlyPheProGlyAlaProGlyGl
72	8 CAGAGAGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGAAGTCCAGCAGCACCCCA 66
49	2 GlyGluProGlyGlyLysGlyGluArgGlyAlaProGlyGluLysGlyGluGLyGlyPro 69
99	8 CGCCCAGGATGAGCAGTGCCAGCTCCAGGGCTGGGATCCGGGCACA
69	2ProdlyvalAlaValProProGlyGlySerGlyProAlaGlyProProGiyProGln 71
.19	7 GCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGGGATGCCCAAGGACA 55
711	ClyVall.v

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A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
1409 GCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTG 1468
                                                                                                                                                                                                                                                                                1516 ------GCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGAC 1558
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                                         535 ThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGln 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    628 roGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro----
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Fatent No. 6110689
GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: in Body Fluids,
TITLE OF INVENTION: Method and Use
TITLE OF INVENTION: Disorders Associated the companion of th
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2939 GGAAGTGGGGGGAACCAGGCTGGGCCAAGAGAGAGGGGTGGTTAGGGAAGCCGTTGAGA 2880
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                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-759-143-110 (1-3410) x US-08-963-825-21 (1-1078)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                               US/08/963,825
IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                 29,714
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INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
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30.798
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                                                                                                                                                                                                                             NAME: Gogoris, Adda C
REGISTRATION NUMBER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                       CLASSIFICATION: 436
                                                                           APPLICATION NUMBER:
FILING DATE:
               OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 AIGIGCCCCCTCTGCTGCTGCAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGG 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 CTAGGCAGTTGGCGGCAGCAAGAAGAGAGGCCGCCGCAGCTTCTGGAGCAGAGCCGAGACGA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 GGTGCCCCACACCACAGCAGGTGTTG-----AGCATGGGCTGAGAAGCTGGACCGGCACCA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 AGCAGTTCTGGAGTGCCTGAACGGCCCCTGAGCCCTACCCGCCTGGCCCACTATGGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 GlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHisHis
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING NUMBER OF SEQUENCES: 105
                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 530
ATTONES/AGENT INFORMATION:
NAME: ROWLAND BETTER 20,015
REGISTRATION NUMBER: 20,015
REPERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 398-3249
TELEPRAY: 910 277299
TELEPRAY: POR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                       STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: Californi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 uGlyGlyAlaLysGlnAlaGlyAspValGly-----
                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-759-143-110 (1-3410) x US-08-397-633A-26 (1-762)
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 AAGGGC-----TGGCAGAAATGGGCGCCTGGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.62e-20
365.00
35.02%
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                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                            NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                 Y: USA
94111-4187
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                    SOFTWARE:
                                                                                                                 COUNTRY:
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1209 CGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGCT-- 1266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 930 TGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCT 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 aGlyAspValGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySe 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  870 AGGAGIGCCICTITIGGCCIGCICACCCICAICTICCICACCIGCGIAGCAGCCACACTGC 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 -GlyalaProGlyThrProGlyGluGlyGlnGlnHisHisLeuGlyGlyAlaLysGlnAl 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 oGly-----ThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyTh 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        816 TGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCC-----CTACCTGGGCACCCAGG 869
                                                                                                                                                                                                                                                                                    211
                                                                                                                                                                                                                                                                                                                                          671
                                                                                                                                                                                                                                                                                                                                                                                                229
                                                                                                                                                                                                                                                                                                                                                                                                                                                      G------GCTGCTGGACTTCTGTGGCCAGGTGTTCACTCCACTGGAGGCCC 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GGACCACTGTC 755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GlyLeuProGlySerProGl 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1107 TCGTGGCTGAGCTGTGCAG-----CTGGATGGCACTCATGACCTTCACGCTGTT----
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456 GCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACT
                                                                                                            516 GGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGC
                                                                                                                                                                                                                                                                                    191 yAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPr
                                                                                                                                                                                                                                                                                                                                                                        11 ollyProGlnGlyLeuProGlySerProGlyAlaProGlyThr-----ProGlyGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 yGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAlaPr
                                                                                                                                                                                                                              576 TGAGCCT----CTTTCTCATCCCAAGGCCGGCTGGCTAGCAGGGCTGCT-----GTGCC
                                                                                                                                                                                                                                                                                                                                             627 CGGATCCCAG-------GCCCCTGGAGCT---GGCACTGCTCATCCTGGGCGTGG
                                 1370 CCTGTGGCTGCCGGTGCCACATGCCTGTCCC-----
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266 rProGly-----
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Dp 1	421 oGlyThrProGlyProGlnGlyLeuP	441
Οy	3GCACTCGAGCAGTCTATT	1
qa	:::	 SerProGlyAl 461
QY	1370 CCTGTGGCTGCCGTGCCTGTCCC	ACAGTGTG 1408
QQ	roglyProglnGlyLeuProglySerProglyAla	ProGlyThrProGl 481
Oy	09 GCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCT	G 1
qq	81 yPro	-ThrProGlyPro 497
, Oy	69 CCCTACAC	1515
d G	498GlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGl	yGluGlyGlnG 515
ð á	16	15
2 6	olo inhishisheddiyGlyAla-LysGlnAlaGlyAsp	aProGly 534
ž 8	1559 AGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCT	CCTTCCCTAAT 1612
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qq	575 ProGlyAlaProGlyThrProGlyGluGlyGlnGlnHisHisLeuGlyGlyAl	lyAlaLysGln 594
οy	1676 GCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCCACCGAGGCC	SGGTGGTTCCG 1735
qq		 -GlyThrProG 608
οy	1736 GGCCGGGCATCTGCCTGGACCTCGCCATCCTGGA-	-TAGTGCCTTC 1780
Dβ	 IIII	 oGlnGlyLeuP 628
οy	1781 CTGCTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGTCT	FCAGCCAGTCT 1840
ΩP	628 roGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGly	SerP
Qy	GTCACTGCCTATATGGTGTCTGCCG	-CATTIACTIT 1894
QQ	647GlyAlaProGlyThrProGlyGluGlyGlnHi	isHisLeu 660
Qy	ATTTGACAAGA	AGAAAACTICC 1954
QQ	661GlyGlyAlaLysGlnAlaGlyAspValGlySerProGl	oglyalaprog 676
Qy	O	STGTTAGCCCC 2014
QQ	676 lyThrProGlyProGlnGlyLeuProGlySerProGlyAla-ProGlyThrP	 IProGlyPro 695
Qy	2015 ATGGGGCTGCCGGCTGCCG 2035	
qa	696 GlnGlyLeuProGlySerPro 702	
RESULT US-08- ; Sequ ; Pate ; GEN	NS-08-397-633A-26 Sequence 26, Application US/08397633A Patent No. 577357 GENERAL INFORMATION: GENERAL INFORMATION	
	2	

Qy 1955 AGCACATTGGGTGGAGGCCTGCCTCACTGGGTCCCGGCTCCTGTTAGCCCC 2014 :::	RESULT 23 US-08-642-255-114 ; Sequence 114, Application US/08642255 ; Patent No. 5773249	GENERAL INFORMATION: APPLICANT: CAPPELLO, Joseph APPLICANT: FERRARI, Franco A. TITLE OF INVENTION: High Molecular Weight Collagen-Like	El . e	: 1 san Francisco E: California Francisco California Francisco Fra	COMPUTER FEADABLE FORM: ** COMPUTER FEADABLE FORM: ** COMPUTER: IBM PC compatible ** COMPUTER: IBM PC compatible	SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/642,255	FILING DATE CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAMME: ROWLAND, BETTEAM I.	TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-8970	TELERA: 910 277299 FHT UR INFORMATION FOR SEQ 1D NO: 114: SEQUENCE. CHARACTERISTICS:	; TYPE: amino acids ; TYPE: amino acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECOLE TYPE: protein	5.62e-20 Length:	e: 365.00 ent Similarity: 35.02% Local Similarity: 30.09% v Match: 5.69%	1 Gaps: -759-143-110 (1-3410) x US-08-642-255-114 (1-762)	Qy 84 GGTGCCCACAGAGAGTGTTGAGCATGGGTGAGAGCTGGACCGGCACCA 137 1	Qy. 138 AAGGGCTGGCAGAAATGGCGCCTGGC	Qy 171 CTAGGCAGTTGGGGGCAGGAGGAGGCGCGAGCTTCTGGAGAGGCGAGAGAG 230
1047 CCCTGCTTCCCCGGCTGCACCAGCTGTGCCGCATGCCCCGCACCCTGCGCCGGCTCT 1106	recognization in the contract of the contract	1209 CGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGCT 1266 	1267GTTCCTGCAGTGCGCCATCTCCCTGGTCTCTCTGGTCATGGACCGGCTGGTGC 1322	1323 AGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTC 1369 ::: :: :: 440 uGlyGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAl 460	1370 CCTGTGGCTGCCGGTGCCATGCCTGTCCCACAGTGTG 1408	1409 GCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTG 1468	1469 CCCTACACACTGGCCTCCCTCTACCACGGGAGAAGCAGGTGTTCCT 1515 	1516	1559 AGCCTGATGACCAGCTTCCTGCCAGGCCTAAGCCTGGAGCTCCCTTCCCT	GGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCACCCGCGCTCTGCGGGGCC	16/3	1676 GCCTGTGATGTCTCCGTACGTGGTGGTGGTGGGTCAGCCCAGGGCCAGGGTGGTTCCG 1735 	1736 GGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTC 1780	1781 CTGCTGTCCCAGGTGGCCCCATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAGTCT 1840	1841 GTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGCTCATTTACTTT 1894	1895 GCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCC 1954

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AGTTGGCGGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGA 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :-----TGGCAGAAATGGGCGCCTGGC-----TGATTC 170
ON:
PPELLO, Joseph
RARI, Franco A.
TUN: High Molecular Weight Collagen-Like
'ION: Protein Polymers
                                                                                                                                                                                                                    ADDRESS:
LLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
bbroadero Center, Suite 3400
encisco
                                                                                                                                                                                                                                                                                              -4187
ABLE FORM:
RICHARD AGE
IBM PC compatible
XYSTEM: PC-DOS/MS-DOS
PATENTIN Release #1.0, Version #1.30
PCATION DATA:
NUMBER: US/08/642,255
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Matches:
Conservative:
Mismatches:
Indels:
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N NUMBER: 20,015
OCKET NUMBER: A5556-3/BIR
TITON INFORMATION:
(415) 494-870
277299 FHT UR
SEQ ID NO: 114:
                                     CTGCCGGGCTGGCCG 2035
                                                    ication US/08642255
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INFORMATION:
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990 CCTTGTCGCCCCACTGCTGTCCATGCCGGCCCGCTTGGCTTTCCG---GAACCTGGGCG 1046
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91 LeuGlyGly---AlaLysGlnAlaGlyAspValGlySerProGlyAlaProGlyThrPro 109
                                                                                                                               GGTGCCCCACAGCAGCAGGTGTTG-----AGCATGGGCTGAGAAGCTGGACCGGCACCA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 CTAGGCAGTTGGCGGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 ------CCAGAGGCTGTGGGTGAGCCG---CCTGCTGCGGGCACCGGAAAGCCCAGC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 TCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 yAlaProGlyThrProGlyGlu-------GlyGlnGlnHisHisLe 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 ATGTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 -----SerProGlyAlaProGly---ThrProGlyProGln------ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        626
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| 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GlyLeuProGlySerProGl 190
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                                                                                                                                                                                                     71 GlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHisHis 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 GCATTGGTCCAGTGCTGGGCCTGGTCTGTGCCCGCTCCTAGGCTCAGCCAGTGACCACT
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US-09-759-143-110 (1-3410) x US-08-707-237A-84 (1-761)
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	1041 AGGTTCCGGAAAGCCAAG	oGlyAla	984 GCCGACAGCCCTTCTGCTGGC			869CCTGGGTGCCCAGGTAG	ySe		 yAspV	759 TGGCGACAGTGGTCCGGG		705 GTGAAGCACACCTGGCCACAG	500 uProGlySerProGly	645 TCCAGGGGCCTGGGATCCGGG	518 rProGlyAlaProGl	585 AAGAGGCTCAGCAGGATGCCC	533 pvalGlySerProGlyAlaPr	528 TAGCGTCCACGCCAGTGGTCA	551	468 ACTGGACCAATGCCCAGCACC	561	408 AGAGGCGGCACATAGGTGATG	569 a							GCCAA	638Procinglybeur		63 CACTCAGATCCT	
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2045CAGAAACTGGCGGCCAGCCCGGCAGGCCTAGGGGCTAACAGGAG 2001	100 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro 119 2000 CGGGGAGCTGGGACCCAGTGAGGCAGGCCCTCCACCCAATGTGCTGGAAGTTTTCTACG 1941	::: 120 GlnGlyLeuProGlySerProGlyAlaProGlyThrPro132	1940 CTGAGTATTTGGCCAAGTCGCTCTTGTCAATACTACCTGTGTAGCAAAGTAAATGGCGA 1881	133 138	1880 CCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGCTGGCTG	139 GlySerProGlyAlaProGlyThrProGlyGlyAlaLysGlnAlaGlyAspValGly 157	1820 TGGAGCCCATAAACAGGGATGGGGCCACCTGGGAGGCAGGAGGCAC 1773	158SerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGly 172	TATCCAGGATGGCGAGGTCCAGGCAGATGCCCCGGCCCG	lyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro	CCTGGCCTCGGTGGGCTCACCCACCACGTACG	G1yThrProG1yProG1nG1yLeuProG1ySerProG1yALaProG1yThrProG1yG1y	1809GAGACAICACAGGCACAGAGGCCCCGCAGAGCGCGGGGGGGG		1			AGAGGGAGGCOAATGTGTAAGGGAATC		1461 TGCAGGGCTGAGAAGGTGAACCCGGTGAGGGGGGCGATGTCACCACGGCCACACTG 1402		1401 TGGGACAGGCATGTGGCACCGGCAGGCACAGGGAAAGCTGCCACACTGGCCAAATAGACT 1342		1341 GCTCGAGTGCCGAATCGCTGCACCAGCCGGTCCATGACCAGAGAGAAGACCAGGGAGATG 1282		1281 GGGACTGCAGGAACA		1254 CCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCGGGCTCAGCTCTG 1198	 335 rProGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAlaProGlyThrProGl 355	1197 GGCACGCCCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAG 1144	::: 355 yProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGly 373	GTCATGAGTGCCATCCAGCTGCACAGCTCAGCCAGAAGAGCCGGCGC	roGlyProGlnGlyLeuProGl	1095 AGGGTGCGGGGCATGCGGCACACACAGTGGTGCAGCCGGGGAAGCAGGGCGCCC 1042
Qy	da oy	qa	Qy	qa	Qy	qa	δλ	QQ	δλ	qq	δλ	an c	දි සි	3 8	රි සි	3 8	ਨੇ ਜ਼ਿੰ	3 3	g qq	ΛO	g qa	Qy	qa	Οy	qq	Qy	qq	٥y	qq	Oy	Оb	δy	QQ (δλ
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qq	.
Qy	1041 AGGITCCGGAAAGCCAAGCGGGCCCGGCATGGACAGTGGGGGCGACAAGGAGGGG 985
qa	
Qy	ACAGCCCTTCTGCTGGCTCGGT
qa	431 rPro 441 431 rPro 441
δλ	927 AGIGIGGCIGCIACGCAGGAGGAGGAIGAGGGIGAGCAGGCCAAAGAGGCACICCI 870
qq	442GlyAlaProGlyThrProGlyProGlyLeuProGl 454
Qy	869CCTGGGTGCCCAGGTAGGGGCCCAGGGCACTGGTGCCCAGTCAATGGCAGGCA
q _Q	454 ySerProGlyAlaProGlyThrProGlyGlyAlaLysGlnAlaGl 469
Qy	813 AGGTAGCCCAGGCAGCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCC 760
QQ	469 yAspValGLySerProGlyAlaPro
Qy	759 TGGCGACAGTGGTCCGGGTAGAGAGGTCAGAGAGCAGGCCTCCAGTGGA 706
qq	480 oGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLe 500
Qy	705 GTGAAGCACACTGGCCACAGAAGTCCAGCAGCACCCCAGGATGAGCAGTGCCAGG 646
qq	500 uProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySe 518
QY	645 TCCAGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCC
QO	518 rProGlyalaProGlyThrProGlyGlyAlaLysGlnAlaGlyAs 533
QY	585 AAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCA 529
QQ	533 pValGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGly 550
٥y	528 TAGCGTCCACGCCAGTGGTCACTGGCTAGGAGCGGGACACACAGACCAGGCCAGC 469
qq	551561
Qy	468 ACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGC 409
qa	561GlnGlyLeuProGlySerProGlyAl 569
Qy	408 AGAGGCGCACATAGGTGATGCCTGCGGCCAAACACACTCCAGGCCAAAGGTTAGCAGG 349
qq	569 a
Qy	348 TTGACCACCAGGAGCTGGGCTTTCCGGTGCCGCAGCAGGCGGCTCACC 301
QQ	580 ySerProGlyAlaProGlyThrProGlyGlyAlaLysGlnAlaGlyAspValGlySerPr 600
Qy	300 CACAGCCTCTGGACCATAGTGGGCCGGGCTAGGGCTCAGGGGCCCGTTCAGGCA 244
Ор	3.nGlyLeuProGlySerProGlyAlaProG
δy	243 CTCCAGAACTGCTTCGTCTCGCCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCC 184
qa	620 hrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 637
Qy	183 GCCAACTGCCTAGGAATCAGCCAGGCGCCCATTCTGCCAGCCCTTTGGTGCCGGTCCAG 124
qa	638ProGlnGlyLeuProGlySerProGlyAlaProGlyThrP 651
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qa .	651 roGlyGlyAlaLysGlnAlaGlyAspValGlyS 662
Οy	63 CACTCAGATCCTGGCGG 46

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	41 bccmmcc	
7 음	11 oGlyAlaProG	
Qy	CTTCTGCTGGCTGGGGGCCCAGCGCTGCCTCTCAGCCACCAGC 92	
qa	GlyLeuProGlySerPro 44	
Οŷ	TGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGGAGGCCAAAGAGGCACTCCT 87	
Dp	442GlyAlaProGlyThrProGlyProGlyLeuProGl 454	
oy d	69CCTGGGTGCCCAGGTAGGGGGCACTGGTGTGTCCCAGTCAATGGCA	
gg «	54 ySerProGlyAlaProGlyThrProGlyGlyAlaLysGlnAlaG	
δŏ dd	GAAGGCATAGACAGAGTAGGCC. 76 	
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0y	AGC 46	
Db	- 56	
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qq	561	
Oy.	08 AGAGGCGGCACATAGGTGATGCCTGCGGCCAAACACACTCCAGGCCAAAGGTTAGCAGG 34	
ορ	69 a	
Οÿ	48 TTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGGC-	
qa	580 ySerProGlyAlaProGlyThrProGlyGlyAlaLysGlnAlaGlyAspValGlySerPr 600	
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S d	183 SCHARUTGCTARGARTCAGCCCCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCAG 124 638	
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qa	1vs 6	
Qy	70 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
Dp	662 erProGlyAlaMet-AspProGlyArg 670	

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2314 AAAAACCCTTCTCTAGGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGT 2255
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2254 AATCCACCIGCAGAGTCCCCGCATTCCAGIGCAIGGAGCCCTTCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: A.58848-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFA: (415) 398-3249
TELEFA: 910 277299
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 682 amino acids
TYPE: amino acid
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249
444
294
56
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-759-143-110 (1-3410) x US-08-397-633A-36 (1-682)
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Matches:
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                   Sequence 36, Application US/08397633A Patent No. 5773577 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
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                                                                                                                                                                                                   CITY: San Francisco
STATE: California
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                          USA
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US-08-397-633A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-397-633A-36
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1095 AGGGTGCGGGGCATGCGGCAGCAGCAGCTGGTGCA-----GCCGGGGAAGCAGGCCGCCC 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1461 TGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGCTGAAGCTGTCACCACGGCCACACTG 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1254 CCCA---TCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTG 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 GTCATGAGTGCCATCCAGC----TGCACACACCTCAGCCACGAAGAGCCGGCGC 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1401 TGGGACAGGCATGTGGCACCGGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACT 1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1733 GAACCACCCTGGCCTCGGTG-----GGCTCACCCACCACCACCACGTACG------ 1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1575 AAGCTGGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGC 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 oGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyTh 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000 CGGGGAGCTGGGACCCAGTGAGGCAGGCCCTCCACCCCAATGTGCTGGAAGTTTTCTACG 1941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 pvalGly-----SerProGlyAlaProGl 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 111 111 374 ------EuproGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGl 391
                                                                                                                                              1940 CTGAGTATTTGGCCAAGTCGCTCTTGTCAATACTACCTGTGTAGCAAGTAAATGGCGA 1881
                                                                                                                                                                                                                                1880 CCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAA 1821
                                                                                                                                                                                                                                                                                                                                                                                                  1772 -----TATCCAGGATGGCGAGGTCCAGGCAGATGCCCGGC---------CCG 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 ------ProGlySerProGlyAlaProGlyThrProGlyGlyAlaLySGlnAlaGlyAs 281
                                                                                                                                                                                                                                                                                                                                                                                                                                     173 SerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 192
100 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro 119
                                                                                                                                                                                                                                                            158 ---SerPro------GlyAlaProGlyThrProGlyProGlnGlyLeuProGly 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 rProGlyGlyAlaLySGlnAlaGlyAspValGlySerProGlyAlaProGlyThrProGl
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                                                                                                                                                                                                                                                                                                                   1820 TGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGAAGGCAC--
                                                                                                       120 GlnGlyLeuProGlySerProGlyAlaProGlyThrPro----
                                                                                                                                                                                        ----GlyProGlnGlyLeuPro---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2089 GCA-----GCACAGGGTGGCAGCAGAGGCCACATTACTTTGGCAGCAA----- 2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2314 AAAAACCCTTCTCTAGGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGT 2255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2209 GGCCTCCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCT 2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProproPheAlaSerAspProMetGlyAlaProGlyThrProGlyProGlnGlyLeuPro 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGly 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 AlaProGlyThrProGlyGlyAlaLySGlnAlaGlyAspValGlySerProGlyAlaPro 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 GluAsnPro-----GlyValThrGlnLeuAsn------ArgLeuAlaAlaHis 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2254 AATCCACCTGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCT----
                                                                                       APPLICANT: CAPELLO, Joseph
APPLICANT: FERRARI, Franco A
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                  ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Faracisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-759-143-110 (1-3410) x US-08-642-255-126 (1-682)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                          Sequence 126, Application US/08642255 Patent No. 5773249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 126:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.04e-20
370.50
35.26%
29.96%
5.95%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 682 amino acids
TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                            RY: USA
94111-4187
                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2045
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٥y	941	CAG
QQ	454	GlyGlySerArgAspProGlyProPro
٥y	968	GGGTGAGCAGGCCAAAGAGGCACT
Д	466	GlyProAlaGlyProLysGlyAlaHisGlyProAlaGlyProLysGlyAlaHisGlyPro 485
Qy	854	AGGGGCCAGGCCACTGGTGTCCCAGTCAATGGCAGGCAGGAGTAGC 807
QQ	486	AlaGlyProLysGlyAlaHisGlyProAlaGlyProLysGlyAlaGlnglyProAlaGly 505
Οy	908	CCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT 747
Db	206	ProGlyGlySerArgAspProGlyProProGlyAlaGlnGly 519
٥y	746	CCGGGTCCCGGAAGAGGTCAGAGAGAGGCCTCCAGTGGAGTGAAGCACACGTGGC 690
Д	520	ProAlaGlyProGlyGlySerArgAspProGlyPro
٥y	689	CACAGAAGTCCAGCAGCCCA
Db	534	AladinglyProAladlyProGlyGlySerArgAspProGlyProProGlyAlaGlnGly 553
οy	650	CCAGCTCCAGGGCCTGGGATCCGGCACAGCAGCCCTGCTAGCCAGCCGG 600
ДD	554	ProAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGln-GlyProAlaGl 573
٥y	599	CCCTTGGGATGAGAAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGG 543
qq	573	yProGlyGlySerArgAspProGlyProProGlyAlaGlnGly-ProAlaGlyProGlyG 593
	542	GCCGCCGCGCCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACAC 483
QQ	593	
Οy	482	AGACCAGGCCCAGCACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTTA 426
qq	613	AspProGlyBroProGlyAlaGlnGlyProAlaGlyProGlyGlySerArgAspProGly 632
Qy	425	CCCCCACTTCCAGCAGCAGCAGCACATAGGTGATGCCTGCGGCCAAACACCCCCA 366
qq	633	ProProGlyAlaGlnGly
Qy	365	GGCCAAAGGTTAGCAGGTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCA 315
QQ	644	GlySerArgAspProGlyProProGlyAlaGlnGlyProAlaGlyProGlyGlySerArg 663
Oy .	314	GCAGGCGGCTCACCCACAGCCTCTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGGGG 255
qq	664	AspProGlyProProGlyAlaGlnGlyPro-AlaGlyProGlyGlySerArgAspProGl 683
oy vo	254	CCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCC 195
Db	683	AlaGlnGlyPro
Qy	194	TAGGAATCAGCCAGGCGCCCATTTCTC
Db	869	pProGlyProProGlyAlaHisGlyProAlaGl 709
Qy	134	TGCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGCTGTGGGGCACCTCAGTGGG 75
Db	709	AlaGlyProLysGlyAlaHis
Qy	74	ACACGICTCATCACTCAGATCCTGGCCGAGGCGCGGGCTGTCACCCGGAGCCA 21
Db	729	ysGlyAlaHisGlyProAlaGlyProLysGlyAlaGlnGlyProAlaGlyProGlyGlyS 749

qq	334	
Qy	1036	CCGGAAAGCCAAGCGGCCCCGGCATGGACAGTGGGGGCGACAAGGAGGGGGCCGACAG 977
Db	354	erArgAspProGlyProProGlyAlaPro
Qy	916	CTICIGCIGGCICGGCCCACGCIGCTCCTCAGCCAC 93
Dp	364	Aspi
δλ	931	87
QQ	377	ro
ΟŊ	872	
qq	389	rgAspProGlyProProGlyAlaProGlyProAlaGlyProProGlySerArgAspPro- 408
٠. دم	829	GTCAATGGCAGGCAGGAGGCCGCCAAGACTGATCATGAAGGCATAGAC 770
ΩQ	409	
'n	769	AGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGAGCAGGCCTC 713
QQ	417	laGlyProProGlySerArgAspProGlyProProGlyAlaProGlyProAlaGlyPro- 436
δ	712	CAGTGGAGTGAAGCACACACACAGAAGTCCAGCAGCCCCACGCCCAGGATGAG 656 .
qq	437	ProGlySerArgAspProGlyProProGlyAlaProGlyProA 451
ογ	655	CAGTGCCAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCC
Dp	451	laGlyProProGlySerArgAspProGlyProProGlyAlaHisGlyProA 468
Οy	6	GGGATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGG 54
qq	468	laGlyProLysGlyAlaHisGlyProAlaGlyProLysGlyAlaH 483
٥y	541	CCGGCGGCCGCCATAGCGTCCACGCCAGTGGTCACTGAGCTGAGCAGGGGACACA 482
Dp	483	isGlyProAlaGlyProLysGlyAlaHisGlyProAlaGlyProLysGlyAlaProGlyP 503
٥٧	481	GACCAGGCCCAGCACTGGACCAATGCCCAGGACCATGGTCATGAACTTCTCCTCTACCCC 422
Dp	503	roAlaGlyProProGlySerArgAspProGlyProProGlyAlaProGlyProAlaGlyP 523
Qy	421	CACTICCAGCAGAGGGGGGCACATAGGTGATGCCTGGGGCCAAACACACCTCCAGGCC 362
Db	523	roProGlySerArgAspProGlyProProGlyAlaProGlyProAlaGlyProProGlyS 543
Oy.	vo	AAAGGTTAGCAGGTTGACCAGCAAGAGCTGGCTTCCGGTGCCCCAGCAG 311
Dρ	543	erArgAspProGlyProProGlyAlaProGlyProAlaGlyProProGlySerArgAspP 563
٥y	310	GCGGCTCACCCACACCTCTGGACCATAGTGGGCCAGGGGTAGGGCTCAGGGGCCGT 251
Dp	563	roGlyProProGlyAlaProGlyPro-AlaGlyProProGlySerArgAspProGlyPro 582
Οy	250	SAAGC
QG	583	ProGlyAlaPro
٥y	190	TGCTGCCGCCAACTG
QQ	593	AspProGlyProProGlyAlaProGl
Qy	2	TTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCC 113
	613	AspProGlyProProGlyAlaProGlyProAlaGlyProPro 626
RESULT 19 US-09-219	-849-	

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2302 CTAGGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCA 2243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2212 TCTGGCCTCCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGC 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2152 CCTAGAGACTGGGGAGAGAGGAGGGACGCCCCAGCCCCAGCTGTGCAGCTACGCACC 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2092 TCAGCAGCACAGGGTGGCAGCAGCAGCACATTACTTTGGCAGCAAGAAACTGGCGG 2033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2359 GGGCTTAGAGAT---GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCT 2303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2032 CCA-----GCCCGGCAGCCCCATGGGGCTAACAGGAGCGGGGAGCTGGGACCCAGT--- 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1939 TGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAATGGCGAC 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 GlnGlyProAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGlnGlyPro 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 SerArgAspProGlyProProGlyAlaGlnGlyProAlaGlyProGly------ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GlyGly-----SerArgAspProGlyProProGlyAla 88
                                                      APPLICANT: VAN HEBENDE, GEORGE V.
APPLICANT: VAN HEBENDE, GEORGE V.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: BOUNGER, FREDERIK A.
APPLICANT: MOOBROBK, ANDREAS
APPLICANT: WERKEW, ANDREAS
APPLICANT: WIND, RICHELE D.
APPLICANT: VAN DEN BOSCH, TANJA J.
TITLE OF INVENTION: SILTVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUTTABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Description of Artificial Sequence: Illustrative ; OTHER INFORMATION: amino acid sequence US-09-219-849-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 AlaGly-------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                               FILE REFERENCE: 2728-2
CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PALENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 -----Gly--SerArg-----
Sequence 6, Application US/09219849 Patent No. 6150081
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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371.00
32.39%
28.78%
5.96%
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                       Patent No. 6150081
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 6
LENGTH: 960
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DB:
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1084 CAIGCGCCAGC:ACAGCIGGIG	 Oy	Db 48 AspProGlyProProGlyAlaProGlyProAla 58
		QY 2146 GACTGGGGAGAGGGAGGGCGCCCAGCCCCAGCTGTGCAGCTACGCACTCAGCA 2087
	gg a	Db 39 Gly
1204 AGCTCTGGGCACGCCCTGGTACAGCCCCTGGCCCTCGCCCTCGCCCTGGTATAGAGAGAG		Qy 2200 GTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGA 2147
291 roProGlyAlaProGlyPro	qq	Qy 2257 GGTAATCCACCTGCAGAGTCCCCGCATTCCAGTGCATGCACCCTTCTGGCCTCCCT 2201
Z/8 roGlývroataclývrovrochýserargasprv 1264 CCCCAGGTGCCCATCGGAACGCCTTCATCATA	<u> </u>	US-09-759-143-110 (1-3410) x US-09-219-849-5 (1-960)
1324 CTGCACCAGCGGTCCATGACCAGAGAGAGCC	Qy	
271 spProGlyProProGly	QΩ	t Similarity: 32.90% conservative:
1384 ACCGGCACCACAGGGAAAGCTGCCACACTGGCC	Qy	Length:
::: 255AlaGlyProLysGlyAlaProGl	qa	US-09-219-849-5
1444 GAACCCGGTGAGGGCGGCTGAAGCTGTCACCACC	OY	
1504 CTFCFCCGGTGGTAGAGGGAGGCCAGTGTGTA 	Qy Op	
	QQ	SEQ ID NO 5 LENGTH: 96
1564 CAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCC	QY	; CURRENT FILING DATE: 1998-12-23 ; NUMBER OF SONS: 50 . COMPURABLE: DATE OF 2 1
	qa 	FILE REFERENCE: 2728-2 CURRENT APPLICATION NUMBER: US/
1605 ************************************	ογ	TITLE OF INV
1651 AGGTGGGAGCAGCCCACTGCCTCCAGCACCC	Qy QD	CANT: CANT: OF IN
 160 laGlyProProGlySerArgAspProGlyPro	qa ——	
141 1YPFOALAGIYPFOFFOGIYSGFAFGASPFFOGI	oy oy	APPLICANT: VAN HEEKDE, GEORGE APPLICANT: VAN RIJN, ALEXIS C APPLICANT: BOUWSTRA, JAN B.
	Qy	, Sequence J. Application 05/09219049 ; Patent No. 6150081 ; General information:
1/89 GOALAGLAGGA - AGGCACIAILCAGAIGGGC 	άδ 	RESULT 18 US-09-219-849-5
	qa	OY 61TGGGCGA 46 :::
GGCAGTGACAGACTGGCTGGACAAT	À Å	Db 728 inHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProG 744
1909 TACTACCTGTAGCAAAGTAAATGGCGACCAGA	λο d	Oy 117 AGCCCATGCTCAACACCTGCTGCTGGGGGCACCTCAGTGGGGACACGTCTCATCA 62
	qa	
1969 CCACCCCAATGTGCTGGAAGTTTTCTACGCTGAG	Qy	177 MCCCMAGGAAMCACCAAGCCCCCAAmmagagCCAACCCTTTTTTTTCATTTTTTTTTTTTTTTTTTT
	qa	Dy 23/ AACTGCFTCGCFTCGCTCTGCTCCAGAAGCTGCGGCCCTCTCCTCGCTGCCGCCCAAC 178
2026 CGGCAGCCCCATGGGGCTAACAGGAGCGGGGAGC	ΟŊ	674 aProGlyThr-ProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProG
ZUBb GCACAGGGTGGCAGCAGAGAGGCCAAATTACTTTG ::: S9 GlyProProGlySerArgAspProGlyProProG	λο —	294 CTCTGGACCATGGGCGCGGGTAGGGCTCAGGGGCCGTTCAGGCACTCCAG 23:
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	2086	GCACAGGGTGGCAGCAGAGGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCC 2027
	59	roProGlyAlaProG
		CGGCAGCCCCATGGGGCTAACAGGAGCGGGGAGCTGGGACCCCACTGAGGCAGCCCT 1970
		roAlaGlyPro 94
	1909	Pro
_	1909	GCAAAGTAAATGG
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	10	-
	1789	GGACAGCAGGAAGGCACTATCCAGGATGGCGAGGTCCAGGC
	1748	AGATGCCCGGGCCGGAACCACCTGGCCT
_	141	lyProAlaGlyProProGlySerArgAspProGlyProProGlyAlaProGlyProA 160
	1711	CTCACCCACCACCACCACGGAACGACATCACAGGCAGAGGCCCCGCAGAGCGCGGGGGG 1652
	1651	AGGTGGGAGCAGCAGC CCACTGCCTCCAGCACCCACGTGTCCATTAGGG 1606
	ì	TOOLY SOLD I GROUP COLUMN TO THE TOOL OF T
	1605	rgAspProGl
	1564	CAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTG 1505
_	219	Pro
	1504	CTTCTCCCGGTGGTAGAGGGAGCCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGT 1445
	4	GACAGGCATGTGGC 13
_	255	A 271
	8	AAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCG 13
•	271	278
	7	AGAGAAGACCAGGAGATGCCGCACTGCAGGAACAG 12
_	278	roGlyProAlaGlyProProGlySerArgAspProGly
	1264	CCCCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTC 1205
	1204	AGCTCTGGGCACGCCCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAA 1145
•	303	erArgAspProGlyProProGlyAlaProGlyProAlaGlyPro 317
	1144	TCATGAGT
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_	1084	CATGCGGCAGC:ACAGCTGGTGCAGCCGGGAAGCAGGCGCCCCAGGTT 1037

90 OX OQ OX	Q Q Q Q Q	2 6 6 6	6			
	CAGCCCCCAGCTGCAGCTACGCACCTCAGCAGGGGTGGGAGCAGAGAG 206	2005 AGGAGCGGGAGCTGGGACCCAGGGCCCTCCACCCCAATGTGCTGGAAGTTTT 1946 ::::: :	1885 GGCGACCAGGCCTGCGCACCACACACATATAGGCAGTGACACACTGGCTGAGCTG 1826	1765 GATGGCGAGCTCCAGGCAGTCCCCGGCCCGGAACCACCTGGCTC 1718	246 oGlyAlaProGlyThrProGlyProGlnGlyJeuProGlySerPro	1426 TGAAGCTGTCACCACGCCACTGTGGGATGTGGCACCGGCAG
90 O O O O O O O O O O O O O O O O O O O	60 60 60 60 60 60 60 60 60 60 60 60 60 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	c d c d	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0	67 67 67 67 67

ФФ	351 GlyT	hrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGlu 370
Qy	1244 CGCCT	TCATCATAGTGTCTCGGGCCTCGGTGCCCGGCTCAGGTCTGGGC
qq .	371 GLyGl	nG1
Qy	1190 CCTG	GTACAGCCCCTCGCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA 1131
qq	391 ProG	::: rodlyThrProGlyProGlnGly
οy	1130 TCCA	GCTGCACACGCACGAAGAGCCGGGGGCAGGGTGCGGGGCATGCGGCAGCACA 1071
qq	401 GlyS	 SerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 420
Qy	1070 GCTG	TIGGTGCAGCGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGC 1014
qq	421 ProG	euProGlySerProGlyAlaProGlyThrP
οy	1013 AT-G	GACAGCAGTGGGCCGACAAGGAGGGGGCCGACAGCCCTTCTGCTGC 964
Οβ	441 GluG	lyAlaLysGlnAlaGlyAspValGlySer
Οy	63	35GG
qq		roGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla-ProGlyThrPr 480
δy	.933 ACCA(SCTGCTACGCAGG
QQ	480 ogly	
QY	873 TCCT	
QΩ	500 uProgly	/SerProGlyAla
Qy	828 TCAA	
QQ	520 yAla	~
ογ	774 TAGA	CAGAGTAGGCCTGGCGACAGTGGT CCGGGT CCCGGGAAGAGGTCAGAGAGC 721
qq	534	GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPr 551
Qy	720 AGGG	SCTCCAGTGGAGTGAAGCACACCTGGCCACAGAAGTCCAGGCAGCCCCACGCCAGG 661
qq	551 oGly	oGlyProGlnGlyLeuProGlySerProGly·····AlaProGlyThrProGlyProGl 569
Qy	660 ATGA(3CAGTGCCAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCC
qa	569 nGly1	
QY	200 GCCC	TTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGT 556
qa	587 sHis	ieuglyglyalatysglnalaglyaspvalglyserProGlyalaProGlyThrPr 607
QY	555 GC	CCCAGATGAAGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAG 499
Qa	607 oglyi	07 oGlyProGlnGlyLeuProGlnS
Qy	498 CCTAC	SGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCATGGTCATG 439
qa	615 rPro	oglyAlaProGlyThrProGlyPro
Qy	438 AACTI	CACATAGGTGA
qq	625	GlnGlyLeuProGlySerProGlyAla
QY	378 AAACA	AA -
QQ	634 oGly1	hrProGlyProGlnGlyLeuProGlySerProGlyAla
Οy	320	
QQ	654 uGlyG	uGlyGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAl 674

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2290 CAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCA------GAG 2240
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237 AACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTCCTTGCTGCCGCCAAC 178
                                                                 177 TGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGCTGCTGCCGGTCCAGCTTCTC 118
                                                                                     117 AGCCCATGCTCAACACCTGCTGCTGGGGCACCTCAGTGGGGACACGTCTCATCA---- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AlaProGlyThrProGlyGluGlyGlnGlnHis 90
                               694 lyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly----
                                                                                                                                                                                                                                                                                 US-08-397-633A-26
Sequence 26, Application US/08397633A
Sequence 2735577
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREFF: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
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259
41
296
259
51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-759-143-110 (1-3410) x US-08-397-633A-26 (1-762)
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Conservative:
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                                                                                                                                                                                                   ----CTCAGATCCTGGCCGA 46
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IBM PC compatible
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TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACFERISTICS:
LENGTH: 762 amino acids
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NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,0
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30.36%
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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              CCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA 1131
                                                                              1130 TCCAGCTGCACAGCTCAGCCACGAAGAGCCGGCGCAGGGTGCGGGGCATGCGGCAGCACACA: 1071
                                                                                                                                                                   UGlyGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAl 674
                                               ----- 400
                                                                                                              401 GlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 420
                                                                                                                                                                                                                     964
                                                                                                                                                                                                                                                                                   933 ACCAGCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAGAGGCAC 874
                                                                                                                                                                                                                                                                                                                                                                                        oGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLe 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           828 TCAATGGCAGGCAGGA-----GGTAGCCCAGGCAGCCCCCAAGACTGATGAAGGCA 775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTGGACCATAGTGGGCCAGGCGGG---TAGGGCCTCAGGGGGCCCGTTCAGGCACTCCAG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aproGlyThr-ProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProG 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1070 GCTGGTGCAGCCGGGGAAGCAGGCGCCCAGGTTCC---GGAAAGCCAAGCGGGCCCGGC
                                                                                                                                                                                                               1013 AT-GGACAGCAG-----TGGGGCGACAAGGAGGGGGCCGACAGCCCTTCTGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                           774 TAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGT---CCCGGAAGAGGGTCAGAGGG
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| 615 rProGlyAlaProGlyThrProGlyPro----
                                          391 ProGlyThr---ProGlyProGlnGly----
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              1190
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117 AGCCCATGCTCAACACCTGCTGCTGGGGGCACCTCAGTGGGGACACGTCTCATCA 62	Qy Dp	2179 CCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGA
61CTCAGATCCTGGCCGA 46 :::	λδ	CAGCCCCCAGCTGCAGCTACGCACCTCAGCAGCACAGGGGGGGG
2,	oy Oy	CCACTTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGAGCCCCCATGGGGCTAAC
Facent No. 57,5249 GENERAL INFORMATION: APPLICANT: CARPELLO, Joseph APPLICANT: FERRARI, Franco A.	QY Dp	2005 AGGAGCGGGAGCCAGTGAGGCAGGCCTCCACCCCAATGTGCTGGAAGTTT 1946 :::::: ::::
ENTION: ENTION: QUENCES: CE ADDRES	Qy Dp	1945 CTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAAT 1886
. 4 E S	QQ QD	GACTGGCTGAGCTG
COUNTY: USA ZIF: 94111-4187 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	δ qα	1825 GACAATGGAGCCCATAAACAGGGATGGGGCCACTGGGACAGCAGGAAGGCACTATCCAG 1766
52"5	oy.	1765 GATGGCGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCCTGGCCTC 1718
APPLICATION NUMBER: US/08/642,255 FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:	Q da	1717 GGTGGGCTCACCACCACACACACAGAGACATCACAGGCAGAGGCCCC 1667
NAME: KOWLAND, BEITTAM 1. REGISTRATION NUMBER: 20,015 REFERENCE/DOCKET NUMBER: A55556-3/BIR TELECOMMUNICATION: INFORMATION:	λ Q	1666 GCAGAGCGGGGGGGAGGAGCAGGCCACCTCCCAGCACCCACGTGTCCATTAGG 1607
TELEFAN: (415) 494-8771 TELEX: 910 277299 FHT UR INFORMATION FOR SEC ID NO: 114:	V da	1606 GAAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGCTCCTCACTGCT 1547
SEQUENCE CHARACTERISTICS: LENGTH: 762 amino acids TYPE: amino acid STRANDENESS: single TODGIAGY: linear	QV Db	1546 AGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGGTTCTCCCGGTGGTAGG 1487 [
⊕ ⊞	Oy Pp	1486 GGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGC 1427
Alignment Scores: 5.68e-22 Length: 762 Score: 391.00 Matches: 259 Secret Similarity: 35.17% Conservative: 41 Best Local Similarity: 30.36% Mismatches: 296 Ouery Match: 6.28% Indels: 259	Oy Db	TGAAGCTGTCACCACGGCCACACTGTGGCACTGTGGCACCGGCAG TGAAGCTGTCACCACGGCCACTGTGGCATGTGGCACCGGCAG TGAAGCTGTCACCACGGCAGCAGCAATGGAGAGCTGCCAAATAGACTGCTCGAAATGCTGCCCGAAATGCTGCCCGAAATGCTGCCCGAAATGCTGCCCGAAATGCTGCCCGAAATGCTGCTGGCCAAATAGACTGCTCGAAATGCTGCTGAAATGCTGCTCCAAATGCTGCTCGAAATGCTGCTCGAAATGCTGCTCGAAATGCTGCTCCAAATAGAATAGAATGCTGCTCCAAATAGAATGCTGCTCCAAATAGAATAGAATGCTGCTCCAAATAGAATAGAATAGAATGAAATGCTGCTCGAAATAGA
Saps: 51 Saps: 51 Saps: 51 Saps: 51 Saps: 51 Saps: 52 Saps: 52	- Op	320 ProGlyThrProGlyProGlnGlyLeuProGlySerPro
76 GlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHis 90 2290 CAACTAGGAGGCTAGCTGTTAACCCTGAGCTGGGTAATCCACCTGCAGAG 2240	Qy	1271 GGAACA
TCCCGCATTCCAGTGCATGCAGCCTTCTGGCCTCCTGTATAAGTCCAGACTGAAACC	Oy Dp	1244 CGCCTTCATCATAGTGTCTCGGGCCTCGGTGCCCGGCTCAGGTCTGGGCACGC 1191 1

2066 158 2006 166 1946 180	1826 198 1766 208 1718	1667 245 1607 260 1547	1487 285 1427 299 1;377 318 1332 331	13 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
CAG Gly CCA Gln AGG :::: Gln	GGCGACCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGACTG		4 , 9 – 4 1 1 4 0	
2119 140 2065 159 2005 2005 167 1945	1885 187 1825 199 1765 208	1717 228 1666 245 1606 261	1546 276 1486 285 1426 300 1376 1331	33 35 37 19 13
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. vo	1070 GCTGG	GAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCCCGG
QG	420 ProG1	GlyThrProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 439
λ ₀ (13 A7	TGGGGCGACAAGGGGGCCGACAGCCTTCTGCTGC 9
ga	40 G]	inHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGly 45
Qy Dp	963 TCGGT(::: 460 AlaPro	TCGGTGGGGCCAGCGCTGCCTCCTCAGGCC 934 ::
0y	933 ACCAG	ACCAGCAGTGTGGTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAGAGGCAC 874
qa	479 oGlyP	
Qy	873 TCCT-	CCTGGGTGCCCAGGTAGGGGGCCCAGGGCACTGGTGTCCCAG 829
qq	499 uProG	uProGlySerProGlyAlaProGlyThrProGlyGluGluGlnGlnHisHisLeuGlyGl 519
Oy	828 TCAAT	TCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATGAAGGCA 775
Dp	519 yAla	ysGlnAlaGlyAspValGlySerProGlyAlaPro532
Qy	774 TAGAC	AGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGGC 721
Dp	533	GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPr 550
Qy	720 AGGGC	CTCCAGTGGAGTGAAGCACACCTGGCCACAGAAGTCCAGCAGCCCCACGCCCAGG 661
οqα	550 oGlyF	oGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGl 568
Qy	660 ATGAG	CAGTGCCAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCC
Dp	568 nGlyI	nGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHi 586
Qy	600 GCCCI	CTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGT 556
Db	586 sHis	euGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAlaProGlyThrPr 606
Qy	555 GC	
QQ	606 oGlyF	roGlnGlyLeuProGly
Qy	498 CCTAGO	AGCGGGACACAGACCAGGCCCAGCACTG
qa	Ρŗ	lyAlaProGlyThrProGlyPro
Oy	438 AACTI	CGGCACATAGGTGATGCCTGCGG
qa	624G	GlnGlyLeuProGlySerProGlyAla
٥y	78 AAA 	CACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGGCTGGGCTTTCCGGT 321
Dp	~	hrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGl 653
Qγ	320	
Db	653 uGlyG	yGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerPrOGlyAl 673
Οÿ	294 CTCTG	TGGACCATAGTGGGCCAGGCGGGTAGGCCTCAGGGGGCCGTTCAGGCACTCCAG 238
Db	673 aProG	lyThr-ProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProG 693
0y	237 AACTG	TTG(
Dp	693 lyPro	oGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 708
Qy	177 TGCCT	CCTAGGAATCAGCCAGGCGCCCATTCTGCCAGCCTTTGGTGCGGGTCCAGCTTCTC 118

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729 TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGGT---CCCGGAAGAGGT 729
                                                                                                                                     549 GlyThrProGlyProGlnGlyLeuProGlySerProGly-----AlaProGlyThrPro 566
                                                                                                                                                                                     668 CGCCCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCAGCCCTGCTA 609
                                                                                                                                                                                                                                                                                                          506 TGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCCAGCACA 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 CCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCC, 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      446 TGGTCATGAACTICTCCTCTACCCCCACTICCAGCAGCAGAGGCGGCACATAGGIGAIGC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       634 -----ProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            710 -----ProGlnGlyLeuProGlySerProGlyAla---ProGlyThrProGlyGl 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     725 uGlyGlnGlnHisHisLeuGly------GlyAlaArgGlnAlaGlyAspValGl 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 AGCTTCTCAGCCCATGCTCAACACCTGCTGCTGGGGCCACCTCAGTGGGGACACGTCTC 66
                                        534 ------GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro
                                                                                        28 CAGAGAGCAGGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGAAGTCCAGCAGCCCCA
                                                                                                                                                                                                                                567 GlyProGlnGlyLeuProGlySerProGlyAla-----ProGlyThrProGlyGluGly
                                                                                                                                                                                                                                                                                                                                                                     563 AGGACAGTG---CCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                605 GlyThrProGlyProGlnGlyLeuProGly------
                                                                                                                                                                                                                                                                             608 GCCAGCCGGCCCTTGGGATGAGAAGA-------GGCTCAGCAGGATGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 84, Application US/08707237A
Patent No. 5830713
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Capello, Joseph
APPLICANT: Crissman, John W.
APPLICANT: Crissman, Mary A.
TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
TITLE OF INVENTION: REPETITIVE DNA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     625 -------GlnGlyLeuProGlySerProGlyAla-----
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San Francisco

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2290 CAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCA-----GAG 2240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2179 CCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGGAGGGACGCCC 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2347 GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTTGGGTGTGTCT--- 2291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 GlyProGlnGlyLeuProGlySerPro---GlyAlaPro-------GlyThrProGly 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 GlySerProGly------AlaProGlyThrProGlyGluGlyGlnGlnHis
                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-759-143-110 (1-3410) x US-08-707-237A-84 (1-761)
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: A-55186-10/WHD TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
ROOK APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-COT-1987
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION ONDER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTOORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
                                                                                                                                                               APPLICATION NUMBER: US/08/707,237A FILING DATE: 03-SEP-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 US 08/053,049
                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 781-1989
             ZIP: 94111-410,
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08 FILING DATE: 22-APR-1993 PRIOR APPLICATION DATA:
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 761 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393.00
35.17%
30.36%
6.31%
United States
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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Best Local Similarity:
                                                                                  COMPUTER:
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209 lyThrProGl	1717 GGTGGGCTCA	229 GlyG	1666 GCAGAGCGCG	1 ::: 246 oGlyAlaPro	1606 GAAGGGAGCT	262GlyAla	1546 AGCACCTCCA	277	.1486 GGAGGCCAGT	286 lyLeuPro	1426 TGAAGCTGTC	301GlnGlnH	1376	320 ProGlyThrP	1331 CGAATCGCTGG	. 333GLyA.	1271 GGAACA	351 GlyThrProG	1244 CGCCTTCATCA	371 GlyGlnGlnH	1190 CCTGGTACAGO	_	1130 TCCAGCTGCAC	401 GlySerProG	1070 GCTGGTGCAG	421 ProGlyThrP	1013	441 GluGlyGlnG	998 GCGACAA(461 AlaProGlyT	941 CCTCAGCCACC	478 GlyThrProGl	881 AGAGGCACTCC			518 LeuGlyGlyAl
qa	Qy	qa	Qy	qa	Qy	qa	δλ	qa	Qy	qa	Qy	qq	Oy	qа	Qy	QO	Qy	qa	Qy	qq	Qý	đ	Qy	qa	Qy	qq	Qy	qq	Οy	qq	γo	qq	δλ	ДQ	δλ	qq
T APPLICATION DAT	ING DATE:	ATTORNEY AGENT INFORMATION: NAME: Rowland, Bertram I	REGISTRATION NUMBER: 20,015 REFERENCE/DOCKET NUMBER: A-58848-1/BTR PROP-011-1		; TELEFAX: (415) 398-3249 ; TELEX: 910 277299	; INFORMATION FOR SEQ ID NO: 31: ; SEQUENCE CHARACTERISTICS:	; LENGTH: 762 amino acids ; TYPE: amino acid	STRANDEDNESS: single TOPOLOGY: linear	MOLECULE TYPE: peptide US-08-397-633A-31		2.8e-22 Length: 395.00 Matches:	t Similarity: 34.50% Conservative: ocal Similarity: 30.06% Mismatches:	6.35% 1	US-09-759-143-110 (1-3410) x US-08-397-633A-31 (1-762)	r)	76 GlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHis				Db 111 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 126		:::	OY 2119 CAGCCCCAGCTGTGCAGCTACGCACCTCAGCAGGGTGGCAGCAGAGAG 2066	Db 141 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGln 159	QY 2065 CCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGGCTAAC 2006		ATGTGCTGGAAGTTTT		GTGTAGCAAAGTAAAT	182	1885 GGCGACCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTG		SCAGGAAGGCACTATCCAG	:::	GGCAGATGC	

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|aProGlyThr---ProGlyProGlnGlyLeu-ProGlySerPro----- 276
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|HisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAla 319
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lyProGlnGlyLeuProGlySerProGlyAlaPro-GlyThrProGlyGlu 228
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qa	518 LeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAlaPro 533	; COUI	DONTRY: U
Qy	782 TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGT 729		MEDIUM TYPE
qa	534GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 548	;	OPERATING S
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CCACAGCCTCTGGACCATAGTGGGCCAGGCGGG---TAGGGCTCAGGGGGCCGTTCAGG 246
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                                         lyThrProGlyProGlnGlyLeuProGlySerProGly-----AlaProGlyThrPro 566
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NVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE ENVENTION: OF PRIXATIC CROSS-LINKING SEQUENCES: 105
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E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                               EADABLE FORM:

YPE: Floppy disk

: ISM PC compatible

SYSTEM: PC-DOS/MS-DOS

:: PatentIn Release #1.0, Version #1.25
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APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

TITLE DE INVENTION: DIAGNOSIS OF PROSTATE CANCER

CURRENT APPLICATION NUMBER: US/09/605,785

CURRENT FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 835

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 706

LENGTH: 123
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APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1490 TACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATAC 1525
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OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Mismatches:
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Matches:
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97.83%
94.57%
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                       6.648
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Wang, Aijun
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US-09-605-785-706
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 -----GlySerProGlyAlaProGlyThrProGlyProGln------- 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-759-143-110 (1-3410) x US-08-642-255-120 (1-762)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
Indels:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REPERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPONE: (415) 494-8700
TELEFAX: (415) 494-8701
TELEFX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 762 amino acids
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Matches:
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34.50%
30.06%
6.35%
                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-642-255-120
                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                    linear
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Best Local Similarity:
Query Match:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                            TCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCCAGTCTATTTGGCCAGT 1357
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                                                                                                                                                                                                                                                                     21 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 40
                                                                                                                                                                                                      GAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTC
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                                                                                                                                                                             US-09-759-143-110 (1-3410) x US-09-525-397-36 (1-255)
                                                                                                                Conservative:
                                                                                                                            Mismatches:
Indels:
                                                                                       Length:
Matches:
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                       TOPOLOGY: linear MOLECULE TYPE: No. 6252047e
                                                                                      7e-91
1287.00
100.00%
100.00%
20.05%
          STRANDEDNESS: single
amino acid
                                                                                                                             Best Local Similarity:
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                                                                                                                 Percent Similarity
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                                                                           Alignment Scores:
                                               US-09-525-397-36
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1673 TCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTT 1732
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                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C9
                                                                                                                                                                                                                                                                                                                                                                                                   944
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Mismatches:
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                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 571
LENGTH: 84
Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan Louise
Jiang Yuqui
Reed, Steven G.
Kalos, Michael
Fanger, Gary
Retter, Mark
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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452.00
100.008
100.008
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                                                                                                                                            Solk, John
Day, Craig
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APPLICANT:
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APPLICANT:
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DB:
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1672

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COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-759-143-110 (1-3410) x US-09-071-710-36 (1-255)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FASLEDG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
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                                                                                                                                                                                                                                                                                                            6083.US.P1
                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
100 Abbott Park Road
                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: No. 6130043e
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER; IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
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100.00%
100.00%
20.05%
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60064-3500
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Best Local Similarity:
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                                          COUNTRY:
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                                                                                  APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KATOCHVIL, JON D.
APPLICANT: RATOCHVIL, JON D.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
GURRESPONDENCE ADDRESS: 41
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/09/525,397
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STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/09525397 Patent No. 6252047 GENERAL INFORMATION:
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APPLICANT: Reed, Steven G.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210/21.44662
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 107
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Best Local Similarity:
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### PRICAMEST Hallocker, Stans Louise Pablicher	; GENER ; APPL	AL INFORMATION: ICANT: Dillon, Davin C.	Qy	_
APPLICANT: N. J. Janagchan: AND DIAGNOSIS APPLICANT: AL Janagchan: AND JANAGCHAN: AND JANAGCHAN: AL JANAGCHAN: AL JANAGCHAN: AL JANAGCHAN: AL JANAGCHAN: AL JANAGCHAN: AL JANAGCHAN: AND MATHODS FOR THEIR USE CURRENT APPLICATION COMPUTED FOR IMMUNOTHERAPY AND DIAGNOSIS AL JANAGCHAN: AL JANAG	; APPL	uis	qa	 221 AlaAla
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERARY AND DIAGNOSIS TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERARY AND DIAGNOSIS TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERARY AND METHODS FOR THEIR USE CONTRIBUTION: COMPOUNDS FOR IMMUNEST INCOME. 1202 1203 1204 1204 1204 1204 1204 1205 1	; APPL ; APPL	ICANT: Xu, Jiangchun ICANT: Mitcham, Jennifer Lynn	Qy	
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NUMBER OF SEQ ID NOS: 1999-07-13 SEG OF ARE: 1999-07-13 EMERCH: 553	; FILE		Qy	1064 CACCAC
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ORGANISM: Homo sapien Organism: 1.61e-211 Length: 553 Organism: 2861.00 Marches: 553 Organism: 2861.00 Marches: 553 Organism: 2861.00 Organism: 2861.00 Organism: 100.004 Mismarches: 0 Organism: 100.004 Mismarches: 0 Organism: 0 Organism: 100.004 Mismarches: 0 Organism: 0 Orga	TYP	53	qq	281 SerTrp
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APPLICANT: MILLON, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: MILCHAM, Jennifer L.
APPLICANT: MITCHAM, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Fanger, Gary
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APPLICANT: Fanger, Gary
APPLICANT: Relea, Mark
APPLICANT: Role, Michael
APPLICANT: Calg
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DAGNOSIS OF PROSTATE CANCER
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CURRENT PRILICATION NUMBER: US/09/439,313
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APPLICANT: MILCHAM, JULION, DAVIN C.
APPLICANT: MILCHAM, JULION, DAVIN C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Handerson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Renger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Davick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITION SAND METHODS FOR THE THERAPY AND
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FILE REFERENCE: 210121.427C16
541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 113
                                                   Sequence 113, Application US/09605785 Patent No. 6321716
                                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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                                                                               GENERAL INFORMATION:
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                                     -09-605-785-113
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TYPE: PRT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                     210121.427C3
                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MAKi, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 anino acids
TYPE: amino acid
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Best Local Similarity:
Query Match:
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                                Homo sapiens
                MOLECULE TYPE: protein ORIGINAL SOURCE:
STRANDEDNESS: single
        linear
                                                                                          Best Local Similarity:
                                                                                 Percent Similarity:
                                        US-09-020-956-113
                                ORGANISM:
                                                        Alignment Scores:
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         GCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT
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STREET: 6300 Columbia Center, 701 Fifth
CITY: Seattle
STATE: WA
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ZIP: 98104
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Patent No. 6262245
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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(without alignments) 6802.181 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                           OM nucleic - protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                   262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                                                                                         BLOSUM62
Xgapop 10.0 , Ygapext (Ygapop 10.0 , Ygapext (Ygapop 6.0 , Ygapext Delop 6.0 , Delext ...
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Maximum DB seq length: 200000000
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                                                                                                                                                                                               Title:
Perfect score:
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Command line parameters:

-MODEL-frame+_n2p.model -DEV=xlp
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-Q=-Cgn2_1/USPTO_spool/US09759143/runat_05062003_111320_23081/app_guery.fasta_1.3591
-DB-ESSWed_Partents_AA -OFMT-fastan -SUFFIX-rai -MINMATCH=0.1 -LOOPCL=0
-LIOOPEXT-0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi
-LIST-45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MN=0 -ALIGN=45
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-USFR-US09759143_eCGN_1_126_erunat_05062003_111320_23081 -NCPU=6 -ICPU=3
-NO_MMAP -LARCEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREOUT=30 -TRANSPOP=10 -XGAPEXT=0.5 -FGAPOP=6

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/cgn2_6/ptodata/2/laa/pcTuS_COMB.pep:*
/cgn2_6/ptodata/2/laa/pcTuS_COMB.pep:* /cgn2_6/ptodata/2/laa/5A_COMB.pep:*/cgn2_6/ptodata/2/laa/5B_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result		Query				
NO.	Score	Match	Match Length DB	DB	ID	Description
-	2861	4 4 4				
4	4004	7	000	,	02-03-070-60-60	113,
7	2861	44.6	553	4	uS-09-030-607-113	
3	2861	44.6	553	4	US-09-605-785-113	113,
4	2861	44.6	553	4	US-09-439-313-113	113,
S	2861	44.6	553	4	US-09-352-616A-113	113
9	2861	44.6	553	4	US-09-602-877A-101	101
7	2861	44.6	553	4	US-09-232-149A-113	113,
8	1420.5	22.1	371	4	US-09-605-785-708	
6	1287	20.1	255	4	115-09-071-710-36	2007
10	1287	20.1	255	4	US-09-525-397-36	, 4
11	452	7.0	84	4	US-09-439-313-571	
12	426	9.9	123	4	US-09-605-785-706	706,

Sequence 120. App	m	84,	114,	26, 4	5. A	9	126	36	84		26,	21,	~	21,	21,	-	31,	62,	132	53, 7	68	103,	101,	75, 1	103,	Sequence 103, App	50, A	72,	4	49	'n	Sequence 73, Appl
US-08-642-255-120	-08-397-633A-	-08-70	-08-64	-08-36.	US-09-219-849-5	Ξ	US-08-642-255-126	-08-397-		US-08-642-255-114	US-08-397-633A-26	US-08-963-825-21	US-09-500-811-21	US-09-570-573-21	US-09-548-608-21	US-08-642-255-120	3-397-633A-	3-64	3-64	US-08-397-633A-53	3-17	US-08-477-509B-103	-08-64	-70,	-482	-444	-08-397-633A	642	US-08-931-820-4	-09 - 219	-08 - 931 - 82	US-08-642-255-73
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ALIGNMENTS

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Sequence 113, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: DILII, Davin C,
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 178
                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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STREET: 6500
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Akimura, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramcto, K., Hiracka, T., Imotani, K., Ishii
"Y., Ito, M., Kawai, J., Koʻjima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Taqawa, A., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Tayanishi, A., Muramatsu, M., and Hayashizaki, Y.
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BB701488 RIKEN full-length enriched, in vitro fertilized eggs Mus musculus cDNA clone 7420429L15 3', mRNA sequence.
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2111 TGGGGGCTGGGGCGTCCCTCTCTCCCCCAGTCTCTAGGGCTGCCTGACTGGAGGCC 2170
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                                  Email: genome.res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayafstsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNa.libraries for rappid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wadiiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                  Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                             2291 AGACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTT 2343
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .000 CCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCG 1059
                                                                                                                                                                                                                      Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5" GAGAGAGAGGACCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 TGGATTTGGCCCTGCTGGTTGGGAGTGGGGCTGGCTGGACTTTTGTGGCCAGGTGTG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 CITTACTCCATTGGAGGCCTTACTCTCCGACCTCTTCCGGGACCCAGACCACTGCCGCCA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 CTTTGGCCTCCTCACCCTCATTTCCTCATCTGCAGCCACTCTGTTTGTGACGGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           940 GGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCTCCTTGTCGCC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 GGAGGCAGTACTGGGCCCACCCGAGCCGCAGAAGGGTTGTTGGTCTGTCCCGTGTCGCG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 CCGATGCTGCCCATGCCACGTTGGCCTGGCTTTCCGGAATCTGGGTACCCTGTTTCCCCG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         582 TCTTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       642 TGGAGCTGGCACTGCTCATCCT - - GGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700 CTTCACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     760 GGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          820 TGCCATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    880 CTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                              /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia
                                        /clone_lib="RIKEN full-length enriched, in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%; Score 352.8; DB 10; Length 509; 83.3%; Pred. No. 2.1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82; Indels
                                                                                                            /tissue_type="in vitro fertilized eggs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1060 GCTGCACCAGCTGTGCTGCCGCATGCCCCG 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 GCTGCAGCTGTGCTGCCGCATGCCTCG 509
/db_xref="taxon:10090"
/clone="7420429L15"
                                                                                                                                 /dev_stage="egg"
/lab_host="DH10B"
                                                                    fertilized eggs"
                                                                                       /sex="female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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41

9, 2003, 19:43:37

completed: June

Search

Job time : 4214 secs

/organism="Mus musculus"

Source

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AW135465
UI-H-BII-aca-e-07-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2713812 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          676 TGATCCCAGGGCCCTGGGAGGCTAGGACTTGTCAATCCTGGGTTTGGGGCTGTGCATTCT 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             736 TGTGGGCCAGGTTTCGTCCTTCGAGGCCTGTCT---TGGCCTTTTCCGGGGACCG 792
                                                                                                                TGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCA-GCAGGTGTTGAGCATGGGCTGAG 120
                                                                                                                                     AAGCTGGACCTGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGTGCTGATTCCTAGGCAA 195
                                                                                                                                                                                                                                                                          AGTTCTGGAGTGCCT---GAACGGCCCCCTGAGCCCTACCCGCC-TGGCCCACTATGGTC 289
                                                                                                                                                                                                                                                                                                                                         CAGAGGCTGTGGGGTGAGCCGCCTGCTGCGCACCGGAAAGCCC--AGCTCTTGCTGGTCA 347
                                                                                                                                                                                                                                                                                                                                                                                                            348 ACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AAGCTGGACC-GGCACCAAAGGGCTGGCAGAAATGGGCGCCTG-GCTGATTCCTAGGCA- 177
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 370)
                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGC----TGCTGGAAGTGGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGTGCA-TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACC-ACTGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             627 CGGAICCCAGGCCCCIGGA-GCIGGCACIGCICAICCIGGGCGGIGGGGCIGCIGGACIIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              686 TGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           575 CTGAGCCTCTTT -- CTCATCCCAAGGGCC ---- GGCTGGCTAGCAGGGCTGCTGTGCC
                                                                  16 GGAACCAGCCTGCACGGCTGGCTCCGGGTGACAGCCGCGCGCCTCGGCCAGGATCTGAG
                                                 2 GGAACCAGCCTGCACGCGCTGGCTCCGGGTGACAGCCGCGCGCCTCGGCCAGGATCTGAG
                                                                                                                                                                                                                                                      •••• GTTGGCGGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGAGC
                 Gaps
                                                                                                                                                                                                 39;
               Indels
                 0; Mismatches 128;
No. 2.3e-38;
   Pred.
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                 Conservative
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   Best Local Similarity
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KEYWORDS
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REFERENCE

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/clone='Inba"kOlicape Sub13"
/lab_host="NALLCAPE Sub13"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)
/lab_host="DH10B (L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-remail.nil.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at:
www-bio.llnl.gov/bbtp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1991 CAGCICCCCGCICCIGITAGCCCCAIGGGGCIGCCGGGCIGGCCGCCAGITICIGIIGCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:2713812"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_LIB-NCI_CGAP_Pr22
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TAG_SEQ=AAGTG"
109 c 101 g
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                                                                                                             Unpublished (1997)
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                                                                             Tumor Gene Index
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Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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          AUTHORS
TITLE
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/dev_stage="45 years old"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; lst
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from 5,000-10
,000 microdissected, histologically normal prostate
epithelial cells. Double-stranded cDNA was ligated to
EcoRI adaptors, 5 cycles of PCR applied to the cDNA with
an adaptor-specific primer, and the resulting PCR product
subcloned into pAMP10 by the UDG-cloning method (Life
Technologies). Average insert size is 600 bp. NOTE: Not
directionally cloned. This library was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index.

Unpublished (1997)

Email: cgapbs-rémail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortiun/LLNL at:

Www-blo.llnl.gov/bbrp/image.html

Seq primer: -40ml3 fwd ET from Amersham
                                                                                                                                                                                                                                                                                                                                                            AA579486 1389 bp mRNA linear EST 03-SEP-1997 of 33907.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:915612 similar to contains element MSR1 repetitive element ;, mRNA
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
                                                                             485 GTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_Pr1"
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/db_xref="taxon:9606"
/clone="IMAGE:915612"
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Location/Qualifiers
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AA579486.1 GI:2357670
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AA579486/c
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="IxaAGE:4297170"
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/clone="IxaAGE:4297170"
/clone="Togan: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggcgcctcggcc); Site_2: Sfil (ggcattatggcc); Site_1: Sfil (ggccattatggcc); Site_1: Sfil (ggccattatggcc); Site_2: Sfil (ggccattatggcc); Site_1: Sfil (ggccattatggcc); 
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                                                                                                                                                                                                                                                                                                   3215 TTTGCAATAATGTCGTCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCA 3274
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                                                                                                                                                 3095 CCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAAACTC 3154
                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 906)
                                                                                                                                                                                     261 CCTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                              Email: cgapbs remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Plate: LLCM1150 row: n column: 19
High quality sequence stop: 564.
Location/Qualifiers
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       Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was
                                                 61 GTGATGAGACGTGTCCCCACTGAGGT - GCCCCACAGCAGCAGGTGTTGAGCATGGGCTG 118
                                                                                                                                                                                                                                                                                          AGAAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAG 178
                                                                                                                                                                                                                                                                                                                                    239 TGGAGTGCCTGAACGGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTG 298
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                                                                                                                                                                                                                                      Score 381.2; DB 10; Length 650;
Pred. No. 3.4e-41;
0; Mismatches 118; Indels 12; Gaps
prepared and sequenced in Mouse Genome Encyclopedia
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120845 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
AW787124
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                                                                                                                                                                                             tch 11.2%; al Similarity 79.2%; 494; Conservative
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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                                                                                                                                              pooled tissue normalized cDNA libraries for
     Euteleostomi;
                                               1 (bases 1 to 537)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTGAACGGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 GCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTGGAGT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.8%; Score 369.4; DB 10; ilarity 85.0%; Pred. No. 1.3e-39; Conservative 0; Mismatches 76;
                                                                                                                                                                EST discovery in swine Unpublished (2000) (Unpublished (2000)) (Unpublished (2000)) (USDA, ARS, US Meat Animal Research Center USDA, ARS, US Weat Animal Research Center Po Dex 166, Clay Center, NE 68933-0166, USDA, 402 762 4366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTACAGGACG
Plate: 45 row: C column: 12
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
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1. .537
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Email: cgapbs_rémail.nih;gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LiAMIll37 row: n column: 24
High quality sequence start: 2
High quality sequence stop: 630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 TIGAGCAIGGGCIGAAAGCIGGACCGGCACCAAAGGGCIGGCAGAAAIGGGCGCCIGGC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 TGATTCCTAGGCAGTTGGCGGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 AGACGAAGCAGTICTGGAGTGCCTGAACGGCCCCTGAGCCCTACCCGCCTGGCCCACTA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 TGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTGG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 TCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 CTCTGCTGCAAGTGGGGGTAGAGGAGATCATGACCATGGTGCTGGGCATTGGTC 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cloud_lib="NCI_CGAP_Lig"
/lab_host="DHIOB (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMv-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.4%; Score 389.4; DB 13; Length 630; 79.4%; Pred. No. 2.9e-42; Live 0; Mismatches 116; Indels 11; Gaps
                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                       /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                        /clone-"IMAGE:5050583"
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Matches 490; Conservative
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FIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

(11), 1757-1771 (2000)

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Email: genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci.P., Shibata.Y., Hayasu.N., Sugahara.Y., Shibata.K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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/clone_lib="RIKEN full-length enriched, adult male urinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
Fre Institute of Physical and Chemical Research (RIKEN)
1-7-2 Suebliro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
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/dev_stage="adult"
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                                                     612 AGTAGGCCCTGCTGATC 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB627844.1 GI:16465416
645 AGCTGGCACTGCTCATC 661
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/note="Site_1: Sall; Site_2: BamHI; cDNA library was

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BI145201 630 bp mRNA linear EST 05-JUL-2001 602909395F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5050583 5',
                                                                                                                                                                                                                                                                                                                                 /note="multiple clone assembly from multiple libraries and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 630)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 CAGCAGCAGGTGTTGAGCATGGGCTGAGAAGCTGGACCGGCACCAAAGGGCTGGCAGAAA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CAGCAGCAGGTGTTGAGCATGGGCTGAGAAGCTGGACCGGCACCAAAGGGCTGGCAGAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACAGCCGCGCCCTCGGCCAGGATCTGAGTGATGAGACGTGTCCCCACTGAGGTGCCCCA 60
Walker,M.G., Volkmuth,W., Sprinzak,E., Hodgson,D. and Klingler,T. Prediction of gene function by genome-scale expression analysis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTTGGCCGCAGGCATCA
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                                                                                                                                                                                                                                                                           /clone_lib="Homo sapiens prostate adult"
                                                                                                                                                                                                                                                                                                                                                                                                                              11.5%; Score 391; DB 9;
ilarity 97.0%; Pred. No. 2.1e-42;
Conservative 0; Mismatches 10
                                                                                                                   Incyte Pharmaceuticals
3174 Porter Drive, Palo Alto, CA 94304,
co-expressed with known prostate-cancer
Location/Qualiflers
                                          prostate cancer-associated genes
Genome Res. 9 (12), 1198-1203 (1999)
                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                               /tissue_type="prostate"
/dev_stage="adult"
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                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IPCA-8"
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20082966
Contact: Walker MG
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      AUTHORS
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                                                                                                                                                                                                                                                                                                                                 /note-"Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF109303 Homo sapiens prostate adult Homo sapiens cDNA clone IPCA-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGTGCCCCATCCCTGTTTATGGGCTTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCC 1849
                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NT0147-
191100-482-h07&t3=2000_11-19&t4=1)
Seq primer: puc 18 forward
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 430)
      Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 395.8; DB 12;
Pred. No. 5.1e-43;
0; Mismatches 2;
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0147"
                                                                                                                                                                                                    High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 g
                                                                                                                                                                                                                                                                                                                   /dev_stage="Adult"
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122 c 13
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                                              Tel: +55-11-2704922
                                                                    +55-11-2707001
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AF109303
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Best Local 9
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ORIGIN
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source			BASE COUNT	, Mat Loce	Matches 401 1795	Db 405 GCC Qy 1855 GGI	Db 345 GGT Qy 1915 CAP	Db 285 CAN Qy 1975 CTG	Db 225 CTG Oy 2035 GCC	165 2095	105 2155	DD 45 TGC RESULT 37 BF922235/C LOCUS	ITION SION ON RDS E E	Mamma REFERENCE 1 (b AUTHORS Dias Nagai	Bruns A.J. A.J. A.J. Simps Simps Societ JOURNAL Proc. MEDLINE 20202 COMMENT CONTA
177 AAAGGGCTGGCAGAAATGGGAACCTGGCTGCCTAGGAGGTTAGTGCTAGTGAGGAGG 236	197 AGAGGCCGCAGCTTCTGGAGCAGCCCAGACGAGTTCTGGAGTGCCTGAACGGCC 256 11	257 CCCTGAGCCCTACCCGCCTGGCCCACYNTGGTCCAGAGGCTGTGGGTGAGCCGCTGCTG 316	317 CGGCACCGGAAAGCCCAGCTCTTGCTGGTCGCTAACCTTTGGCCTGGAGGTGFG 376	377 TTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGGA-AGTGGGGGTAGAGGAAA 435 	436 GITCATGACCATGGTGGTGGTTGGTCCAGTGCTGGCTTGG-TCTGTGTCCCGCTCC 494	495 TAGGCTCAGCCAGTGACCACTGGCGTG3ACGCTATGGCCGCCCGGCCCTTCATCTGGG 554	555 CACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCAAGGGCGGGC		675 TGCTGGACTTCTGTGGCCAGGTGTGC-TTCACTCCACTGGAGGCCCTGCTCTGACCTC 733	734 TTCCGGGACCCCGCCCCG 760 	AW175665 A12 how and 11 seems	N RC3-BT0046-310899-002-F07 BT0046 Homo sapiens CDNA, mRNA sequence. AW175665.1 GI:6441806 EST. human.		Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil	Tel: 192-11-27/04922 Fax: +55-11-27/04922 Fax: +55-11-27/07001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3.BT0046- 310899-002-F07&t3=1999-08-31&t4=1) Seq primer: puc 18 forward High quality sequence stop: 411.
QQ	dy Db	Qy Dp	oy Op	oy Db	Qy Db	Qy Dp	Qy Dp	Qy	Qy Dp	Qy Db	RESULT 36 AW175665/c LOCUS	DEFINITION ACCESSION VERSION KEYWORDS SOURCE	ORGANISM REFERENCE AUTHORS TITLE JOURNAL	COMMENT	FEATURES

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/db_xref="taxon:9606"
/clone_lib="BT0046"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: breast; Vector: pucl8; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and oDNA amplification were performed under low stringency conditions."
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s Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
al,M.A., da Sllva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
dmn,G.H., Carvalho,A.F., Matsukma,A., Baia,G.S., Simpson,D.H.,
nstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                          SCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATAT 1854
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0
                                                                                                                                                                                                                                                                                                                                      11.7%; Score 398.6; DB 10; Length 412;
.larity 99.0%; Pred. No. 2.2e-43;
Conservative 0; Mismatches 4; Indels 0;
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oratory of Cancer Genetics
ig Institute for Cancer Research
/organism="Homo sapiens"
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Local Similarity 77.4%;
nes 578; Conservative
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                                                                                                                                                                                       /note-"Site_1: Sal1: Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GTGATGAGACGTGTCCCCACTGAGGT - - GCCCCACAGCAGCAGGTGTTGAGCATGGGCTG
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numan genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.rlken.go.jp) for
further details.
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es 127; Indels
                                                                                                                                                    /tissue_type="urinary bladder"
/dev_stage="adult"
/lab_host="DH10B"
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                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                        /clone="9530024M01"
                                                         Location/Qualifiers
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197 c
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BG246497 13-FEB-2001 844 bp mRNA linear EST 13-FEB-2001 602360526F1 NCI_CGAP_Maml Mus musculus CDNA clone IMAGE:4488895 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTGAGGT -- GCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAGAAGCTGGACCGGCACC 136
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murlnae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.c. column: 08
plate: LLAM10336 row: c column: 08
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                                                                                          567 AGACCCTTTATCTGGGCTTTGTCCTGGGGGTGCTGTAAGCCTCTTTCTCATCCGGGGG
                                                                                                                                                                                              GCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTC
                                                                                                                                                                                                                            507 GITTCTGTTCCACTCCTAGGCTCAGCCAGTGACCAGTGGCGTGGGCGCTATGGCCGCGG
                                                               CGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 9.5e-44;
0; Mismatches 153;
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="lMAGE:448895"
/clone_lib="NGI_CGAP_Man1"
/tissue_type="tumor, blopsy samp
/dev_stage="10 months, virgin"
/hab_host="DH108"
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Computational Analysis of Full-Length Mouse cDNAs Compared with
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                                                                                                                                                                 Depublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-Temail.nih.gov
Tissue Procurement: Jeffrey, F. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be informed through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM9810 row: 1 column: 07
High quality sequence start: 3
High quality sequence start: 3
High quality sequence stop: 756.
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                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="FVBAN"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
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/clone=lib="NCI_CGAP_Kid14"
/lab_bost="DHIOB (TI phage-resistant)"
/note="Organ: Kidney: Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: Kidney: Vector: pCMV-SPORT6; Site_1: Not1;
/note="Tolone undirectionally. Primer: Oligo dT.
Average inser: size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
a 218 c 243 g 167 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 ACGIGICCCCACIGAGGI -- GCCCCACAGCAGCIGITIGAGCAIGGGCIGAGAAGCIG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 GACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTGGCGGC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGAGCAGCAGTTCTGGAGTGC 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 759)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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 BF789072.1 GI:12094108
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Mulauryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (1092) a to 692) a rakawa.T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A. Hiramoto,K., Hori,F., Ishi,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,H., Kouda,D., Shibata,K., Sahai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
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URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
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487 CCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCCTT
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Contact: Yoshihide Hayashizaki
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667 CCCTCTACCACCGTGAGAAGCCGGTGTCC 695

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SOURCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
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Arakway..., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, K., Saraki, T., Sano, M., Tagami, M., Shinagaki, F., Takadashi, C., Sakai, K., Sano, H., Sasaki, Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashi, Zaki, Y.,
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Contact: Yoshihide Hayashizaki
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                                                                                               BB610495 RIKEN full-length enriched, adult male stomach Mus musculus cDNA clone 2210413P12 5', mRNA sequence.
BB610495 GI:16452013
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UR.:http://genome.gsc.riken.go.jp,

Carninci,P., Shibata,Y., Haydstsu,N., Sugahara,Y., Shibata,K., Itoh

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'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
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Fax: 81-45-503-9216
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/db_xref="taxon:10090"
/clone="2210413P12"
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Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGCCCAACTCGAGTTTTTTTTTTTTTVN 3'], cDNA was
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602104930F1 NCI_CGAP_Kidl4 Mus musculus cDNA clone IMAGE:4222998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998 CCGCTCCTGTTAGCCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTTCTGTTGCTGCCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2058 TAATGTGGCTCTCTGCTGCCACCCTGTGCTGAGGTGCGTAGCTGCACACAGCTGGGGGC
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                                                                                                                                                                                                                                                                                                                                             DB 10; Length 700;
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                                                                                                                                                                                                                                                                                        0; Mismatches 124;
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                                                                                                                                                                                                                                                   12.3%; Score 419.6; DB 1
78.8%; Pred. No. 2.9e-46;
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Matches 547; Conservative
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                                                                                                                                                                                                                                                                        /clone="Index:1420415"
/clone_lib="NCI_CGAP_CO24"
/lab_host="bH10B_(TI_phage: resistant)"
/note="Organ colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; cloned unidirectionally. Primer: Oligo dT-Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9803 row: p column: 16
High quality sequence start: 2
High quality sequence stop: 680.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 12.7%; Score 433.8; DB 12; Length 700; al Similarity 84.5%; Pred. No. 3.9e-48; 582; Conservative 0; Mismatches 97; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTCTACCACCGGGAGAAGCAGGTGTTC 1513
                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
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          /clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="blu108"
/fissue_type="carcinoid"
/lab_host="blu108"
/note="Organ: lung; Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; plasmid bNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991. and 1520904-1522439). Subtraction by Bento soares and M. Fatima Bonaldo. " 412 c 96 g 114 t
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700 bp mRNA linear EST 12-DEC-2000
602100464F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4220415 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
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NIH WG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                           tch 12.8%; Score 435.4; DB 10; Length 448; al Similarity 99.6%; Pred. No. 3e-48; 447; Conservative 0; Mismatches 1; Indels 1;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /nac.nost="United" Site_1: SalI; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo. CDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E1.5 female mesonephrosygonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT). Not primers. References include: (i) Genome-wide expression profiling of mid-gestation placenta and embryousing a 15,000 mouse developmental CDNA microarray, 2000, proc. Nall. Acad. Sci. U S A, 97; 91127-9132; (2) iarge-scale CDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127:1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the x chromosome, 1998, Hum Mol Genet 7:1967-1978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute on Aging/National Institutes of Health National Institute on Aging/National Institute on Aging/National Institutes of Health Email: casell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3066 row: G column: 04
Seq primer: -21M13 Reverse
High quality sequence stop: 549
                                                                                                                                                                     EST 26-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka, T.S., Carter, M.G. and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Verification and initial annotation of NIA mouse 15K cDNA clone set
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                    #3066004-5 NIA Mouse 15K CDNA Clone Set Mus musculus cDNA clone BG081576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="H3066G04"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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         3276 TCAGAGTATAATGTTTATGGTGACAAATTAAAGGCTTTCTTATATGTT 3324
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Pred. No. 1e-48;
0; Mismatches 69; Indels 0;
                                 /db_xref="niaEST:H3066G04-5"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: George J. Kargul
Laboratory of Genetics
                                                                                                                                                                                                                                                             BG081576.1 GI:12564144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Other_ESTs: H3066G04-3
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Best Local Similarity 87.4%;
Matches 480; Conservative (
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BG081576
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JOURNAL
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KEYWORDS
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CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BEG74096 448 bp mRNA linear EST 08-SEP-2000 7d74g04.xl NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278742 3' similar to contains element MER22 repetitive element; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                 1482 CCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAG 1541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1542 GTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTC 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1602 CCTTCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGC 1661
                                                                                                                                                                            1242 GCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTC 1301
                                                                                                                                                                                                                                                                                                1302 TEGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGG 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TGTACCAGGGTGTACCCAGAGCCGAGCCAGGCACCCGGGGGCCCGGAGACACTATGATGAAG 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 448)
NCI-CGAP http://www.ncbl.nlm.nlh.gov/ncicgap.
National Cancer Institute; Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                               121 GCATTCGAATGGGCACCTGGGGCTCTTCCTGCAGTGTGCCATCTCCCTGGTCTTCCCC
                                                           1182 TGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCCCCGAGGCCCCGGAGACACTATGATGAAG
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Homo sapiens
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ORIGIN
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                                                                                                      Length 934;
                                                                                               Score 453; DB 14; Length 9
Pred. No. 1e-50;
0; Mismatches 130; Indels
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Best Local Similarity 77.5%;
Matches 636; Conservative
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BASE COUNT
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AI703348.1 GI:4991248

human. EST

mRNA sequence. AI703348

DEFINITION

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ACCESSION KEYWORDS SOURCE VERSION

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In Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Emmail: Grapbs-remail.nlh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.linl.gov/bbrp/image/image.html
Insert Length: 566 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCL_CGAP_Lun5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-152439). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2857 AAGGTAGAGGGTGGGGGTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCTTTGGC 2916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 CTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAAGTGCGGTTTCCCAAGC 230
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Engaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 469)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:2339129"
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Outhoursing (1937).

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: capabs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.AG.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mammary: Vector: pCNV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator Library amples: Smith, NIH"

193 c 168 g 140 t
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1426 AGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTC 1485
                                                                                                   1486 CCTCTACCACCGGGAGAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGC 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        788 AGTCTTGGGGGCTGCCTGGCCTACCTCCTGCCATTGACTGGGACACCAGTGCCCTG 847
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                        622 CAGTGCCCTCACGGGGTGCACTTCTC-GGGCTGGAGATACCGGCTTACACGCCACT 679
                                                                                                                           680 CCTCTACCACCGTGCGAAGCAGTGTGTC--TGCCCAATACCGAGGGCACCTGAGGTGAC 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute. Cancer Genome Anatomy Project (CGAP),
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/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, blopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH108"
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86.7%; Pred. No. 6.5e-51;
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High quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                         1546 TAGCAGTGAGGACAG 1560
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Unpublished (1997)
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Mus musculus
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1148 ACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAG 1207
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                                                                                                                                                                                                                                                                              1028 GCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCTGTGCTGCCGCATGCCC 1087
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                                                                                                                                                                                      968 GCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCCACTGCTGTCCATGCCGGGCCCGCTTG 1027
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/lab_host="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                       302 GCTTTCCGGAATCTGGGTACCCTGTTTCCCCGGCTGCAGCAGCTGTGCTGCCGCATGCCT 361
                                                                                                                                                                                                                                                                                                                                                                                                                        421
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                        122 GCCCCTACCTGGGTACTCAGGAAGAATGCCTCTTTGGCCTCCTCACCTCATTTTCCTC 181
                                                                                                                                                                                                                                  242 GCAGAAGGGTTGTTGGTCTCTGCCGTGTCGCCGATGCTGCCCATGCCACGTTGGCCTG 301
                                                                                        908 ACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCA 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs.remail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tobna Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
III.gov i column: 05
High quality sequence stop: 634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 CGCACCCTACGCCGACTCTTTGTGGCTGAGCTGTGCAGCTGGATGGCACTTATGACTTTC
848 GCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCTTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGENCOURT_8881033 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:6396364 5', mRNA sequence.
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/clone="IMAGE:6396364"
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/organism="Mus musculus"
NIH-MGC http://mgc.nci.nih.gov/.
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al Similarity 80.8%;
594; Conservative
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Best Local Similarity
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                                                                                                          /note—"Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I: oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                    2956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3017 CCCCAACTTTCCCCACCAGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCAC 3076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATCTCACAGAAACTCAGGAGCACCCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCA 3196
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 929)
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Pred. No. 4.4e-51;
0; Mismatches 7; Indels 3
                                                                                 /tissue_type="normal prostate"
/lab_host="DH10B"
                                                                                                                                                                                                                              116 t
              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1158206"
/clone_lib="NCI_CGAP_Pr22"
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98.0%;
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Matches 484; Conservative
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1066 CCAGCTGTGCTGCCGCATGCCCCGCACCTGCGCGCTCTTCGTGGCTGAGCTGTGCAG 1125
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Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: eqapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9855 row: j column: 10
High quality sequence stop: 610.
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                                                                TTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCATG 1084
                                                                                                                                  1085 CCCCGCACCCTGCGCCGCTCTTCGTGGCTGTGCAGCTGGATGGCACTCATGACC 1144
CCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCGC 1024
                5;
                                                                                  422 CCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGGAGCTGGATGCCACTCATGACC 481
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MNH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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289 c 287 g 194 t
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://imag.llnl.gov e column: 03
High quality sequence stop: 608.
Location/Qualifiers
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Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
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Pred. No. 1.6e-51;
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/clone_lib="NCI_CGAP_Man1"
/tissue_type="tumor, biopsy sam
/dev_stage="10 months, virgin"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .969 // /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                            BG173136.1 GI:12679748
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al Similarity 82.9%;
583; Conservative
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BG173136
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TITLE
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KEYWORDS
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959 ACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGG 1018
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                        121 CCCGACCGGCAGAAGGGTTGTTGTTCGCCGTGTCGCGCGGATGCTGCCCATGCCAG
                                                                                                                                                                                                                               241 GGCATGCCTCGCACCCTACGCCGACTCTTTGTGGCTGAGCTGTGCAGCTGGATGGCACTT 300
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Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 491)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
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                                                                                                                    181 GTTGGCCTGGCTTTCCGGAATCTGGGTACCCTGTTTCCCCGGCTGCAGCAGCTGTGCTGC
                                                                                         1019 GCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGC
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www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 919 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 472.
Location/Qualifiers
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Unpublished (1997)
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AA631143
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AA631143/C
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/clone="IPCA-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.6%; Score 463; DB 13; Length 9 78.5%; Pred. No. 5e-52; Live 0; Mismatches 165; Indels
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                      /strain="1129.CSTBL/61,FVB/N"
/db_xref="taxon:10090"
/clone="twAGE:5337073"
/clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
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                                                 e: LLAM11855 row: p column: 02 quality sequence stop: 778.
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AF109299 482 bp mRNA linear EST 28-JAN-2000 AF109299 HOMO sapiens prostate adult Homo sapiens cDNA clone IPCA-2
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/note="multiple clone assembly from multiple libraries and
                                                                                                                                                                                 716 GCCCTGCTCTCTGA--CCTCTTCCGGGACCCGGACCAC-TGTCGCCAGGCCTACTCTGTC 772
692 GATCTTGGGAGTGGGGCTGCTGGACGT-TGTGGCCAGGTGTGCTTGTACTCCATTTGGAG 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 482) Walker, M.G., Volkmuth, W., Sprinzak, E., Hodgson, D. and Klingler, T. Frediction of gene function by genome-scale expression analysis: Genome Res. 9 (12), 1198-1203 (1999)
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3174 Porter Drive, Palo Alto, CA 94304, USA
co-expressed with known prostate-cancer genes.
Location/Qualifiers
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Pred. No. 7.6e-52;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                           831 GGGACA-CCAGTGCCCTGGCCCCTACCTGG 860
                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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1192 CGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGA- 1250
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                                                                                                                                                                                             241 GGACACCAGCGTTCTGGCCCCCTACCTGGGTACTCAGGAAGAATGCCTCTTTGGCCTCCT
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CCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCA
                                                                                                 653 CTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTG
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602334219F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:4457452 5',
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC).
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact
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                                                                                                                                                                                                                                                                                            GCGTGGGGCTGCTGCTCTG--TGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCT 723
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 786)
                                                                                                                                                                                                                         781 TGATCAGCCTTGGGGGCTGCCTGGGTTACTTTTACCTGGCATTGACTGGAACACAG-G
TCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGGCT
                                                                                                 GGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGG
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/db_xref="taxon:10090"
/clone="IMAGE:4457452"
/clone=lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               843 CCCTGGCCCCTACCTGGGCACCCAGG 869
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BG174399.1 GI:12681102
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901 bp mRNA linear EST 12-SEP-2001
603296208F1 NCI_CGAP_Mâm3 Mus musculus cDNA clone IMAGE:5337073 5',
mRNA sequence.
B1650119
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed, by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 901)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Unpublished (1999)
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                      TITLE
JOURNAL
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/clone="IMAGE:5473696"
/clone=lib="NIF,MGC 41"
/tissue_lib="NIF,MGC 41"
/tissue_lib="NIF,MGC 41"
/tissue_lype="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
FOOTE="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor:
GGCAGGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library.

NIH-MGC Library.

10 a 665 c 258 g 418 t 16 others
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BG864609
BG864609.1 GI:14215147
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BG864609
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Ste_2: Not!, Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation? 3.31 (1996)."
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13 GAATTGGCACTAAAGGGCTGGCAGAAATGGGAACCTGGCTGCACCCTAGGAGGTTAGTGC 190
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                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
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/clone="IMAGE:4919513"
/clone=lib="NoT_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                       http://image.llnl.gov
Plate: LLAM10834 row: i column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                              Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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231 CAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCT
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/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: DCTD/DTP
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                                     61 AACAGCTAGCCTCCTAGTTGAGACACACTAGAGAAGGG-TTTTGGGAGCTGAATAAACT 119
CTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCAT 361
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone-lib="NIH_MGC_90"
/clone-lib="NIH_MGC_90"
/tissue_type="bell admoracrinoma, cell line"
/tasue_type="Defl admoracrinoma, cell line"
/lab_nost="bell admoracrinoma, cell line"
/lab_nost="Defl admoracrinoma"
/note="lorgan: liver; Vector: pcWv-SpORT6; site_1: Not!;
Site_2: Sall; cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                   2784 CAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTT
                                                                                                                                       482 AGGGTGTTGAACGGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAAACCAC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Plate: LLAM10238 row: p column: 05
High quality sequence stop: 689.
Location/Qualiflers
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/db_xref="taxon:9606"
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AGENCOURT_6613122 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5473696 BM912193
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                                                                                                                                                                                                                                                                                                                                                                               299 GTC-TTTTGCTGATCCACCCCCTCTTACCTTTATCAGGATGTGGCCTG-TGGTCCTTC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           594 GCCAAATGATAATTCCAAATGCTGTTACC -- AAGGTAGGGTGTTGAAGGAAGGTAGAGGG 651
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1667)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1985 row: 1 column: 17
High quality sequence stop: 448.
Location/Qualifiers
1. 1667
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                                                                                                                            2450 GTAGGGGAAGAGTCCTGAGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACT
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Similarity
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                         RESULT 16
BG469586
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JOURNAL
COMMENT
                                                                                                                                                               ACCESSION
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                                                                                                                                                                                                                  KEYWORDS
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                                                                                                                             /db_xref="taxon:gofo"
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/note="Organ: muscle: Vector: poTB7; Site_1: Site_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 CTGAACGCCCCCTGAGCCCTACCGCCTGGCCACTATGGTCCAGAGGCTGTGGGTGAG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAGAAGCTG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTGGCGGC 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 AGCAAGGAGGAGAGGCCGCAGCTTCTGGAGCAGACGCGAGAGCAGTTCTGGAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487 CCCGC-TCCTAGGCTCA-GCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.8%; Score 538.2; DB 12; Length 1035; 93.1%; Pred. No. 5.9e-62; tive 0; Mismatches 33; Indels 14;
                                                                                                         /organism="Homo sapiens"
High quality sequence start: 3
High quality sequence stop: 602.
Location/Qualifiers
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35 a 153 c 133 g 168 t
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BG469586 1-1-MAR-2001 589 bp mRNA linear EST 21-MAR-2001 602533622F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661500 5',
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                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information.can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM1460 row: k column: 05
High quality sequence stop: 587.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 589)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.7%; Score 534.8; DB 12; Length 589; 98.8%; Pred. No. 2.2e-61; Live 0; Mismatches 2; Indels 5;
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2.2e-61;
2;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                               mRNA sequence.
BG469586
BG469586.1 GI:13401861
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-	qq	δλ	qa	Qy	qq	ò	Db	Oy	qa	Oy	qq	δŏ	qa	δλ	qa	QY	qa	Qy	qa	ογ	qa	ΔO	7 7	ga 	RESULT	LOCUS	DEFINIT	ACCESSIC	KEYWORDS	ORGANI	REFERENC	AUTHO	COMMENT			
	3D1 AGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTG 3,60	1896 CTACACAGGTAGTATTTGACAAGGGGGACTTGGGCGAAATACTCAGGGTAGAAAACTTCCA 1955	361 CTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAACTTCCA 420	1956 GCACATTGGGGTGGAGGCCTGCCTCACTGGGTCCCAGCTCCCGCTCCTGTTAGCCCCA 2015	421 GCACATIGGGGIGGAGGCCTGCCTCACTGGGTCCCAGCTCCCCGCTCCTGTTACCCCCA 480	2016 TGGGGCTGCCGGGCTGGCCGCAGTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTG 2075	481 TGGGGCTGCCGGCCTGCCGGCAGGTTCTGTTGCTGCCAAAGAAATGTGGCTCTCTACTG 540	2076 CCACCCTGTGCTGCTGAGGTGCGTAGGTGCGGG 2115	541 CCACCCTGTGCTGCTGTGTGTGTTGTTGTGTGTGTGTGTG	T. 14	597	ITION	ACCESSION BG242597 VERSION BG242597.1 GI:12752412	S EST.	NISM Mus musculus Entermote: Determote Changette Canadata	Eukalyota, metazoa; Chordata; Crahata; Vertebrata; Eureleostomi; Manmalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. FRNCE: 1 (hases 1 to 1116)	AUTHORS NIH-MGC http://mgc.ncl.nih.gov/. TITLE National Institutes of Health. Mammalian Gene Collection (MGC)	ΑĽ	Email: cgapbs-remailmin.or.	JISSUE FIOCULEMENT: GILDER SMITH, PA.D. CONA Library Preparation: Life Technologies, Inc.	CDNA LIDRARY ARRAYED BY: The 1.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	http://image.llnl.gov	Figure: Limmildary 10W: C COllumi: US High quality sequence stop: 666. RRS Incation/Onallfiers	rce	/organisms muscurus /strain="FVB/N"	/db_xref="taxon:1009()" /clone="IMAGE:4482362"	/clone_lib="NCI_CGAP_Mam1" /tissue_type="tumor, biopsy sample"	/dev_stage="10 months, virgin" /lab_host="DH10B"	/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.	;	OUNT 209 a	Query Match 15.9%; Score 543.4; DB 12; Length 1116; Best Local Similarity 84.8%; Pred. No. 1.2e-62; Matches 644; Conservative O: Mismatches 111; Indels 4: Gans 3:	1023 GCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCTGTGCTGCTGCCGCA 10		1083 TGCCCCGCACCCTGCGCCGCCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGA 1142
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1035 bp mRNA linear EST 22-MAY-2001

MRNA sequence.

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                                           1143 CCTTCACGCTGTTTTACACGGATTTCGTGGGCGGGGGGGTGTACCAGGGCGTGCCCAGAG 1202
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69 TGCCTCGCACCCTACGCCGACTCTTTGTGGCTGAGCTGTGCAGCTGGATGGCACTTATGA 128
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1035)
                                                               369 CTGCCACCTGCCACTGCCACGAGGGTGGTAGTGACAGCCTCAGCTGCCCTCACCGGGT
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1807 row: i column: 03
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1836 AGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGCTCGCCATTTACTTTG 1895
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98.3%;
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TITLE
JOURNAL
                                RESULT 13
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KEYWORDS
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                                                                  /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
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/organism="Homo sapiens"
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/clone="IxMAGE:5480245"
/clone="IxMAGE:5480245"
/clone=lib="NIH_MGC_113"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dr prining, Dixectionally cloned
into ECORI/XhoI sites using the following 5; daptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BM914562 1060 bp mRNA linear EST 12-MAR-2002 AGENCOURT_6615475 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480245
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.3e-65;
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BI107873 858 bp mRNA linear EST 26-JUN-2001 602901816F1 NCI_CGAP_Mam3 Mus musculus CDNA clone IMAGE:5031771 5',
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1510 GTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGAC 1569
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng i
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng i
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can i
Cloud through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
plate: LLAM11088 row. o column: 04
High quality sequence stop: 810.
High quality sequence stop: 810.
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/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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/lab_host="bullOB (phage-resistant)"
/nab_host="bullOB (phage-resistant)"
/note="oran colon, Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XioI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
73 a 272 c 264 g 185 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: agapba-remain.nih.gov
Email: agapba-remain.nih.gov
Tissue Procurement: Arrayed
Tissue Procurement: Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM1458 row: a column: 09
High quality sequence stop: 671.
                                                                                                                                                                                                                                                                              661 CCCAGAAGAATATCTGGGCTTTGGGGAAACCCCCCCGGAAATCTCGGGGACCCCCCC 720
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
NIH-MGC http://mgc.nci.nih.gov/.
Nathonal Institutes of Health, Mammalian Gene Collection (MGC)
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                                                  2998 ACCCCCAACTTTCCCCTACCCCAACTTTCCCCACCAGCTCCACAACCCT-GTTTGGAGC
                                                                     3057 TACTGC--AGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCC
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/organism="Homo sapiens"
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                        2 GCCTACACACACTGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCG
                                                            1528 AGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCC
                                                                          TGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGCCATCTGCCTGGACCTCGCCATCCT
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//dev_stage="adult, 70 yr"
/lab_host="DH10B"
/note="Vector: pcMv-SPORT6 (Life Technologies); Site_1:
/note="Vector of the pcm of the 
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13621 row: f column: 03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6202754"
/clone_lib="Lupski_sciatic_nerve"
                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
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Location/Qualifiers
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Jupublished (1999)
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17.4%; Score 594.6; DB 12; Length 850;
Best Local Similarity 92.9%; Pred. No. 2.4e-69;
Matches 733; Conservative 0; Mismatches 44; Indels 12;
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http://image.llnl.gov
Plate: LLCM1196 row: a column: 08
High quality sequence stop: 675.
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1. .850
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/clone="inAGE:431407"
/clone=linH_MGC_46"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
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NotI: Site_2: Salı; CDNA made by Oligo-dT priming.
Directionally cloned using the following adaptors:
5. TCGACCCACGCCACCA: and
5. GACTAGTTTTAGATCCCAGCGCCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Madicine) and is available through Life
Technologies."
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                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Consortium/LLNL at:
High quality sequence start: 2
High quality sequence store: 490.
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                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="lyAGE:6204253"
/clone_lib="Lupski_sciatic_nerve"
/sex="male"
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0; Mismatches 13
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/dev_stage="adult, 70 yr"
/lab_host="DH108"
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IMAGE: 6204253 5', mRNA sequence.
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                                       BQ950805.1 GI:22366283
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Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebratå; Euteleostomi;

Bukaryota: Metazoa; Chordata; Craniata; Vertebratå; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 850)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Contact: Robert Strausberg, Ph.D.

Email: Gapbs-remanil.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be
1974 CCTGCCTCACTGGGTCCCAGCTCCCGCTCCTGTTAGCCCCCATGGGGGCTGCCGGGCTGGC 2033
                                                                                                                                                                                                                                                                                                            2153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   2154 CTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAA 2213
                                                                                                                                                  2034 CGCCAGTITCTGTTGCTGCCAAAGTAATGTGGCTCCTCTGCTGCCACCCTGTGCTGCTGAG 2093
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                                          483 GTGCGTAGCTGCACAGCTGGGGGCTGCCTCTCCTCTCTCCCCAGTCTCTAGGG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF972601 850 bp mRNA linear EST 22-JAN-20
602243025F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4331407 5',
                                                                                                                                                                                                                                                                                                2094 GTGCGTAGCTGCACAGCTGGGGGCTCCCTCTCCTCCTCTCCCCCAGTCTCTAGGG
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                                            CTGTGATGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGG 1737
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                                                                  62 GETGGGTGCTGGAGGCAGTGGCCTCCCACCTCCACCGCGCGCTCTGCGGGGCCCTCTGC 121
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 718)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov. a column: 04
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                                                                                                                                                             181 CCGGGCCATCTGCCTGGACTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                              361 GAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 CAGTTTCTGTTGCTGCCAAAGTAATGTGGCCTCTCTGCTGCCACCCTGTGCTGCTGAGGT
                                                                                                                                                                                                                                  CCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGT
                                                                                                                                       CCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             860 GGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGAC 1415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACT 180
                                                                                                                                                                                          Library constructed by Life
                                                                                                                       /tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GGCCTCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGG
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                                                                                                                                                                                                                                                                              19.4%; Score 660.2; DB 12; Length 718; 97.7%; Pred. No. 6.2e-78; tive 0; Mismatches 14; Indels 2;
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                                                  /organism="Homo sapiens
                                                                                     /clone="IMAGE:3846411"
/clone_lib="NIH_MGC_65"
High quality sequence stop: 693
Location/Qualifiers
                                                                      /db_xref="taxon:9606
                                                                                                                                                                                                               Technologies.
227 c
                                                                                                                                                                                                                                                                                                                     690; Conservative
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2277 TAGCCTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCA 2336
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                                                                                         þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2455 GGAAGAGICCIGAGGGGCAACACAAAAACCAGGICCCCICAGCCCACAGCACIGICII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.6%; Score 703.2; DB 14; Length 916; 98.8%; Pred. No. 1.2e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                              /clone="IMAGE:6205362"
/clone_lib="Lupski_sciatic_nerve"
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0; Mismatches 3
                                                                                                                                                                                                                                                                          /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
                                                                                                                http://image.llnl.gov
Plate: LLAM13628 row: b column: 19
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                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
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/note="Orli0B (phage-resistant)"
/note="OrlinB (phage-resistant)"
/note="O
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2992
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602532993F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4660703 5',
                                    2875 TCAGGTCTCAACGC-TTCCCTAACCACCCCTCTTCTCTTGGCCCAG-CCTGGTTCCCCC
                                                                                                                                                                                                                                                                           2933 CACTTCCACTCCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTT
                                                                                                                                                                                                          601 TCAGGTCTCAACGGCTTTCCCTAACCACCCTCTTCTTTGGCCCAGCCCTGGTTCCCCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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High quality sequence stop: 741.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BM915082
BM915082.1 GI:19365461
EST
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//tissue_type="amelanotic melanoma, cell line"
//tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant);
/note="Organ: skin; vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dr priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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                                                               1080 GCATGCCCGCGCCCTGGGCCGGCTCTTCGTGGCTGGCGCTGC--ATGCCACT 1137
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1022 CGCTTGGCTTTCCGGAA--CCTGGGCGCCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCC 1079
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               720 GGCATGCCCGGAACCTGCGCCCGGCTCTTCGTGGCTGTGCAGCTGGCAGCATGGCAACT 779
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1025)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: Rhe I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2005 row: f column: 03
High quality sequence start: 35
High quality sequence stop: 657.
                                                                                                                                  1138 CATGACCTTCACGCTGTTTTACACGG - - ATTTCGTGGGCGAGGGGCTGT - ACCAGGGCGT
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/db_xref="taxon:9606"
/clone="IMAGE:5481218"
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Contact: Robert Strausberg, Ph.D.
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Subaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 916)
12 CCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCCAGTCTGTCACTGCCTATATGGTG 71
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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602533345F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:4661075 5',
                                                                                                                                               ACTGGGTCCCAGCTCCCGCTCCTGTTAGCCCCCATGGGGCTGCCGGGCTGGCCGCCAGTT
                                                            ACTGGGTCCCAGCTCCCGGTCCTGATAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTT
                                                                                                                                  CTGCACAGCTGGGGCTGGGGCGTCCCTCCTCTCTCCCCAGTCTCTAGGGCTGCCTGA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 94). NIH-WGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                  mRNA sequence.
BG469889
BG469889.1 GI:13402164
                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                     Homo sapiens
                                                                                                             human.
DEFINITION
                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                            ACCESSION
                                                                 VERSION
KEYWORDS
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/clone_lib="NiH_MGC_15"
/lissue_type="adenocarcinoma cell line"
/lab_nost="bH10B (phage-resistant)"
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ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
20 a 331 c 296 g 199 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can lefound through the I.M.A.G.E. Consortium/LLNL at: http://mage.llol.gov
Plate: LLCM1459 row: i column: 12
High quality sequence stop: 798.

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                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4661075"
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                                                                                                           /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGCCCCC.3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
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                                                                                                                                                                                                                                                                                               23.0%; Score 784.2; DB 14; Length 885; 95.1%; Pred. No. 2.7e-94;
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                                                                                                                                                                                                                                                                                                                            0; Mismatches
/organism="Homo sapiens'/db_xref="taxon:9606"
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                                                      /sex="male"
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/organism="Homo sapiens"
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/issue_type="amelanotic melanoma, cell line"
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/inco corent./AnoI sieve susing the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH,MGC Library."
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AGENCOURT_6701857 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5481717
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                                                   780
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.j column: 22
High quality sequence start: 131
High quality sequence stop: 308.
Location/Qualifiers
                         803 CTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGC
745 GACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTC - - TTGGGGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Gaps
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                                                                                                                                                                                                                                          863 A -- CCCAGGAGAGAGCCTCTTTGGCCTGCTCACCTCATCTTCC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 9
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283 c 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM915527.1 GI:19365906
                                                                                                                                                                                                                                                                                                                                                                                                                                                5', mRNA sequence.
BM915527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 95.0
Matches 847; Conservative
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(without alignments)
13136.682 Million cell updates/sec
                                                                                                                                                                                                                            9, 2003, 15:13:08 ; Search time 4204 Seconds
                                                                                                                                                                                                                                                                                                                                                              32308132
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                     16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                        OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
                                                                                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                 US-09-759-143-110
                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                              June
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em_gss_mus:* em_gss_other:* em_gss_mam:* gb_est4:* gb_est5:* em_estfun:* gb_gss:* em_gss_hum:* em_gss_pln:* em_gss_vrt:* em_gss_fun:* em_gss_pro:* em_gss_inv:* em_gss_rod:* em_estom:* em_estov:* em_estpl:* em_esthum:* em_estba:* em_estro:* em_htc:* em_estin:* gb_est2:* gb_est3:* em_estmu:* qb_htc:* qb_est1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query					
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П	784.2	23.0		14	BQ948390	B0948390	AGENCOURT
7	767.2	22.5		14	BM915527	BM915527	AGENCOURT
m	749.6	22.0		12	BG469889	BG469889	602533345
4	748.6	22.0	1025	14	BM915082	BM915082	AGENCOURT
Ŋ	703.2	20.6		14	BQ950912	BO950912	AGENCOITET
9	667.4	19.6		12	BG469487	BG469487 602532993	602532993

source

FEATURES

	BM9124502 ACENCOURT BG2842597 602354010 BG828841 602752813 BG469586 602533622 BG122427 60235334 BM912193 ACENCOURT BG864609 602798469 BG174399 602334219 B1650119 603296208 AF109299 AF109299	nq75908.3 60211243 AGENCOUR. wd93b09.x H3066G04 60210046 60210495 60210495 60210493	RC3-BT OV2-NT F10930 602909 BB6278 120845 f33907 602156 UI-H-B
BE86724 BQ95080 BF97260 BQ94202 BG46952 BI10787	BGB BGB BGB BGB BGB BGB BGB BGB BGB	AA6311. BF7855 AW412. AW412. BO934. AI7033. AI7033. BE674. BF581. BB610. BB627. BB627.	AW17566 BF92223 AF109303 BE114520 BB62784 AW76779486 BF68099 AW13546
718 1 859 1 8850 1 8875 1 8894 1		9491 9 9299 10 9392 110 9342 14 1448 12 700 110 692 110 844 12	4464446444
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7 8 9 10 11 12 13	114 116 117 118 118 120 120 120	0 0 2022 2022 2033 3033 3033 3033 3033 3	00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

EST 21-AUG-2002 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13611 row: b column: 08
High quality sequence stop: 615.
Location/Qualifiers
rce 1. .885 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 885)
NIH-MGC http://mgc.nci.nih.gov/. BQ948390 885 bp mRNA linear EST 21-AUG-AGENCOURT_8803099 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:6198823 5', mRNA sequence, BQ948390.1 GI:22363868 Unpublished (1999) Homo sapiens BQ948390 human. EST VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION TITLE JOURNAL ACCESSION REFERENCE AUTHORS RESULT 1 BQ948390 COMMENT

AGGAGCGGGGACCTGGGACCCAGTGAGCCCTCCAC	GCCTGGGGGGGGCACTATALGSGIYGIUAPTOGIYGIUAATGGIYGIUAAIGG 305 GCCTGGGGGAGACACTATAGGCAGACTGGACAATGGAGACCAT. 1811	GlyGluSerGlyArgPro	
1 1	Db 290 Qy 1870 Db 305 Qy 1810 Db 325 Qy 1757 Db 345 Qy 1702 Db 365 Qy 1649 Db 385 Qy 1649 Db 385 Qy 1500	Oy 1529 Oy 1529 Oy 1469 Oy 1469 Oy 1469 Oy 1409 Oy 1409	

CCCCCAGGTTCC	TAG 171 oar 820	1 80	212	l rPr 787	AGG 258	 Gly 767	GGC 306	Pro 751	CCA 366	rogly 743	CTA 426	Arg 730	GGA 486	721	TGA 546	sGly 713	AGCC 606	val 693	TGA 657	31y 674	3GG 717	yGlu 654	AGA 771	645	CCC 831	рьу 631	3CA 888	ile 619	3CG 948	/al 606	AGT 1002	eu 586	0 5	,
Compared	CCAACTGCC 1 0GlyPr	yProLeuG1	1 1 1 1	uLysGlyse	GTAGGGCTC	Pro	SCAGCAGGC	i	AACACACCT	GlyAsnPro	ACTICICE	ProGlyAla	CTAGGAGCG		GTGCCCAGA	Ę	5	ProGl	SCCCAGG	slyGluPro	CAGAGAGCA	ArgGl	TGAAGGCAT	-	G	roGlyAs	rGAGGGTGA	GlyPro	rggggcccA	AlaAspGly	ATGGACAGC.	ArgGlyGly	-	17 FI OF 1 OG 1)
6 CGCC 7 Proj 1 GGCC 7 G1y3 6 GCT 7 G1y3 6 GCT 7 GGCC 8 SGC 7 GGCC 8 GGC 8 GGC 1 G1y 1 G1y 1 G1y 1 G1y 2 G1y 2 G1y 3 GGCC 4 A Lang 1 G1y 2 GGC 4 A Lang 1 G1y 2 GGC 2 GGC 4 A Lang 1 GGC 1 GGC 2 GGC 4 A Lang 1 GGC 1 GGC 2 GGC 4 A Lang 1 GGC 2 GGC 4 A Lang 1 GGC 2 GGC 4 A Lang 1 GGC 2 GGC 2 GGC 4 A Lang 1 GGC 2 GGC 2 GGC 4 A Lang 1 GGC 2 GGC 4 A Lang 1 GGC 2 GGC 2 GGC 4 A Lang 1 GGC 2 GGCC 2 GGCC 2 GGCC 2 GGCC 2 GGC 2 GGCC 2 GG	TTGCTGCCG oGlyMetPr	yAlaProGl	TGCTCCA	 nProGlyGl	-ccaegcee	::: ThrGlyAla	TCCGGTGCC	1	CGG	GlySerAsn	TGGTCATGA	1	TGGCTGAGC	Pro	CCAAGGACA	 GlyProGln(GGCACAGCA	 GlyGlyPro	GCAGCCCCA	 GlyGlnAsn	GGAAGAGGT		GACTGATCA	-	366	GlyGln	TGÂGGAAGA		creecrees	3lyProGly	200000000000000000000000000000000000000	ProGlyGlu#		styntantat
CGCCCTCTCCCCCTCCCCCCCCCCCCCCCCCCCCCCCC	CTCTCCTCC aGlyProPr	G1	TCTCGGCTC	pAlaGlyGl		 AlaGlyAsn	GCTGGGCTT	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	aggtgatgc	Pro	CCAGCACCA	AlaGlyPhe	AGTGGTCAC	ProGlyGly	GCAGGATGC	 GlyProPro	TGGGATCCG	::: LysGlyGlu	AGAAGTCCA	 GlyAlaPro	CGT CCC	Glu	AGCCCCCAA	 GlyIleAla	GGT AGG		CTACGCAGG		SCCTTCTG	3luProGly	AAGCCAAGC	31nGlyMet		ory dry Lysi
6 CGCCC 7 Proj 7 GLY 7 GLY 8 SELI 7 GCCC 8 CCCT 8 SCCC 7 GCC 8 SCCC 8 SCCC 7 GCC 8 CCCT 8 CCC 8 CCCT 8 CCC 8 CCCT 1 GLY 1 GLY 1 GLY 1 GCC 2 GLY 1 GCC 2 GLY 1 GCC 2 GCC 3 GCC 4 Ala 4 Ala 8 SCCC 6 CCC 7 GCC 8 CCC 8 CCC 8 CCC 9 CCC 1 GLY 1 GLY 1 GCC 1 G	AGCTGCGGC gGlyLeuAl	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ACTGCTTCG	III -LysGlyAs	TAGTGGG	 ProGlyPro	CCAGCAAGA		590	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GACCAATGC	GlyAla	GTCCACGCC	ArgGlySer	AGAGGCTCA	 GlyProAla	225	 ProGlyGlu	CCTGGCCAC	III GlyPhePro	GGT CCG	serProGly	AGCCCAGGC	 31yLeuPro	SGGTGCCCA	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	srerecere	3lyProThr	GGCCGACA	AspLysGly	GGA	ProGlyLeu		ary riveru
6 CGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GA rGlyAlaAr	yProPro	CACTCCAGA		TCTGGACCA	 AspGlyPro	SCAGGTTGA	::: SerGlySer	SCAGCAGAG	Pro	CCAGCACTG	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GCCATAGC	Glu	GGATGAGAA	 3lyGlySer	ccAGGG	ArgGlyAla	FGAAGCACA	::: 3lyProAla	GCGACAGT	ArgGly	SCAGGAGGT	lla AlaPro	ACTCCTCCT	roAla	CACCAGCA	lly SlyProArg	AGGAGG	4		\laGlyThr		TYFIOFIO
6 CGCC 7 Proj 1 GGGCC 7 GLY, 7 GLY, 6 CTTGC 6 CTTGC 6 CTTGC 6 CTTGC 7 CTGC 6 CTTGC 6 CTTGC 7 CTGC 8 GCCT 1 GLY 8 CCCC 7 CTGC 8 CTTGC 9 GLY 1 GCCC 1 GCCCC 1 GCCCC 1 GCCCC 1 GCCC 1 GCC	aGlyileTh	yAlaGlnGl	CCGTTCAGG	 ProGlyval	CCCACAGCC	.:: Lys	CAAAGGTTA	 ProGlyPro	CCACTTCCA		AGACCAGGC		၁၁၅၁၁၅၁၁၅	1	CGGCCCTTG	 SlyProPro	STGCCAGCT	sG1	CCAGTGGAG	111 31yProPro	AGTAGGCCTC	1 1 1 1 1 1	CAATGGCAGG	::: 31uGlyGly#	SAAAGAGGC	roProGlyE	CTCCTCA	lyLysAs	CGACA	erProGly		 roGlyAla	COMBOOKO	тубтумтас
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::: 82 LeuProGlyMetLysGlyH1sArgGlyPheSerGlyLeuAspGlyAlaLysGlyAspAla 101	1876 ACCCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAA 1821 	1820 TGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGGA 1782 	1781 GGAAGGCACTATCCAGGATGCCGAGGAGATGCCCCGGCCCGGAACCACCTGG 1722 	1721 CCTCGGTGGGCTCACCCACCACCACGTACGGAGACATCACAGGCAGAGGCCCCGC 1665	1664 AGAGCGCGGGTGGAGGTGGGAGCAGGCCACTGCCTCCAGCAC 1623	1622 CCACGTGTCCATTAGGGAAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGC 1572	1571 TGGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGA 1512 ::::	1511 ACACCTGCTTCTCCCGGTGGTAGAGGGCCAGTGTGTAGGGCAGGATCTGCAGGCTG 1452	1451 AGAAGGTGAACCCGGTGAGGGCGGCTGAGCTGTCACGGCCACACTGTGGGACAGGC 1392	1391 ATGTGGCACCGGCAGCCACAGGGAAAGCTGCCACACAGCCAAATAGACTGCTCGAGTGC 1332	1331 CGAATCGCTGCACCAGCCGGTCCATGACCAGAGAAGAACAGGAGATGGCGCACTGCA 1272 :::		1241CTTCATCATGTGTCTCCGGGCCTCGGTGCCGGGCTCAGCTCTGGGCA 1194	1193 CGCCCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTG 1134	3 CCATCCAGCTGCACAGCTCAGCCACGAAGAGCCGGCGCGGGGTGCGGGGGATGCGGCAGC 10	345GIJ 345 1073 ACAGCTGGAGGAGGAAGGAGGCGCCAGGTTCCGGAAAGCCA 1026 1016 11111 11111111111111111111111	GlualaglyArgProGlyGlualaGlyLeuProGlyAlaLysGlyLeuThrGlySerPro	1025 AGUGGGCCCGCATGGACAGCAGTGGGGCGACAAGGAGGGGGCCGACAGCCCTTCTGCTG 966 	965 GCTCGGTGGGCCCCAGCGCTGCCT942
q a	QY	Qy	Oy Db	VQ da	· Qy	Qy Dp	QQ	δγ	Oy Db	Qy	Q	Oy Db	Qy Dp	oy da	Qy	QV DD	qa (qa qa	Oy
OY 170 GAATCAGCCAGGCGCCCATTCTGCCAGCCTTTGGTGCCGGTCCAGCTTCTCAG 116	115	27 [20 g	48		; Patent No. 6150081 ; GENERAL INFORMATION: ; APPLICANT: VAN HEERDE, GEORGE V.	APPLICANT: BOUWSTRA, JAN B. APPLICANT: DE WOLF, FREDERIK A. APPLICANT: MOORPORK, ANDREAS APPLICANT: WIRPHEN WARP W. W.		; TITLE OF INVENTION: PREPARATION THEREOF; FILE REFERENCE: 2728-2; CURRENT PAPLICATION NUMBER: U.S./09/219, 849	; NUMBER OF SEQ ID NOS: 50 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 49	TYPE: PRT: ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence:	ATION: amino acid sequence	Alignment Scores: Pred. No.: 6.84e-19 Length: 822 Score: 351.00 Matches: 244 Percent Similarity: 32.94% Conservative: 37 Best Local Similarity: 28.60% Mismarches: 37	Indels: Gaps:	TCAGCAGCACAGGGTGGCAGC	2071	Db 27 GlyGluProGlyGluProGlyGlySerGlyProMetGlyProArgGlyProFroGlyPro 46 Qy 2011 GCTAACAGGAGGGGAGCTGGGA	47 ProGlyLysAsnGlyAspAspGlyGluAlaGlyLysProGlyArgProGlyGluArgGly	Qy 1972 CCTCCA	GTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAG

ą	384 GlyArgProGlyProAlaGlyProProGlyAlaArgGlyGlnAlaGlyValMetGlyPhe 4	03
λ	941 CCTCAGCCACCAGCAGTGGCCTGCTACGCAGGAGGAGATGAGGGTGAGCAGGCCAA 8	882
ð		418
Á,	AGAGGCACTCCT	870
Q		438
Y do	869CCTGGGTGCCCAGGTAGGGGGCCAGGGCACTGGTGTCCCAGTCAATGGCAGGCA (816 458
χ		780
, q	::: rProGlyPheGlnGlyLeuProGlyProAlaGlyProProGlyGluAlaGlyLys	478
λλ		729
	479 ProGlyGluGlnGlyValProGlyAspLeuGlyAlaProGlyProSerGlyAlaArgGly	498
	728 CAGAGAGCAGGGCCTCCAGTGAAGCACACTGGCCACAGAAGTCCACAGCCCCA :::	. 699
		51.7
		639
	518 ArgGlyAsnAsnGlyAlaProGlyAsnAspGlyAlaLysGlyAspThrGlyAlaProGly	537
		579
		555
	578 TCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCAC	519
		573
	518 GCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAA	459
		290
	458 TGCCCAGCACCATGGTCATGAACTTCTCTCTACCCCCACTTCCAGCAGCAGAGGCGCA	399
		. 009
	398 CATAGGTGATGCCTGCGGCCAAACACCTCCAGGC	3,63
		. 029
	362CAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGCCTTTCCGGTGCCGCAGCA	312
		640
	311 GGCGCTCACACACCTCT	291
	641 AspGlyGlnProGlyAlaLysGlyGluProGlyAspThrGlyValLysGlyAspAlaGly	099
	290GGACCATAGTGGGCCAGGCGGTAGGGCTCAGGGGCCGTTCAGGCACTCC	240
	661 ProProGlyPro-AlaGlyProAlaGlyProProGlyProIleGlyAsnValGlyAlaPr	089
	st:	180
	680 oGlyProLysGlyProArgGlyAlaAlaGlyProPro-GlyAlaThr-	695
		120
	696GlyPheProGlyAlaAlaGlyArgValGlyProProGlyProSerGlyAsnA	713
	119 TCAGCCCATGCTCAACACCTGCTGCTGGGGCACCTCAGT	75
	713 laGlyProProGlyProProGlyProValGlyLysGluGlyGlyLysGlyProArgGlyG	733

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1966 ------CCCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTT 1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2110 GCTGTGCAGCTACGCACCTCAGCACACAGGGTGGCAGCAGAGAGCCACATTACTTTGGC 2051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2050 AGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAACAGGAGCGGGGAGCTG 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 GlyAlaPro---GlyProGlnGlyPheGlnGlyProProGlyGluProGlyGluProGly 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 AlaSerGlyProMetGlyProArgGlyProProGlyProProGlyLysAsnGlyAspAsp 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --G 45
                                                                                                                                                                                                                    APPLICANT:
TITLE OF INVENTION: Assay for collagen degradation
NUMBER OF SEQUENCES: 4
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-759-143-110 (1-3410) x US-08-931-820-1 (1-1057)
 74 ACACGICICATCACTCAGAICCIGGCCGA--
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/931,820 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
FILING DATE:
                                                                                      44 GCGCGCGCTGTCACCCGGAGCC 22
                                                                                                                                                 Sequence 1, Application US/08931820; Patent No. 6010863; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OKGANISM: Homo sapiens;
TISSUE TYPE: Collagen type I
US-08-931-820-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.16e-18
345.00
32.73%
28.01%
5.54%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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q			
	107 ArgGlyPheSerGlyLeuAspGlyAlaLysGlyAspAlaGlyProAlaGlyProLysGly 126	3 8	of serious and ser
ΟY		ž 2	A15 Glabalacture
QQ	$_{\rm GI}$	3 3	
δ	1795 CACCTGGGACAGCAGGAAGGCACTATCCAGGATGGCGAGGTCCAGGCAGAT 1745	Š ī	
qq	142 roArgGlyLeuProGlyGluArgGlyArgProGlyAlaProGlyProAlaGlyA 160	2	429 GLYGLuProGLYLYSA
Qy	1744 GCCCCGGCCCGGAA	ΟŊ	
qq	GlyAlaThrGlyAlaAlaG	qq	449 AlaGlyLysAspGlyG
Qγ		Οy	839 IGGIGICCCAGICAAT
qq	180 lyProProGlyPheProGlyAlaValGlyAlaLySGlyGlyAlaGlyProGlnGlyProA 200	qq	469 GluArgGlyGluGlnG
οy		Qy	803 GGCAGCCCCCAAGACT
QQ	rgGlySerGluGlyProGlnGlyValArgGlyGluProGlyProProGlyP	QQ	489 GlyProProGlyGluA
οy		ογ	746 CCGGGTCCCG
qq		qq	509 ProGlyProSerGlyA
ογ	ď	Οy	692 GGCCACAGAAGTCCAG
οg	:::::: 337 GlyAlaAsnGlyAlaPro	Dp	528 GlyProProGlyProA
οy		QY	647G
οp	247 AlaProGlyPhoGlyPhoGlyGlyProglyBrogl	qa	548 LysGlyAspAlaGlyA
Οy	GGATCTCCAGGGCTGAGGTGAACCCGGTGAGGGCGGCTGAAGCTGAAGCTACACCACAA	Qy	602 CGCCCTTGGGATGAG
QQ	::	QQ	566 GlnGlyMetProGlyG
0y		ΟŊ	542 GCCGGCGGCGGCCATA
Op	ProProGlyProSerGlyGlu	qa	584 ArgGlyAspAlaGlyP
οy	1367 AAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCAGCGGGTCGA 1308	Οy	485 CACAGA
QQ	305 GluGlyLysArgGlyProAsnGlyGluAlaGlySerAlaGlyProProGlyPro 322	qa	601 ValArgGlyLeuThrG
δy	1307 TGACCAGAGAGAAGACCAGGGAGATGGCGCACTGCAGGAACAGCCCCAGGCTGCCCATCC 1248	. Оу	452
Db		qq	619 AspLysGlyGluSerG
δy		δλ	446 TGGTCATGAACTTCTC
Db		qa	. 639 GlyAspArgGlyGluPi
Οy	ACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCC	Qy	386 CTGCGGCCAAACACACA
Db		qa	655P ₁
δy	1127 AGCIGCACAGCICAGCCACGAAGAGCCGGCGGGGGTGCGGGGGTGCGGCATGCGGCACAGCI 1068	οy	338 AGAGCTGGGCTTTCCGC
QQ		QQ	670 AspAlaGlyAlaLysG
ογ	1067 GGTGCAGCCGGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGG 1020	δy	278 GCCA
Dp		Db	687 yProProGlyProlleC
٥y	1019 CCCGGCATGGACAGCAGTGGGGGGGGGGGGGGGGGGGGG	ΟŊ	230 TCGTCTCGGCTCTGCT.
qq	386 ProGlyProAspGlyLysThrGlyProPro 395	qa	704ArgGlySerAla
2	010 CT	òò	176 GCCTAGGAATCAGCCAG

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-------GCAGTGTGGCTGCTACGCAGGTGA 906
                                                                                                                                                                    GAAAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGGATGAAGG 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyPheProGlyProLysGlyAlaAla------- 428
                                                                                                                                             GCAGGCCAAAGAGGCACT-----CCTCCTGGGTGCCCAGGT--- 855
                                                                                                                                                                                                                      GluAlaGlyAlaGlnGlyProProGlyProAlaGlyProAlaGly 468
                                                                                                                                                                                                                                                                                                   TGGCAGGCAGGA------BGTAGCCCA 804
                                                                                                                                                                                                                                                                                                                                      GlyProAlaGlySerProGlyPheGlnGlyLeuProGlyProAla 488
                                                                                                                                                                                                                                                                                                                                                                          TGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT--- 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAAGAGGTCAGAGAGGGCCTCCAGTGGAGTGAAGCACACCT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGCCCCACGCCCAGGATGAGCAGTGCCA------- 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCCAGGGGCCTGGGATCCGGGCACAGCAGCCTGCTAGCCAGC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGCG---GGA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProLysGlyAlaAspGly-----SerProGlyLysAspGly 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyProlleGlyProProGlyProAla-----GlyAlaProGly 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GCACCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyProSerGlyProAlaGlyProThrGlyAlaArgGlyAlaPro 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCTACCCCCACTTCCAGCAGCAGAGGCGCACATAGGTGATGC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| ||||||| ProGlyProAlaGlyPheAlaGly------ 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTCCAGGC------CAAAGGTTAGCAGGTTGACCAGCA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||||||
|ProProGlyalaAspGlyGlnProGlyAlaLysGlyGluProGly 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGCCGCAGCAGCGGCTCACCCACAGCCTCTGGACCATAGTGG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GGCGGGTAGGGCTCAGGGGGCCGTTCAGGCACTCCAGAACTGCT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||
eGlyAsnValGlyAlaProGlyAlaLysGlyAla------ 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aGlyProProGlyAlaThrGlyPheProGlyAlaAlaGlyArgVa 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGCGCCCATTTCTGCCAGCCTTTGGTGCCGGTCCAGCTTCTCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P----CCAGAAGCTGCGGCCTCTCCTTGCTGCTGCCGCCAACT 177
:= 2
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1199	TGGGCAC ProAlaG	1140 326
1139	TGAGTGCCATCCAGCTGCACCACCACGAAGAGCCGGCGCC	1080 339
1079	GGCAGCACAGCTGGTGCAGCCGGGAAGCAGGCGCGCCCAGGTTGCTGCTGCTGCTGCTAGTTTT:: ::: :: GlyAlaGlnGlyProAlaGlyProGlyGlySerArgGlyAspProGlyProProGlyAl	. 0 2
1034	GGAAAGCCAAGCGGGCCCGGC :::	975 3.75
974 376	CTTCTGCTGGCTCGGTGGGGCCC	933
932	CCAGC ProGl	873 407
872 408		822
821	CAGGCAGGAAGCCCAGGCAGCCCCAAGACTGATCATGAAGGCA' 	762
761	CCTG 	705
704		645 456
644		585 467
584	AGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGCCATAGC	525
524		9 . 0
464	to c	, 405 522
404		345 533
344	AGAGCTGGGCTTTCCGGTGCCGCAGCGGCGGCTCA	303 553
302		246 571
245 571	CACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTG 1	86 84

ΟŻ	185	GGAATCAGCCAGGCGCCCATTTCTGCCAG	-
qq	584	584 rArgGlyAspProGlyProProGlyAlaHisGlyProAlaGlyProLysGlyAlaH1 603	Э
Qy	130	CTCAGCCCATGCTCAACACCTGCTGCTGTGGGGCACCTCAGTGG	
ФФ	603	603 sGlyProAlaGLyPr 608	80
Qy	7.1	71 CGTCTCATCACTCAGATCCTGGCCGAGGCGCGCGGGTGTCACCCGGAGCCAGCGCGTGCA 12	
qq	809	608 oLysGlyalaMet-AspProGlyargTyrGlnLeuSerAlaGlyargTyrH1sTyrG 627	_
Οy	11	11 GGCFGGTT 4	
рр	627	:: 627 InLeuVal 629	
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957-00-51	10-143-17 011-3410 v 000VIF / 1-6041	
- 60	7-145-110 (1-5410) A 258700 (1 004)	
Qy Db	193 GAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAAACGAAGCAGTTCTGGAGTGCCTGAAC 25 1	8
δλ	GGCCCCTGAGCCCTACCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGTGAGCCGCCT	8
QQ	45 GlyGluMetAsnAspSerAsnLeu	
Qy Dp	313 GCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGT 37: :::! ::: 1 ::: :::::::: 59 *ValArdAsnSerLeuLeuThrLeuIlelEuSerCysThrValAlaAlaGlyValGlnPh 78	2
· YO	373 GIGITIGGCCGCAGGCAICACCIAIGIGCCGCCICIGCIGGAAGIGGGGGIAGAGGA 432	2
qq	::::	
Qy	433 GAAGITCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCT 492	7
QQ	98 sAlaPheSerSerPhelleTrpLeuCysGlyProlleThrGlyLeuValValGlnProCy 118	8
oy E	493 CCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCGCCCTTCATCTG 552 :::	2 6
3 8	GGD ACHGGCCTHTGGGC BHCCTTGCTTGAACCCTTTCTTTTTTTTTTTTTTTTTTTTT	
B	8 elleGlyAlaValMetileSerileAlaValileIleIleIGlyPheSerAl	
è	D#333	vo
qq	5 aAspileGlyTyrLeuLeuGlyAspThrLysGluHisCysSerThrPheLysGlyThrAr	
٨٥	637 GCCCCTGGAGCTGCCACTGCTCATCCTGGGGCTGCTGGACTTCTGTGGCCAGGT 696	9
qq		5
٥y	697 GIGCITCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGGACCCGGACCACTGTCG 756	9
QQ		4
Qy	757 CCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCT 816	9.
qq	::: ::: 214 nThrAlaAsnAlaValPheCysSerTrpWetAlaValGlyAsnIleLeuGlyPheSerAl 234	14
Qy	GACACCAGTGCCCTGGCC	4
qq	234 aGlyAlaSerGlyGlyTrpHiSArgTrpPheProPheLeuThrAs 24	249
οy	CCAGGAGGAGTGCCTCTTTGGCTGCTCACCCTCATCTT :::	33
ΩΩ	nArgAlaCysCysGluProCysGlyAsnLeuLysAlaAlaPheLeuValAlaValValPh	
Oy		096
qa	269 eLeuThrLeuCysThrLeuValThrLeuTyrPheAlaAsnGluValProLeuSerProLy 28	289
Qy	961 CGAGCCAGCAGAAGGGCTGTGCGCCCCTCCTTGTCGCCCAC10	1003
qa	LeuLeuAspSerProGlnAsnThrGlyPh	309
٥y	ı	1042
Dp	309 eAspLeuSerGlnSerLysArgGluLeuGlnTyrArgAsnSerValAlaAsnAsnGluSe 32	62
0y	1042 1042	1042
QQ	329 rGluMetGlyHisValAlaAspAsnSerProLysAsnGluGluGlnArgProAspLysAs 3	349
Qy	1043	1074

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1795 GGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATAT 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------GTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCT 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1675 TGCCTGTGATGTCTCCGTACGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1735 GGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGT 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1396 GTCCCACAGAGTGGCCGTGGTG-----ACAGCTTCAGCCGCCCTCACCGGGTTCACCTT 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1615 ACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGGGGCTCTGCGGGGCCTC 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1255 CAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCG 1314
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                                                                                                                                                                                                                                                                                   | | ::: ||| ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: || | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | :: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :
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                                                                                                                                          1075 CTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGC 1134
                                                                                                                                                                                                                                                                                                                                                                                                  ::::::|||
467 lCysMetAlaCysThrAlaIleIleSerValValSerIleSerAlaAsnThrGlnGlyVa 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427 yAlaPheGlyLeuLeuLeuAsnSerValValLeuGlyValSerSerPheLeuIleGluPr 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 pGlnGlyAspSerPheAlaAspSerProGlyAlaValLeuValAsnLeuLeuThrSerLe 369
                                                                                                                                                                                                                                   ---------GluLeuThrAlaAspAlaGly-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532 ------GlyGlyGlnGlyLeu-------
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Š á		ACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGGCCT 3	10
3	v	rorroserser-asnueulyslyslleValValValAlaSerIleAlaAlaGlyVa	
Qy	367	GGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGCAAGTGGGGGT 426	10
qq	42	3	
Qy	427	AGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGT 486	
qq	62	eProHisThrTrpAlaAlaPheIleTrpLeuCysGlyProIleSerGlyMetLeuValGl 82	
οy	487	CCCGCTCCTAGGGTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCCTT 546	
Dp	82	::::: ProlleValGlyTyrHisSerAspArgCysThrSerArgPheGlyArgArgArgProPh 102	
οy	547	CATCTGGGCACTCTTGGGCATCCTGAGCCTCTTTCTCATCCCAAGGGCC 601	
Db	102	elleAlaAlaGlyAlaAlaSerValAlaValAlaValPheLeurleGlyTyrAlaAlaAs 122	
Qy	602	-crecrereccesarcccassecce	
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Οy	655	CICAICCIGGGCGIGGGGCIGGACTICIGIGGCCAGGIGGIGCIICACIC	
QQ	142	epheValvalGlyPheTrpIleLeuAspValAlaAsnAsnMetLeuGlnGlyProCysAr 162	
ΟÝ	715	GGCCCTGCTCTCTGACCTCTTCCGGGACCGGGACCACTGTCGCCAGGCCTACTCTGT 771	
qq	162	:::	
Οy	772	SCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTA	
pp	182	: rPhePheMe	
Οy	830	TGGGAUACCAGTGCCCTGGCCCTACCTGGGCACCCA 867	
qq	202	_	
Qy	898	1	
qq	222	: sThrCysPhePheIl	
Qy	925	ACTGCTGGTGGCTGAGGAGGCAGCGCTGGCCCCCACCGAGCCAGCAGAAGGGCTGTC 981	
Db	242	¥	
Qy	982	GGGC 102	0
pp	260	ValAspGlyAspAspGluAspGlyProValGluAlaAlaProLeu 274	
Qy	1021	TGGCTTTCCGGAACCTGGGGGGGCTTCCCCGGCTGCACCAGCTGTGCTGCCG 108	0
Db	275		
Οy	1081	CCCTGCGCCGCCTCTTCGTGGCTGAGCTGCAGCTGGATGGCACTCAT 114	0
υр	288		
Qy	1141	- 55	0
qq	306	eProPheLeuLeuPheAspThrAspTrpMetGlyArgCluValTyrGlyGlySerSerAs 326	
Οy	1201	CTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAG	0
Db	326	٠ н	
٥y	1261	GGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTCTCTGGTCATGGACCGGCTGGT 1320	0

QQ	26 LeuPheLeuAlaCysMetValAlaGlyGlyValGlnTyrGlyTrpAlaLeuGlnLeuSer 45		
ò	4	δλ	139
qq	::: ::: ::: ::: ::: :::::::::::	qq	37
ΛÓ	455 GGCATTGGTCCAGTGCTGGGCCTGTGTCCCGCTCCTAGGCTCAGCGAGTGACCAC 514	Qy	145
g Q	LeuCysGlyProlleAlaGlyLeuIleValGlnProCysValGlyLeuTyrSerAspLys	qa	37
'n		Qy	151
qq	86 CysThrSerSerLeuGlyArgArgArgArgProPhelleLeuThrGlyCysIlellelleCys 105	qq	38
0y	575 CTGAGCCTCTTTCTCATCCCAAGGCCGGCTGGCTAGCAGGGCTGCTGC 625	Qy	157
QQ	::: ::: ::: 106 IleSerVall1eVall1eGlyPheSerSerAspIleGlyTyrAlaLeuGlyAspThrThr 125	qq	36
ογ	626 CCGGAT	Qy	163
qq	 126 GluAspCysLysValTyrArgGlyProArgTyrHisAlaAlaAlaAlaPheIleLeuGly 145	ga .c	940
Qy	668 GIGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCGACTGGAGGCCCTGCTCT 727	3 E	700
q	146 PheTrpLeuLeuAspPheSerAsnAsnThrValGlnGlyProAlaArgAlaLeuWetAla 165	3 0	174
δō :	GACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTTGCCTTC	i qa	4.3
QQ O	AspLeuSerGlyArgHisGlyProSerAlaAlaAsnAlaIlePheCysSer	O	180
δο δ	2 ATGATCAGTCTTGGGGGCTGCCTGCCTGCCTGCCATTGACTGGGACACC	qa	4.5
g (3 TrpMetAlaLeuGlyAsnIleLeuGlyTyrSerSerGlySerThrAsnAspTrp	δλ	183
λo		qq	47
qq	Met	RESIILT	44
δ	CICITIGGCCIGCICACCICATCIICACCIGCGIAGCAGCCACACIGCIGGIG 93	M53	35 Q9M535
g	221 AlaAlaPheLeuValAlaValValPheLeuGlyLeuSerThrAlaValThrMetValPhe 240		Q9M535; 01-0CT-
Qy	GCTGAGGAGGCAGCGCTGCCACCGAGCCAGAGAGAGGCTGTCGGCCCCCTTG		01-0CT- 01-JUN-
qq	241 AlaArgGluValAlaLeuAspProValAlaAlaAlaAlaLys253		Sucrose
Qy	995 TCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGC 1045		Eukaryc
qq	254ArgAsnGluGlyGluAlaSer 260		eurosic
Ολ	GCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCGCACCCTG	RP	[1] SEQUENC
q .	GlyLeuLeuAlaValPheLysGlyMetLysAsnLeuProValGlyMetProSerValLeu		TISSUE- Anderso
ογ Έ	1097 CGCCGGCTCTTCGTGGCTGAGCTGGATGGCACTCATGACCTTCACGCTGTTT 1156		"Identi Euphorb
3 8	CARACACACACACACACACACACACACACACACACACAC		EMBL; A
S &	Acontrol to the control of the contr	X 20 2	Pfam; F
ìò	GAGGCCGGAGACACTATTCGATTCGCATTCGCATGCCCACCTCTCTCT		SEQUENC
d d	317 ValThrAlaPheGlnGluGlyValArgGlnGlyAlaPheGlyLeuLeuAsn 334	Alignment Pred. No.:	nment Sc . No.:
Qy	1277 IGCGCCAICTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACT 1336	Score: Percen	Score: Percent Simi
Db	::: ::: ::::::::::::::::::::::	Best Local Query Matc	Best Local S Query Match:
Qγ	1337 CGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTG 1396	DB:	759-17
qq		.60-50	US-09-759-T4

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7 TCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCC 1456
                                                                                             CTGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTG 1516
                                                                                                                                                                                                   CCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTC 1576
                                                                                                                                                                                                                                                                                                 CTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGT 1636
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                                                                                                                                                                                                                                                                                                                              7 GGCCTGCTCCCA------CCTCCACCCGCGCTCTGCGGGCCTCTGCCTGTGAT 1684
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ification of mRNAs expressed in underground adventitious buds of bia estula (leafy spurge).";
ted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
AF242307; AAF65765.1; -.
ro; IPR003662; sub_transporter.
ro; IPR003662; sub_transporter.
Ms; TIGR01301; GPH_sucrose; 1.
CE 530 AA; 55843 MW; 059C1ED3BB02D356 CRC64;
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-2000 (TrEMBLrel. 15, Last sequence update)
-2002 (TrEMBLrel. 21, Last annotation update)
-2002 (TrEMBLrel. 21, Last annotation update)
bia esula (Leafy spurge).
bia esula (Leafy spurge).
cta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
tophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
ds I; Malpighiales; Euphorbiaceae; Euphorbia.
                                                                                                                                                                                                                             6 AlaLeuPheValPheLeuGlyLeuProPheAlaValLeuCys------
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Conservative:
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                            2 ------ValSerValLeuSerAla----
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TGCTACGGGGGCGCGACAGGCCTTCTGGTGGTGGGGCGCACGCGGGGGCGACGGGGGCGACGGGGGCGCACGGGGGCGCACGGGGGCGCACGGGGGCGCACGGGGGCGCACGGGGGCGCACGGGGGCGCACGGGGGCGCACGGGGGCGCACGGGGGCGCACGGGGGCGCACGGGGGCGCACGCGGGGGCCACG		GGTGCAGCCGGGGAAGCCGCCCCAGGTTCCGGAAAGCCAAGCGGCCCGGCA	013
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JykrgaladiyAspprodlyLeu			39
			98
TGCTAGGGGAGAGAGGGTGAGCAGGCCAAAGGCACTCCTCGTGGTGCC TGCTAGGGGAGAGAGGTGAGCAGGCCAAAGGCACTCCTCCTGGTGCC TGCTAGGGGAGAGAGGAGGTGAGCAGCCAAAGGCACTCCTCCTGGTGCC TGCTAGGGGAGAGAGGGGGAGAGGGCAAAGGCACTCCTCCTGGTGCC TGCTAGGAGGAGAGAGGGGAAGAGGCATGGTACCCAGTCAACAGGCAGG		1.11.11	20
		TGCTACGCAGGTGAGGAAGAAGGAGTGAGCAAGTYFLOASÚGLYFLOFLU	0.2
CAGGT			17
rodiydlnargdlydlukrgdiypheProdiyLeuProdlyProSer			15
GAGGTAGCCCAGGCAGCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCG -[1]	_		32
"GlyGluProGly		GAGGTAGCCCAGGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCG	55
ALGEOTYCOTTON COORDINATION COOR		-GIYGLUProGIYLysGlnGlyAlaProGlyA	43
		ncacioni 	63
IngluproGlyArgGluGlyThrProGlyAlaAspGlyPro		GGCCTCCAGTGGAGTGAAGCACCTGGCCACAGAAGTCCAGCAGCCCCACGCCCAGGA- 	09
rgaspGlyAlaalaGlyValLysGlyAspArgGlyGlualaGlyAlaLeuGlyAlaProG GGGCCTGGAACCGGGCACAGCCAGCTGCTGGCTGCTGGCTGCTGGCTG		lyGluProGlyArgGluGlyThrProGlyAlaAspGlyProProGlyA	62
GGGCC		redencivalsalscivusivesivessivesvesivesivesivesvesivesives	41
GGGCGGCCAGGCCAGGGCACAGCAGGCAGGCCGGCGCGGCGGGCGGGGCGGGGGG			
GATGAGAAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGTGAAGGGCCG		GGGCCTGCTTGGGGTGCGGGCACAGCGCTGCTAGCCAGCGGCCCTTGG I I I I I I I I I	93 014
1yLysGinGlyAspArgGlyGluAlaGLy-AlaGlnGlyProMetGlyProAlaGlyPro GCGGC		GATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGCCG	39
GCGGC		lyLysGlnGlyAspArgGlyGluAlaGly-AlaGlnGlyProMetGlyProAlaGlyPro	033
CACGCCAGTGGTCACCTCGTCAGGAGCGGCACACAGA		GCGGCGCCCATAGCGTC	22
GlualaglygluargGlyceutysGlyHisargGlyPherhrGlyLeuGln 107 GlualaglygluargGlyLeuLysGlyHisargGlyPherhrGlyLeuGln 107		AtacıyatanıycıyırıcıloriyricinciyrroniyetyaspLyselyciuAlacıy	
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		GlyLeuProGlyProProGlyProSerGlyAspGlnGlyAlaSerGlyProAlaGlyPro	060
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1111 IleProGlyProlleGlyProProGlyProArg-------GlyArgSerGly 1125
                                                                             1145 oGlyProGlyIleAspMetSerAlaPheAlaGlyLeuGlyProArgGluLysGlyProAs 1165
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389 TGCCTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGG
                                                                                                                     272 CGGG----------TAGGGCTCAGGGGGCCGTTCAGGCACTCCAGA
                                                                                                                                                                                                                                             176 GCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Orgza sativa (Rice).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. NIPPONBARE: TISSUE-PANICLE;
Hirose T., Scoffeld G.N., Whitfeld P.R., Aoki N., Furbank R.T.,
Terao T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation and characterisation of a cDNA for a novel sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transporter, OsSUT3, from rice.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB071809; BAB66368.1;
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
TIGRRAMS: TIGR01301; GPH_sucrose; 1.
SEQUENCE 506 AA; 52776 WW; 0844DC10E1E63E75 CRC64;
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1165 pProLeuGlnTyrMetArgAlaAspGluAlaAlaGly------
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143
77
207
129
21
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Last annotation update)
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Matches:
Conservative:
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
Sucrose transporter.
OSSUT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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327.50
39.57%
25.72%
5.10%
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                                                                                                                                                                                                                                                                                                                                                                                                                             14 GCAGG 10
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Best Local Similarity:
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                                                                                                                                                                                                                                                                           1178
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Qy	AGACCTGAAGCC	i	
Db		QQ	
è		Qy	1934 ATTTG
, (qa	448 eProG
3	Į Lyski O.	Qy	1912
οy	AAGGTCCTGGGTTAGGCATTTTGGGGGGCCCAGACCCCCAGGAGAAGATTCTGGCAATG	qa	468 yLeuA
qq	183 190	Qy	1877 -GACC
δλ		qa	::: 483 yGluE
Op	191 ProGlyLysSerGlyGluArgGlyProProGlyBro 202	Qy	1818 GAGCC
0y	2672 AAATATTAGACACCAACACAGAAAGCTAGCAATGGATTCCCTTCTACTTTGTTAAATAA 2613	qq) 500 aGlyE
QQ	203	ò	1775
οy	2612 ATAAGTTAAATATTTAAATGCCTGTGTCTCTGTGATGGCAACAGAAGGACCAACAGGCCA 2553	i 6	520 opro
QQ	215 oGlyValLysGlyHisArgGlyTyrProGlyLeuAspGlyAlaLysGlyGluAlaGlyAl 235	3 2	1755 TCCAC
Qγ	2552 CATCCTGATAAAAGGTAAGAGGGGGTGGATCAGCAAAAAAGACAGTGCTGTGGGCTGAGG 2493	. qq	1 540 yAla
q Q	235 aProGlyValLysGlyGluSerGlySerProGlyGluAsnGlySerProGlyProMetGl 255	òO	1716 GTGG
Qy	2492 GGACCTGGTTCTTGTGTGTGTGCCCCTCAGGACTCTTCCCCTACAAATAAGTCATATGTTC 2433	ි සි	560 ragl
qq	Arg	ž 0	1656 GGTG0
Qy	2432 AAATCCCATGGAGGAGTGTTTCATCCTAGAAACTCCCATGCAAGAGCTACATTAAACGAA 2373	: E	
Ор	260	a a	ייונדט מצעו
οy	2372 GCTGCAGGTTAAGGGGCTTAGAGATGGGAAACCAGGTGACTTGTTTTTCAGC 2319	ζ, <u>6</u>	
QQ	268 oalaGiyalaalaGiyalaargGiyAsnaspGiyGinProGiy	3 6	
Οÿ	2318 TCCCAAAAACCCTTCTCTAGGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCT 2259	I d	
QQ	1	QQ -0	Unio and
٥y	2258 GGGTAATCCACCTGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCCTGT 2199	ò i	100 AGG
Db		ga (Y199 GGT
ογ	2198 ATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCA	δō :	1503 TTCT
qq	313AlaArgGlyProGluGlyAlaGlnGlyProArgGlyGluProGlyTh 328	qo ,	657 yThr
ò	2158GGCAGCCCTAGAGACTGGGGAGAGAGAG	δŏ	
QQ	328 rProGlySerProGlyProAlaGlyAlaAlaGlyAsnProGlyThrAspGlyIleProGl 348	a o	677 ogly
οy	2131 2120	λ Σ	1405 ACTG
q	 348 yalaLysGlySeralaGlyAlaProGlyIleAlaGlyAlaProGlyPheProGlyProAr 368	90	
ΛO	2119 -CAGCCCCCAGCTGTGCCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAGAGA 2067	δħ	
7 6		QQ	716 rgGl
l è		δλ	1295
S 6		qq	736 luVa
3 6		Qy	1243 GCCT
δ d	CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	DÞ	755 rg
an d	YFIOGINGLYALGKLYKIOALYKIOKIYALYALYALYALYALYALYALYALYALYALAKI	δŏ	1183 CA
δ _€	1981GAGGCAGGCCCICCACCCCAAIGIGCIGGAAGITIICIAGGCIGAGGI 1955	-	

428		
1934	SCCAAGTCGC	
448	 eProGlyGlnAspGlyLeuAlaGlyProLysGlyAlaProGlyGluArgGl	
ō	y Leuntactyrionys	
1877	-GACCCAGGCCTGCGGCAGCACCATATAGGCAGTGACAGACTGGCTGAGCTGGACACACAC	
1818	GAGCCCATAAACAGGGATGGGGCCA 	
1775	CACTI	
າ ທ	TCCAGGCAGATGCCCGGCCGGGAACCACCCTGG 17	
. 540		
1716	GTGGGCTCACCCACCACCACGTACGGAGACATCACAGGCAGAGGCCCC	
1656	GGTGGAGGTGGAGCAGCAGCAGCAGGAGGAGGAGGAGGAGGAGGGAG	
e o	CCACTGCCTCCAGCACCCACGTGTCCATTAGGGAAG	
1602	GGAGCTCCAGGCTTAGGGCCTGGCAGGAAG 	
3 6	AGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTG	
2 0	TTCTCCCGGTGGTA:::	
1458	GGGCTGAGAAGG ::: GlyLeu-GlnG	
1405	5 ACTGTGGGACAGGCATGTGGCACCGGCAGCACAGGGAAAGCTGCCACACTGGCCAAATA 1346 14	
4 4	GACTGCTCGAGTGCCGAATCGCTGCACCAGCCGGTCCATGACCAGAGAGA	
1295	AGACCAGGGAGATGGCGCAC GlyProProGlyProAlaGlyTh	
1243	3 GCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGCCCTGGTA 1184	
8	3 CA	

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1319 GIGCAGCGATICGGCACICGAGCAGICIAI --- TIGGCCAGIGIGGCAGCITICCCIGIG 1375
                                                                                                       1376 GCTGCCGGTGCCACATGCCTGTCC-----1399
                                                                                                                                                                       ------CACAGTGTGGCCGTGGTGACAGCTTCAGCCGCC 1432
                                                                                                                                                                                                                              459 MetAlaGlyThrAlaValIleSerLeuMetSerLeuSerAspAspLysAsnGlyIleGlu 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3032 GIGGGGAAAGTIGGGGGTAGGGGAAAGTIGGGGGTAGGGGAAATITIGGGCAGTGCCIIC 2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2972 ATCAGCCCAGTCCTAGAGAGATAGAGGGGAGTGGAAGTGGGGGGGAACCAGGCTGGGCCA 2913
                                                                                                                                                                                           479 TyrileMetArgGlyAsnGluThrThrArgThrAlaAlaValIleVal-----PheAla 496
                                                                                                                                                                                                                                                             497 LeuLeuGlyPheProLeuAlaIleThrTyrSerValProPheSerValThrAla---- 514
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SEQUENCE OF 18-68 FROM N.A.
SEQUENCE OF 18-68 FROM N.A.
MACLEGOD J.N., Fubini S.L., Gu D.N., Tetreault J.W., Todhunter R.J.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; UGC528; AAB05773.1; -.
InterPro; IPR000087; Collagen.
InterPro; IPR000885; Fib_collagen.
InterPro; IPR000885; Fib_collagen.
                                                                                                                                                                                                                                                                                          1493 CACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT 1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eguus caballus (Horse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                               515 ------GluValThrAlaAspSerGlyGly 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1418 AA; 134343 MW; 115FCD19EB8696A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Richardson D.W., Dodge G.R.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Type II collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pram; PF01410; COLFI; 1.
Pram; PF01391; Collagen; 18.
Probom; PD00007; Collagen; 4.
Probom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
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30.778
26.268
5.278
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Best Local Similarity:
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Q28396;
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Db 59 SerLeuValThrLeuVall		381GlyAspPheGlyGlySerValGlnAspAlaAlaArg 392	qq
OY 347 AACCTGCTAACCTTTGGCC		CCCAA	δλ
US-09-759-143-110 (1-3410) x 0806	_		qa
Query Match: 5.12% DB: 10		1457 CTGCAGATCCTGCCCTACACAGTGCCCTCCTAACCACCGGGAGAAGCAGGTGTTCCTG 1516	٥٧
Percent Similarity: 38.638 Best Local Similarity: 24.148			qq
		1397 TCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCC 1456	Qy
Alignment Scores:	_	:::::	qa
KW Transmembrane. SQ SEQUENCE 594 AA; 63972 MI			Qy
		335 SerIleValLeuGlyIleSerSerPheLeuIleGluProMetCysArgArgLeuGlyAla 354	qa
		1277 IGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACT 1336	Oy
CC -!- SUBCELLULAR LOCATION: II		317 ValThrAlaPheGlnGluGlyValArgGlnGlyAlaPheGlyLeuLeuAsn 334	qa
		1217 GAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAG 1276	ολ
RA Meyer S., Truernit E., Huem		297 AspThrAspTrpMetGlyArgGlulleTyrHisGlyArgProAspGlySerProAlaGlu 316	qa
		1157 TACACGGATTTCGTGGGCGAGGGCTGTACCAGGCGTGCCCAGAGCTGAGCGGGGCACC 1216	Qy
RA Shen M., Ronning C.M., Frase RT "Arabidopsis thaliana chrome		281IleValThrGlyLeuThrTrpLeuSerTrpPheProPheIleLeuPhe 296	QQ
		1097 CGCCGGCTCTTCGTGGCTGAGCTGTGGATGGCACTCATGACCTTCACGCTGTTT 1156	Qy
RN [1] RP SEQUENCE FROM N.A.			qa
		1046GCCCTGCTTCCCCGGCTGCACCAGCTGCCGCATGCCCCGCACCCTG 1096	Qy
OC Eukaryota; Viridiplantae; S: OC Spermatophyta; Magnoliophyta		254	QQ
		995 TCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGC 1045	QY
		241 AlaArgGluvalAlaLeuAspProvalAlaAlaAlaLys253	qq
01-NOV-1998 (TrEMBLrel. 01-NOV-1998 (TrEMBLrel.		GGCCCCACCGAGCCAC	Qy
ID 080605 PRELIMINARY; AC 080605;		::: ::::: 221 AlaAlaPheLeuValAlaValValPheLeuGlyLeuSerThrAlaValThrMetValPhe 240	qa
RESULT 41 080605		878 CICITIGGCCIGCICACCICAICTICCICACCIGCGIAGCAGCCACACIGGIG 934	δλ
Db 477 AlaSerValPheAlaAla		-::: ::: -:: 201 HisLysTrpPheProPheLeuMetThrArgAlaCysCysGluAlaCysAlaAsnLeuLys 220	qq
OY 1835 CAGTCTGTCACTGCCTAT		839 AGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGC	δλ
Db 457 LeuGlyAlaGlyProTrp		::::::	QQ
Qy 1805 CIGITTAIGGGCICCAIT		782 ATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG	δλ
Db 439 LeuCysThrGly			QQ
Qy 1745 ATCTGCCTGGACCTCGCC.			ογ
Db 420ServalProPheAla			qq
Qy 1685 GTCTCCGTACGTGGTG		668 GIGGGGCIGCIGGACTICIGIGGCCAGGIGCTICACICCACIGGAGGCCCTGCICTCI 727	Qy
Db 406 AlaLeuPheValPheLeu			qq
Oy 1637 GGCCTGCTCCCA		626 CCGGAT	οy
Db 393		::: ::: :::	qa
QY : 15/7 CTGCCAGGCCCTAAGCCT		575 CTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGC 625	Qy

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GGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGT 1636
                                                                               -----CCTCCACCCGCGCTCTGCGGGCCTCTGCCTGTGAT 1684
                                                                                                                                                            GTGGGTGAGCCCACGAGGCCAGGGTGGTTCCGGGCCCGGGGC 1744
                                                                                                                                                                                                                                             ATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCC 1804
                       ||||||
|---AlaProAlaGluGluGlyGlyValArgAlaSerAlaLeu 405
                                                                                                                                                                                                                                                                       :::|||::: ::: ::: :::: ||||:::||| ::: | ValLeuAsnIleSerIleValValProGlnMetAlaIleAla 456
                                                                                                                                                                                                                                                                                                                                                      :::|||
AspGluLeuPheGlyGluGlyAsnIleProAlaPheAlaMet 476
                                                                                                                                                                                                     ValThrAlaGlnLeuThrAlaSerArgGlyGlyGlyGlnGly 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGAGGTGTTTTGGCCGCAGGCATCACCTAT----- 397
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transporter from Arabidopsis.";
EMBL/GenBank/DDBJ databases.
NTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                      ||||
|GlyLeuProPheAlaValLeuCys------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ear cress).
Treptophyta; Embryophyta; Tracheophyta;
a; eudicotyledons; core eudicots; Rosidae;
rassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S., Shea T.P., Fujii C.Y., Mason T.M., ser C.M., Somerville C.K., Venter J.C.; coome II BAC T17M13 genomic séquence."; EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
er (Sucrose transporter).
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120
72
174
131
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Db	640 nGlyAlaThrGlyGluProGlyLysAlaGlyGluGlnGlyGlyProGlyGluValGly 65	_
^0		1134 QY
7 A	GlyProGlyProSerGlySerArgGlyAspArgGlyPheProGlyGluArgGlyGlvIle	da 679
· >0	DOTTOPACTED TO THE TOTAL OF THE	1074 QY
' සි		069 Pp
οy		1032 QY
qq	700 ArgGlyGluSerGlyAlaAlaGlyAlaProGlyGlyMetGlyAlaProGlyLeuGlnGly 7	719
οy	1031 AAGCCAAGCGGGCCCGGCATGGACAGCAGCAGGGGGCCGACAAGGGGGCCGACA 9	978
οp		739
Οy	977 GCCCITCTGCTGGCTGGGGCCCAGGGCTGCCTCCTCAGCCACCAGCAGTGTGGCTG 9	918 Db
QQ		748 BESHIT A
Qy		0944V ID
Op	749GlyLysAspGlyMetArgGlyMetThrGlyProIleGlyProPro 7	763 AC Q944
οy		798 DT 01-1
Db	764 GlyProThrGlyAlaHisGlyGluLysGlyGluGlyGlyLeuGlyGlyProProGlyPro 7	783 DE Suci
Qy		744 OC EUK
q	784 ThrGlyGlyArgGlySerProGlyGluArgGlyGluHisGly 7	797 OC Ehri
Qy	743 GGTCCCGGAAGAGGTCAGAGAGCAGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGA 6	684 RN [1]
qa		817 RC STRI
Qγ	683AGTCCAGCACCCCACGATGAGCA 6	654 RA Furi
QQ	SlyProGlyGlyPro	837 RT (OS:
Οy		
Ор		857 DR Pfar
Qy	596 TTGGGATGAGAAAGAGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGC 5	
qa		869 Alignmen
Ογ	536 GGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACACAGACCA 4	477 Score:
Db	AlaPro	883 Best Local
Oy	476 GGCCCAGCACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCCCACTT 4	417 DB:
qq	Gly	068 US-09-75
Qy	416 CCAGCAGCAGCAGCACATAGGTGATGCCTGCGGCCAAACACCCTCCAGGCCAAAGG 3	357 QY
Db		901 da da
οy	356TTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGT 3	321 Qy
QQ		921 Db
Οy		288 Qy
Ωp	922 SerGlyAlaSerGlyAlaLysGlyAsnAspGlyProMetGlyAlaProGlyThrProGly 9	941 Db
Οy		258 Qy
Db	942 Pro-GlyGlyIleAlaGlyGlnArgGlyIleValGlyGlyProGlyGlyArgGlyProSe 9	961 Db

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991 tGly-ProProGlyLeu-----SerGlyAlaProGlyGluAlaGlyArg---GluG 1007
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                          395 TATGTGCCGCCTCTGCTGCAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTG 454
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257 GGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTC 198
                                                                                         197 TCCTCCTTGCTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTT 138
                                                                                                                                       976 nGlyProGlyGlyProValGlyGluArgGlySerProGly-------ProMe 991
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                                                                                                                                                                                     137 TGGTGCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGCTGCTGTGGGGCACCTCAGTG 78
                                                                                                                                                                                                                                                                               94 ----- 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      za sativa (indica cultivar-group).
aryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
rmatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae;
hartoideae; Oryzeae; Oryza.
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Lfeld P.R., Aoki N., Scofield G.N., Hirose T., Terao T.,
Dank R.T.;
                                                                                                                                                                                                                                                                               77 GGGACACGTCTCACTCAGATCCTGGCCGA--------
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mitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
BL; AR419298; AAL14982.1; -.
BL; AR41903662; sub_transporter.
In: PF00083; sugar_tr; 1.
SRFAMS; TIGR01301; GPH_sucrose; 1.
SRFAMS; TIGR01301; GPH_sucrose; 1.
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4W2;
DEC-2001 (TrEMBLrel. 19, Created)
DEC-2001 (TrEMBLrel. 19, Last sequence update)
JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Matches:
Conservative:
Mismatches:
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ProGlyPheProGlyGlyAlaGlyAlaLySGlyGluThrGlyProGlnGlyGlyArgGly GAGGCAGCCCCTCCACCCCAATGTGCT [SerAsp61yProGlnG1ySerArg61yGluProG1yAsnProG1yProAlaG1yAlaAla GGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGC	3/4 GIYFIGSer 376 1894 AAAGTAAATGGCGACCCAGCCCTGCGCAGACACCATATAGGCAGTGA 1842 1877 GIYAlaProGlyGlyAspGlyGlnAlaGlyGlyLySGlySerThrGlyAlaAlaGlyIle 396	1841	1805 GGGATGGGGCCACCTGGACAGCAGGAGGCAC	17721ATCCAGGAGGGGAGGTCCAGCAGATGCCCCGGCCG 1734	1733	1697 CACGTACGGAGACATCACAGGCCCAGAGAGCGCGGGGGGGG	1637 CACTGCCTCCAGCACCCACGTGTCCATTAGGAAGGAGCTCCAGGC	1590TTAGGG	1568 TCATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGTATT 1521 :: :: :: ::	1520	1490 AGAGGGAGGCCAGTGTGTAGGCAGATCTGCAGGCTGAGAAGG 1446	1445 TGAACCCGGTGAGGGCGGCTGAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGG 1386	1385 CACCGGCAGCACAGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATC 1326	1325 GCTGCACCAGCCGGTCCATGACCAGAGAAGACCAGGAGATGCGCACTGCAGGAACA 1266	1265 GCCCCAGGCTGCCCATCCAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCG 1209	1208 GCTCAGCTCTGGGCACGCCTGGTACAGCCCTCGCCCACGAAATCCGTGTGAAAACA 1152 ::::::
qa .	8 & E	9 y	Qy	Qy	Qy Db	Qy	Qy Dp	Qy Dp	Qy	oy Ob	Oy Db	QY	QY	QY	da Db	QY	Oy
Db 474 lAlaAlaThrValSerGlyIleIleAlaLeuThrAlaLeuProSerProProSer 492 Qy 1666 CGGGGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGGT 1708	SULT 10B9 09	DT 01-DEC-2001 (TrEMBLrel. 19, Created) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-UN-2002 (TrEMBLrel. 21, Last annotation update) DE Collagen a3(I).	Oncor Eukar Actir Prote		RA Saito M., Takenouchi Y., Kunisaki N., Kimura S.; RT "Complete primary structure of rainbow trout type I collagen RT consisting of al(1)a2(1)a3(1) heterotrimers."; RL Bur. J. Blochem. 268:2817-2827/2001)	DR EMBL; AB052836; BAB55662.1; - DR InterPro; IPR000087; Collagen. DR InterPro; IPR000885; Fib_collagen_C. DR InterPro; IPR001007: WWF C.	DR Pfam; PF01410; COLFI; 1. DR Pfam; PF01391; Collagen; 18. DR ProDom; PD0000007; Collagen; 1. DR ProDom; PD002078; Fib. collagen C: 1	PROSITE; PS01208; VWFC; UNKNOWN_1. SEQUENCE 1458 AA; 137758 MW; Plument Scores	Pred. No.: 3.74e-13 Length: 1458 Score: 330.50 Matches: 247 Percent Similarity: 30.72% Conservative: 47 Best Local Similarity: 25.81% Mismatches: 320	5.31% Indels: 13 Gaps: 3410) x 0910B9 (1-1458)			GAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCTCCCT	ACTGG	Qy 2140 GGACAGAGAGGAGAGGACCCCCAGCCTGTGCAGCTACGCACCTCAGCAGCACAG 2081	CAGAAACTGGCGGCCAGCCGGCAG	13

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1621 GGGTGCTGGAGGCAGTGGCCTG--
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-TAGGGCTCAGGGGGCCGT 251
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MEDLINE-21444505; PubMed-11523659;
MEDLINE-21444505; PubMed-11523659;
Monop C., Voltsekhovskaja O., Lohaus G.;
"Sucrose transports in two members of the Scrophulariaceae with different types of transport sugar.";
Planta 213:80-91(2001).
EMBL; AF191025; AAF04295.2; -.
Interpro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
SEQUENCE 502 AA; 52327 MW; E754CD030536522D CRC64;
                                                                 250 TCAGGCACTCCAGAACTGCTTCGTCTCGCTCTGCTCCAGAAGCTGCG 203
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nGlyProCysArgAlaLeuLeuAlaAspMetSerAlaGlyAsnAlaLysLysMetSerSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::: |||| |||||| ::: |||| ||||||| 326 nSerValValLeuGlyValAlaSerLeuGlyValGlnValThrAlaArgGlyLeuGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ACTCGAGCAGTCTATTTGGCCAGTGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 yValLysArgLeuTrpGlySerValAsnLeuLeuLeuAlaIleCysLeuAlaMetThrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 lLeuIleThrLysMetAlaGlnHisHisArgGluTyrAlaSerValGlyGlyAlaAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1390 ATGCCTGTCC-----CACAGTGTGGCCGTG---GTGACAGCTTCAGCCGCCCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SerSerAsnSerGlyAlaGlyGlyLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ATGACCAGCTTCCTGCC
                                                                      760 GGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTAC-----
                                                                                                                                                                        -------CTCCTGCCTGCCATTGACTGGGAC---ACCAGTGCCCTGGCCCCTA
                                                                                                                                                                                                                                                                                                                        rCysAlaAsnLeuLysSerCysPhePheIleSerValAlaLeuLeuLeuThrValThrIl
                                                                                                                                                                                                                                                                                                                                                                             tTrpMetLeuLeuLeuValThrAlaLeuAsnTrpValAlaTrpPheProPheLeuLeuPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uGlyIleProLeuAlaAlaThrPheSerIleProPheAlaLeuAlaSerIleTyr----
                                                                                                   ySerTyrThrArgLeuTyrLysValPheProPheSerLysThrGluAlaCysAlaVaLTy
                                                                                                                                                                                                                                                                         CCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GluAlaGlyThrValLysLysHisThrValProValPheGlyGluLeu----
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                                                                                                                                                                                                                                                                                                                                                                                                                               229 eIleAlaLeuCysIleValArqGluThrProTyrThrAlaProProGlu----
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531 yGluArgGlyProSerGlyLeuAlaGlyProLysGlyAlaAsnGl 546	1883 GGACCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGC 1837	TOOLOGE THE STREET STREET STREET STREET STREET STREET STREET SOUTH	563 rdlyArgProGlyAspAlaGlyProGlnGlyLysValGlyProSerGlyAlaProGlyGl 583		 583 uAspGlyArgProGlyProProGlyProGlnGlyAlaArgGlyGlnProGlyValMetGl 603	1773 CTATCCAGGATGGCGAGGTCCAGGCAGATGCCCCGGC	603 yPheProGlyProLysGlyAlaAsnGlyGluProGlyLysAlaGlyGluLysGlyLeuPr 623	1734 GGAACCACCCTGGCCTCGGTGGGCTCACCCACCACGTACGGAGACATCACAGGCA 1675	623 o-GlyalaProdlyLeuArgGlyLeu-ProGlyLysAspGlyGluThrGlyAlaAla 641	1674 GAGGCCCCGCAGAGCGCGGTGGAGCAGG	642 GlyProProGlyProAlaGlyProAlaGlyGluArgGlyGluGlnGlyAlaProGlyPro 661	1638 1603	662 SerGlyPheGlnGlyLeuProGlyProProGlyProProGlyGluGlyGlyLySProGly 681	1602	682 AspGlnGlyValProGlyGluAlaGlyAlaProGlyLeuValGlyPro-ArgGlyGluAr 701	1571TGGTCATCAGGCTGTCCTCACTAGCACCTCCAGTGTCCCCTCGGTAT 1522	701 gGlyPheProGlyGluArgGlySerProGlyAlaGlnGlyLeuGlnGlyProArgGlyEr 721	1521 TTGGGCAGGAACACCTGCTTCTCCCGGTGGTGGGGGGGGG	721 uProGlyThrProGlyThrAspGlyProLySGlyAlaSerGlyProAlaGlyProPr 740	1476 GIGTAGGGCAGGATCTGCAGGGCTGAGGTGAACCCGGTGAGGCTGAAGGTG 1419	740 oGlyAlaGlnGlyProProGlyLeu-GlnGlyMetProGlyGluArgGlyAlaAlaGlyI 760	1418TCACCACGCCACACTGTGGGACAGGCATGTGGCACCGGGAGCCACAGGGAAAGC 1364	760 leAlaGlyProLysGlyAspArgGlyAspValGlyGluLysGlyProGluGlyAlaP 779	1363 IGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCAGCGGGTC 1310	779 roGlyLysAspGlyGlyArgGlyLeuThrGlyProlleGlyProProGlyProAlaGlyA 799	1309 CATGACCAGAGAGAAGACCAGGGAGATGGCGCACTGCAGGAACAGCCC 1262	sGlyGluValGlyPro	1261 CAGGCTGCCCATCCAAGGCCTTCATAGTGTCTCCGGGCTCGGTGGCCCGGGTCAGC 1202	818 rgGlyAlaProGlyGluArgGlyGluThrGlyProProGlyProAlaGlyP 835	1201 TCTGGGCACGCCTGGTACA 1182	835 heAlaGlyProProGlyAlaAspGlyGlnProGlyAlaLysGlyGluGlnGlyGluAlaG 855	1181GCCCTCGCCCACGAAATCCGTGAAAACAGCGTGAAGGT 1142	855 lyGlnLysGlyAspAlaGlyAlaProGlyProGlnGlyProSerGlyAlaProGlyP 874	1141 CATGAGTGCCATCCAGCTGCAGGAGGAGGGGGGGGGGGG	874 roGlnGlyProThrGlyValThrGlyProLySGlyAlaArgGlyAlaGlnGlyProP 893
qq	Oy 1			Qy 1	qa	0y 1	qq		qq				qq	0y 1	QQ	0y 1	qa	0y 1	qq	0y 1	qa	0y 1.	qq	0y 1:	Dp	Oy 1:	q	0y 1:	qq	0y 1:	Dp	0y 1:	qa qa	0y 1:	ପୁପ

į	1001		
S G	1001	GUGGGGGCCCCAGGTTCCGGAA III :: III II	1031
Qy	1030		
Db	913	aArgG	933
Qy	1010	r) -	953
qq	933	-GlnGlyP	949
Qy	952	D	938
QQ	949	-	696
Qy	937		878
Db	696		981
Qy	877	:	855
Dp	981		1001
Qy	854	AGGGGG	849
Db	1001	 yProProGlyP	1021
Qy	848	STAGCCCAGGCA	800
QQ	1021	YProProGlyLeuThrGlyProSerGlyGluProGly-	1035
Qy	799		740
qq	1036	::: gGluGlySerProGlyAlaAspGlyProP	1046
Qy	739		704
Dp	1046		1064
Qy	703		647
Db	1065	GlýðlaProGlyAlaProGlySerProGlySerProGlyProAlaGlyProT	1082
Qy	646		587.
Db	1082	 aGlnGlyProMetGlyP	1099
Qy	586	909	536
Db	1099	 roGlnGlyProArgGlyAspL	1118
Οy	535	GCGGCCATAGCGTCCACGCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACACAGA 4	180
QQ	1118	ysGlyGluAlaGlyGluAlaGlyGluArgGlyLeuLysGlyH1SArgGlyP 1	.135
ΟY	479	T 4	28
pp	1135	heThrGlyLeuGlnGlyLeuProGlyProProGlyProSerGlyAspGlnGlyAlaSerG 1	1155
Oy	457	CCAGCAGCAGAGG	404
Db	1155	::: yProSerGlyLysA	1175
Qy	403		344
Db	1175	spGlyAlaAsnGlyIleProGlyProIleGlyProProGlyProArg 1	190
Qy	343		287
Db	1191	 roAlaGlyProProGlyAsnProGlyP	1210

Db 249 yLysPro 251 Qy 2792 AAGGTCCTGGGTTAGGCATTTTGGGGGCCAGACCCCAGGAGAAGAATTCTGGCAATG 2733	Oy 2732 ATCAGCCCAATGACCAGCTATCTCAGGGAACCTGATTGTTGGGGATCCCCCACCCTACCC 2673	OY 2672 AAATATTAGACACCAACAGAAAAGCTAGCAATGGATTCCCTTCTACTTTGTTAAATAA 2613 :::	OY 2612 ATAAGTTAAATTTTAAATGCCTGTGTCTCTGTGATGGCAACAGAGGCCAACAGGCCA 2553	Qy 2552 CATCCTGATAAAAGGTAAGAGGGGGTGGATCAGCAAAAAGACAGTGCTGTGGGCTGAGG 2493 ::: ::	OY 2492 GGACCTGGTTCTTGTGTGTTGCCCTCAGGACTCTTCCCCTACAATAAGTCATATGTTC 2433	OY 2432 AAATCCCATGGAGGGTGTTTCATCCTAGAAACTCCCATGCAAGAGCTACATTAAACGAA 2373 ::	QY 2372 GCTGCAGGTTAAGGGGCTTAGAGATGGGAAACCAGGTGACTGAGTTTATTCAGC 2319 . 11	QY 2318 TCCCAAAAACCTTCTCTAGGTGTCTCTCAACTAGGAGGCTGGTTA 2270	OY 2269	Qy 2234 GCATTCCAGTGCATGGAGCCTTCTGGCCTCCCTGTATAAGTCCAGACTGAAACCCC 2178	Qy 2177 CTTGGAAGGCCTCCAGTCAGGCAGCAGAGACTGGGGAGAGG 2133 :: :: :: Db tyhrAspGlyIleProGlyAlaLysGlySerAlaGlyAlaProGlyIleAlaGlyAlaPr 431	Oy 2132 GGGAGGGACGCCCCAGCTGTGCAGCTACGCACCTCAGCAGC 2085	Qy 2084 ACAGGGTGGCAGCAGAGAGCCACATTACTTTGGCAGCAAACTGGCGGCCAGCCG 2025 ::: :::	Qy 2024 GCAGCCCATGGGGCTAACAGGAGCGGGAGCTGGGACCCAGT	Qy 1981GAGGCAGGCCCTCCACCCAATGTGCTGG 1953 11 1 1 1 1 1 1 1 1	Qy 1952 AAGTTTTCTACGCTGAGTATTTGCCCAAGTCGCTCTTGTC	Qy 1912
454 ServalGlyGlyGlyProPheAspGluLeul 1592 CCTGGAGCTCCCTTCCCTAATGGACACGTG 111 1 1 1 1 1 1 1 1 1	1646CCACCTC 111111 488 ThrValLeuProSerProProProf	30L 775		·	RN (1) RP SEQUENCE FROM N.A. RX MEDIINE=98340920; Pubmed=9676231; RA Du F., Acland G.M., Ray J.;		RX MEDLINE=20480698; PubMed=11024291; RA Du F., Acland G.M., Ray J.; RT "Cloning and expression of type II collagen MRNA: evaluation as a RT candidate for canine oculo-skeletal dysplasia.";	RL Gene 255:307-316(2000). DR EMBL, ARC021169; AAC62178.2; DR InterPro; IPR000087; Collagen. DR InterPro; IPR000885; Fib_collagen_C.			PROSITE; PSULZUB; VWFC; L. Collagen. SEQUENCE 1487 AA; 141875 MW; 25873EACIE311DB8 CRC64;	2.79e-13 332.50 31.42%	: 25.25 Mismacones: 5.34% Indels: 6 Gaps:	-09-759-143-110 (1-3410) x 077753 (1-1487) 3032 GTGGGAAAGTTGGGGGTAGGGGAAAGTTGGGCAGTGCCTTC :::[1] :::[1]	203 MetGlyProMetGlyProArgGlyProProLighProAlgGlyAlghrochyPro 2972 ATCAGCCCAGTCCTAGAGAGAGTACAGGGGAAGTGGAAGTGGGGGAACCAGGCTGGGCA [Db 221	Db 231 GlyGluProGlyValSerGlyProMetGlyProArgGlyProProGly-ProProGl 249 Qy 2852 CAACACCCTAACCTTGGGTAACAGCATTTGGAATTATCATTTGGGATGAGTAGAATTTCC 2793

qa		qa	 123 GlyAspGlnLeuAspLysProProArgThrArg
Qy Db	178 CTGCCTAGGAATCAGCCAGGCCCATTCTGCCAGCCCTTGGTGCCGGTCCAGCTTT 119 	Qy	671 GGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTC ::: 143 TrplleLeuAspValAlaAsnAsnThrLeuGln
δλ	118 CAGCCCATGCTCAACACCTGCTGCTGTGG	Qy	
g i	GlyProThr	qa	163 LeuSerAlaGlyAsnAlaLysLysThrArgThr
O.Y	58 AGATCCTGGC 49 1561 yProprodly 1564	Qy Db	788 AGTCTTCGGGGCTGCCTGGGCTAC
RES	RESULT 36	δ	827 GACTGGGACACCAGTGCCCTGGCCCCTAC
A L S	QBYXX3 ID QBYXX3 PRELIMINARY; PRT; 508 AA. AC 08YXX3:	g qa	
0 0 0 0 0	01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Sucrose transporter SUC2.	Oy Db	884 GGCCTGCTCACCCTCATCTTCCTCACCTGCGTA :: :: 223 LeuSerlleThrLeuLeuLeuValThrPhe
08 00 00	SUC2. Brassica oleracea (Cauliflower). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Qy	944 GCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGG
888	Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica. MCBT TaxTD=3713.	λŏ	TGC
R R	SEQUENCE FROM N. A.	qq	::
RA RA	Coupe S.A., Sinclair B.K., Bucknell T.T., Greer L.A., Eason J.R., Heyes I A	Qy	1058 CGGCTGCACCAGCTGTGCTGCCGCATGCCCCGC
RT	"The isolation and characterization of sucrose transporter homologs from broccoli and their role in sucrose mobilization during	qa	111 271LysArg
RT RL DR	senescence "; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AX1065840; AAL58072.1;	Qy	1118 CTGTGCAGCTGGATGGCACTCATGACCTTCACG
DR OS	InterPro; IPR003662; sub_transporter. Pfam; PF00083; supar_tr; 1. SROTERVE 408 as a 4.016 Ms. B1222A10100ERN06.	oy ba	
Ali	Alianment Scores:	qa	::: 302 GluValTyrGlyGlyAsnSerAspAlaThrAla
Pred. Score	2.34e-13 Length: 332.50 Matches:	ΟY	1238 GAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTC
Per	ilarity: 41.578 Similarity: 24.518	QQ	322 AspGlyValArgAlaGlyAlaLeuGlyLeuMet
Que DB:	Indels: Gaps:	QY	
-sn	US-09-759-143-110 (1-3410) x Q8VYX3 (1-508)	qq	
상 점	332 CAGCTCTTGCTGGTCAACCTGTACCTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATC 391 :::::::	Oy Dp	1358 GTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACA ;: 361 AlaValAsnPheIleLeuAlaIle
ò	' '	Qy	1414
q	SerLeuleufhrProTyrValGlnLeuleuGlylleProHisLysTrpAlaSerLeulle	qq	378 LysGlnAlaGluAsnHisArgArgAspHisGly
δò	452 CIGGGCAITGGTCCAGTGCTGGGCCTGTGTCCCCGGTCCTAGGCTCAGCCAGTGAC 511	δ	1415 GTGACAGCTTCAGCCGCCCCTC
QQ	66 TrpLeuCysGlyProlleSerGlyMetLeuValGlnProlleValGlyTyrHisSerAsp 85	q a	
δο á	CACTGGCGTGGACGCTATGGCCGCCGCCGTCATCTGGGCACTGTCCTTGGGCATC	yoy Qo	1451 TCAGCCCTGCAGATCCTGCCCTACACACTGGCCT 11
3 8	10	Qy	1505
S 8	5/2 CIGCLEARDCLUCTTCTCARGGGCGGGTGGCTGGGTGGGTGGGTGGGTGGGGGGGGGG	qa	434 GlyGlnGlyLeuSerLeuGlyValLeuAsnLeu
δō ,		Qy	1532 GACACTGGAGGTGCTAGCAGTGAGGACAGCCTG

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SGCTGTCGGCCCCCTCCTTGTCGCCCCAC 1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTTCCGGAACCTGGGCGCCCTGCTTCCC 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCCTGTTTTACACGGATTTCGTGGGCGAG 1177
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                                                                                                                                                                                                                                                                                                                                     TAGCAGCCACACTGCTGGTGGCTGAGGAG 943
                                                                                                                                                                                                                                                                                                                                                              heMetSerLeuCysTyrValThrGluLys 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -CAGGTGTTCCTGCCCAAATACCGAGGG 1531
:::|||:::
rgAlaIleAlaIlePheAlaLeuGlyPhe 142
                                                                            hrAlaAsnAlaPhePheSerPhePheMet 182
                                                                                                                                                                                                                            lySerTyrLysAsnLeuTyrLysValVal 202
                                                                                                                                                                                                                                                                ACCTGGGCACCCAGGAGGAGTGCCTCTTT 883
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rgProMetTrpMetLeuLeuIleValThr 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aSerValAlaSerLysLysLeuTyrAsn 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stLeuAsnAlaIleValLeuGlyPheMet 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||
|stGly---GlyAlaLysArgLeuTrpGly 360
                                                    TCACTCCACTGGAGGCCCTGCTCTGAC 730
                                                                                                                         AGGCCTACTCTGTCTATGCCTTCATGATC 787
                                                                                                                                                                                                -------826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yGlyAlaLysThrGlyProProGlyAsn 397
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aSerIlePheSerThrAsnSerGlyAla 433
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uAlaIleValValProGlnMetValVal 453
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Tue Jun 10 11:28:25 2003

1354 yProAla-----LysGlnAspGlyProProGlyAsp-----LysGl 1366 1461 roGlyPro-----MetGlyProProGlyLeuProGlyLeuLysGlyAspSerGlyProL 1479 1479 ysGlyGluLysGlyHisProGlyLeuIleGlyLeuIleGlyProProGlyGLuGlnGly- 1498 1499 GluLysGlyAspArgGlyLeuProGlyProGlnGlySerSerGlyProLysGlyGluGln 1518 1256 oArgGlyPro------SerGlyAlaProGlyAlaAspGlyProGlnGl 1270 1110 ACGAAGACCGGCGCAGGG---TGCGGGGCATGCGGCAGCACAGCT-----GGTGCAGC 1060 1059 CGGGGAAGCAGGCGCCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGCATGGACAGCAGTGG 1000 1310 uLysGlyGluSerGlyProSerGlyAlaAla------GlyProProGlyProLy 1326 1381 yGluProGlyProSerGlyProProGlyLysArgGlyPro------ 1394 1170 ACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACAGCTCAGCC 1111 367 CAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGGC- 309 286 CATACTGGG------CCAGGCGGGTAGGGCTCAGGGGGCCGTTCAGGCACTCCA 239 1230 TGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCCCCTCGCCC 1171 879 AGGCACTCCT------CCTGGGTGCCCAGGTAGGGGGCCAGGGCACTGGTG 835 834 TCCCAGTCAATGGCAGGCAGGCAGGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGCA 775 717 GCCTCCAGTGGAGTGAAGCACCTGGCCACAGAAGTCCAGCAGCCCCAGGATG 658 597 CTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCCAAGGACAGTGCCCAGATGAAGGGCCGG 538 537 CGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTG-----AGCCTAGGAGCGGGAC 485 484 ACAGACCAGGCCCA---GCACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTC 428 427 TACCCCCACTTCCAGCAGCAGAGGCGGCACATAGGTGATGCCTGCGGCCAAACACACCTC 368 -----GGCTCACCCACAGCCTCTGAC 287 999 GGCGACAAGGAGGGGGCCGACAGCCCTTCTGCTGGCTCGGTGGGGCCCAGCGCTGCCTCC 940 939 TCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAG 880 774 TAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGTCCCGGAAGAGGTCAGAGAGCAGG 718 αq qq op qq οp οy QQ ŏ g δ q à QQ οy g δλ ŏ a ò ŏ ò qq ò q õ q ò à qq ò g δ Db δ g δy

qa	۸٥	. <u>8</u>	Oy	qq	Qy	qa	Oy	qa	Oy	qα	Qy	qa	Qy	qa	δλ	qa	٥y	qa	Qy	qa	Qy	QQ	Oy.	qa	Qy	qq	Qy	qa	Qy	qa	Qy	qq	Qy	Db	,
Db 1166 uLysGlyGluThrGlyLeuLeuGlyAlaTyrProGlyProLysGl 1181	QY 306 CTCACCACACACATGGACCATAGTGGGCCAGGCGGGTAGGGCTCAG 259		Qy 258 GGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCT 199	Db 1201 roGlyArgLysGlyValMetGlyAspValGlyProGlnGlyProFroGlyThrAlaGlyL 1221	0y 198 CTCCTCCTTGCTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCT 139	Db 1221 euProGlyProProGlyLeuProGlyAlaileIleProGlyProL 1236	QY 138 TTGGTGCCGGTCCAGCTTCTC 118	Db 1236 ysGlyAspArgGlyLeuProGlyLeuArgGlyAsnProGlyGluProGlyProProGlyP 1256	Qy 117 AGCC 113	Db 1256 roPro 1257	SUI 509	ID Q15094 PRELIMINARY; PRT; 1838 AA. AC Q15094;	DT 01-NOV-1996 (TrEMBLrel. 01, Created) DT 01-NOV-1996 (TrEMBLrel. 01, Last Sequence update)	01-JUN-2002 (TrEMBLrel. 21, Last annotatio Pro-alpha-1 type V collagen.	COL5A1. Homo sapiens (Human).	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	NCBI_TaxID=9606; [1]		RA Greenspan D.S., Cheng W., Hoffman G.G.; RT "The pro-alpha 1(V) Collagen Chain. Complete primary etructure					InterPro;		DR ProDom: PD000007; Collagen; 1. DR ProDom: PD0000078: Fit collagen; 7.	ì	SMART; SM00210; TSPN; PROSITE; PS00294; PREN	KW Collagen. SQ SEQUENCE 1838 AA; 183610 MW; 5078307F6F00F0BA CPC64.	res:		larity: 31.57% Conservative: imilarity: 26.54% Mismatches:	5.35%	US-09-759-143-110 (1-3410) x Q15094 (1-1838)	

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3169 GCAGGGGGGCTCCTCAGGTTTCTGTGAGATTCCCCAAGCACAGATATACTCTGGGGGC 3110
                                                                                                                                           3109 TGAGATGGACAAAGGCTTGGGAAACCGCACTTTGT-------GCTTCTGGTCCT 3063
                                                                                                                                                                                                                                          3062 GCAGTAGCTCCAAACAGGGTTGTGGAGCTGGGGGAAAGTTGGGGGGTAGGGGAAAGTTG 3003
                                                                                                                                                                                                                                                                                                                                     2943 ------GAGTGGAAGTGGGAACCAG 2922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2921 GCTGGGCCAAGAGAAGAGGGGTGGTTAGGGAAGCCGTTGAGACCTGAAGCCCCACCCTCT 2862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2861 ACCTTCCTTCAACACCCTAACCTTGGGTAACAGCATTTGGAATTATCATTTGGGATGAGT 2802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2801 AGAATTTCCAAGGTCTGGGTTAGGCATTTTGGGGGGCCAGACCCCAGGAGAAGATT 2742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2703 ACCTGATTGTTGGGGATCCCCCACCTACCCAAATATTAGACACCAACAGAAAAGCTA 2644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2583 CTGTGATGGCAACAGAAGGACCAACAGGCCACATCCTGATAAAAGGTÅAGAGGGGGGTGG 2524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2523 ATCAGCAAAAAGACAGTGCTGTGGGCTGAGGGGACCTGGTTCTTGTGTGTTGCCCCTCAG 2464
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                                                                                              728 AlaGlnGlyLeuProGly------ProGlnGlyAlaIleGlyProProGly 742
                                                                                                                                                                          743 GluLysGlyPro---LeuGlyLysProGlyMetProGlyAlaAspGlyPro 761
                                                                                                                                                                                                                                                                                                                                                                         2643 GCAATGGATTCCCTTCTACTTTGTTAAATAAGTTAAATAATTAAATTAAATGCCTGTGTCT 2584
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708 LysGlyAsnValGlyProGlnGlyGluProGlyProProGlyGlnGlyAsnProGly 727
                                                                                                                                                                                                                                                                        762 ProGlyHisProGlyLysGlu--GlyProProGlyGluLysGlyGlnGlyProProG 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    797 laAspGlyIleArgGlyLeuLysGlyThrLysGlyGluLysGlyGluAspGlyPheProG 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  846 ysGlyArgGlyGlyProAsnGlyAspProGlyProLeuGlyProProGlyGluLysGlyL 866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          927 hrGlyLysProGly------ProLysGlyAsnSerGlyGlyAspGlyP 941
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Qy Db

3217 AAACGGCACTTAAACCCCCCCTGAGAGATAAGACCTCCCTTAGCTCAG------ 3170

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863 y	883 0	1164 T	n E06	1104 A	913 9	1044	927 9	1005 0	946 .	971	966	900	ט ממ	866	825	1014	165	1025	720	1045	099	1065	009	1077	543	1097	483	1111	444	1131	399	1151	360
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2131AGAGGGACGCCCCAGCCCCCAGCTGTGCAGCTACGCACCTCAG :::		ProProGlyProProGlyPheProGlyProProAlaGlyProA	CCCGGCAGCCCCATGGGGCTAACAGGACCGGGGGGCTGGGACCCCAGTGAGGCA			alProGlyValLeuGlyProPro	1929 GCCAAGTCGCTCTTGTCAAATACTACCTGTGTGTGAAAAGTAAATGGCCAACAAGAAAAAAAA	CTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGGCCATA	VProProGlyProPro		661GlyProProGlyGlnAlaGlyProArgGlyLeuProGlyDr		:::: 677 oValGlyLysCysAspProGlyLeuProGlyProAspGlyGluProGlyIleProGluAl	1730CCACCCTGGCCTCGGTGGCCTCACCACCACCACCACGTACGGACACACAC	-GlyAsnGlnGlyPheProGlyThrLySGly	TCACAGGCAGAGGCCCGCAGAGCGCGGGTGGAGGTGGGAGCAGCAGCACTGCAGCA	717 SerProGlyCysProGlyGluMetGlyLysProGlyArgProGlyGlu	1623 CCCACGTGTCCATTAGGGAAGGGACTCCAGGCTTAGGG	ProGlyIleProGlyAla	1585	753 ProGlyPheProGlyGluArgGlyAsnAlaGlyGluAsnGlyAspIleGlyLeuProGly	CTGGCAGGAAGCTGGTCATCAGGCT	773 LeubroGlyLeuProGlyThrProGlyArg			1485 GAGGCCAGTGTGTAGGGAGGATCTGCAGGCTGAGAGGTGAACCCGGTGAGGGCG			yLeuLysGlyGlnProGlyArgArgGlyAspinrGly			ATGACCAGAGAGAA 	1248 CGAACGCCTTCATCATGATGTCTCCGGG
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US-09-759-143-110 (1-3410) x Q9QZSO (1-1669)

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2939 GGAAGTGGGGGGAACCAGGCTGGGCCAAGAAGAAGAGGGGTGGTTAGGGAAGCCGTTGAGA 2880
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3029 GGGAAAGTTGGGGGTAGGGGAAAGTTGGGGGTA-------GGGGAAATTTTGGGC 2982
                                                                                                                                 --CTAGAGAGAGTAGAGGGGAGT 2940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2208 GCCTCCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTA 2149
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                                      373 ProSerGlyProProGly--ValProGlySerPro----------- 383
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                                                                                                                                                                     338 ProGlyPheProGlyProThrGluTyrTyrAspAlaTyrLeuGluLys------ 353
                                                                                                                                                                                                                                                                                                          354 GlyGluArgGlyMetProGlyLeuProGlyProLysGlyAlaArgGly---ProGlnGly 372
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------ValProGlyLeuLys---GlyAsnProGly------ 513
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Db	258 gGlyGluAspGlyMetAlaGlyAsnProGlySerValGlyProIl 273	ā	1361
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δō	1910 ATACTACCTGTGTGGCAAAGTAAATGGCGACCAGACCCAGGCCTGCGGACACC 1855	qq	657 laGl
gn i	TOTOCOLUMN TOTOCOLON TOTOC	Qy	940 CTCA
à t	ATATAGGCAGTGACTGGCTGAGCTGGACATGGAGCCCATAAACAGGGATGGGGCCC	QQ	677 rog1
a ·	OGLÝSEIGLIGGLÝGIUVALGLÝALAALJAGLÍKTIOGLÝALAGTHGT. SOGRADO	Qy	880 GAGG
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ð í	1585 GCCTGGCAGGAAGCTGGTCATCAGCTGTCTGCTAGCACCTCCAGTGTCCC 1529	qa	756 ThrG
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Š 2		qa	776 AlaA
3 6		QY	508 ACTG
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1261	CAGGCTGCCCATCCGAACGCCTTCATCATGATGTCTCCGGGCCTCGGTGCCCGGCTCAGC ::	1202 587
1201	TCTGGGCACGCCCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGT	1142
1141	CATGAGTGCCATCCAGCTGCACAGCTCAGCAAAAAGCCGGCGCAGGGTGCGGGGCAT	1082 617
1081	GCGGCAGCACCAGCTGCAGCCGGGAAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGGGGGCGCCCAGGTTCCGGAAAGCCAAGGGGGCGCCCAGGTTCCGGAAAGCCAAGGGAAAGGTAGGT	1022 637
1021	GGCCCGGCATGGACAGCAGGGCGACAAGGAGGGGGCCGACAGCCCTT	972 657
971		941
940	CTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGAA (881 687
980	GAGGCACTCCTCGGGTGCCCAGGTAGGGGCCAGGGCACTGGTGTCCCAGTCAATGGC	821 698
820	AGGCAGGAGGTAGCCCAGGCAGCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGCCCCCAAGACTGATCATGAAGGCATAGACAGAGAAGCCAAGATAGAT	761 708
760	CTGGCGACAGTGGTCCGGGTCCCGGAAGATCAGAGAGCAGGGCCTCCAGTGG	707 728
706	AGTGAAGCACCCT:GGCCACAGAAGTCCAGCAGCCCCAGGATGAG	656
655	CAGTGCCAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAC	596 755
595	51yGluMetGlyGlnThrGlySerAspGlyLysAspGlyAlaLysGlyAspThrGly	569 775
9	CAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCAgGCC :::	509 790
506	CTGAGCCTAGGAGCGGGACACAGGCAGG 	449 809
448	TGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGAAA	389 824
386	TGCGCCAAACACCTCCAGGCCAAAGGTTAGCA	351 844
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3077 TGTGCTTCTGGTCCTGCAGTAGCTCCAAACAGGGTTGTGGAGCTGGTGGGGGAAAGTTGGG 3018
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101 ---GlnGlyAsnValLysAlaAlaProAlaTyrSerProGlnTyrTyrSerProGlyAla 119
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                                                                                                                                                                                                                                                                                                                                                                                                                            140 MetArgGlyGluSerGlyAspProGlyProProGlySerThr-Gly------ 154
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δλ	US-09-759-143-110 (1-3410) x Q9XHL6 (1-524)	
Qy	5,19% Indels: 10 Gaps:	
qa	39.39% Conservative: 25.18% Mismatches:	
Qy	Scores: 2.18e-13 Length:	
qa	SEQUENCE 524 AA; 55279 MW; B5CE3F880D2C1E6B	
Qy	TIGREAMS; TIGR01301; GPH_sucrose; 1. Transmembrane.	
qa	InterPro; IPR003662; Pfam; PF00083; sugar_	
φ.		
Qy Db		
qa		
O.Y		
qq		
Qy		
Qy D		
qa .	Q9XHL6 PRELIMINARY; PRT; 524 AA.	
Qy	RESULT 32	
G G	1032 CCACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	
3 .	401 ValValelyAla	
Oy 40	1.607 CCTAATGGACAC	
q _Q	Db 467 ProTrpAspAspLeuPheGlyGlyGlyAsnLeuProGly	
ογ	1547	
g da	447 LeuGlyValLeuAsnLeuAlaIleValValProGlnMetLeuValSerLeuValGlyGly 466	
2 0	4.2/ ILEKIOFHEALGDEUALGSELILEFHESSELSELASHALGSELSTGLIGTYSTHOLTST 14.0	
QY 4	1466 CTGCCCTACACACTGGCCTCCTCTACCACGGGAGAAG	
qa	407 LysileGlyAla	
Qy	Qy 1448 1465	
qa	387 AlaGluLysSerArgGlnH	
QY	Qy 1418 1447	
qa	Db 370 AsnPheValLeuAlaIleCysLeuAlaMetThrIleLeuValThrLysMet 386	
٥٧	SCTGCCG	
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	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	351 GiyiaiGuinhecorocorocorocorocorocorocorocorocorocor

256 CCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCT 315

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AGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCA 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 userGlyAlaPheLysGluLeu----- 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GlyGlyThrValGlyGluGlyHisAlaTy 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rLysLeuTyrHisValPheProPheThrLysThrGl 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCAT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::: ||| ||| ||| |||::
nLeuLysSerCysPhePheLeuSerIleAlaLeuLe 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aPhePheSerPhePheMetAlaValGlyAsnValLe 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-----TGGGACACCAG 840
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                                                                                                                                                           -------348
                                                                                                                                                                                                                                                                                                                                                                         STGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAAGTTCATGACCATGGTGCTGGCCATTGGTCCAGT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lvalGlyTyrHisSerAspArgCysThrSerArgPh 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3GCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCT 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGCTG-----CTGTGCCC 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCT 804
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l oy	qa	QY	qq	VO .	q a	oy.	ଫୁପ	0y	ସ ପ	ογ 	q a	0y	q a	δδ	qq	φ	qa	ον	qa		qa —	, o	qa —	 	ng (λο 	qa	ογ	qq	yo .	qa	Qy	අ	۵y	qa —
QY 1475 ACACTGGCCTCCTCTACCACGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGC 1534	Db 384GlnHisGlnArgGlnHis389	QY 1535 ACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCT 1594	Db 389 389	CTGCTCCCACCTCCA 16	:::	TCTCCGTACGTGTGGTGAG	Db 399 SerAlaGlyValLysAlaGlyAlaLeuSerLeuPheSerIleLeuGlyIlePro 416	Qy 1715 ACCGAGGCCAGGGTGGTTCCG	 Db 417 LeuSerIleThrPheSerIleProPheAlaLeuAlaSerIleTyrSerSerGlySerGly 436	OY 1739 CGGGGCATCTGCACCTCGCCATCCTGGATAGTGCCTTCCTGCTGCTGCCAGGTGGCC 1798	Db 437 AlaGlyGlnGlyLeuSerLeuGlyValLeuAsnLeuAlaIleValValProGlnMetIle 456	OY 1799 CCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTAT 1852	Db 457 ValSerValLeuAlaG1yProPheAspSerLeuPheG1yG1yG1yG1yAsnLeuProAlaPhe 476	Qy 1853 ATGGTGTCTGCCGCAGGCCTGGGTCGCCATT 1888	Db 477 ValValGlyAlaIleSerAlaAlaIleSerGlyValLeuAlaIle 491	31	36	Q43653; 01-NOV-1996 (TTEMBLTS) 01 CTOSTORY	Lrel. 01,	Sucrose transport protein.	Solanum tuberosum (Potato), Enkaroota: Viridialantas, etrontonhuta, Embancalantas	OC Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;		RC STRAIN=CV. DESIRBE; TISSUE=LEAF; RX MEDLINE=94146554; PubMed=8312741:	mer W.B.;	in phloem loading.";	-1- St	EMBL; Abylbs; CAA4891 InterPro; IPR003662;	DR Pfam; PF00083; sugar_tr; 1. DR TIGRFAMs; TIGR01301; GPH sucrose; 1,	Transmembrane. SEQUENCE 516 AA; 5483]		2.18e-13 Length:	t Similarity: 41.938 ocal Similarity: 24.688	5.19% Indels: 10 Gaps:	US-09-759-143-110 (1-3410) x Q43653 (1-516)

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1004 TGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG 1063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 GlyAsnIleLeuGlyTyrAlaAlaGlySerTyrSerHisLeuPheLysValPheProPhe 210
278 CCCACTATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 --- CTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGCTG 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        677 CTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTCACCTCTTC 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 LeuAspValAlaAsnAsnMetLeuGlnGlyProCysArgAlaLeuLeuAlaAspLeuSer 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               737 CGGGACCCGGAC---CACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTT 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 GlyGlyLysSerGlyArgMetArgThrAlaAsnAlaPhePheSerPhePheMetAlaVal 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 SerLysThrLysAlaCysAspMetTyrCysAlaAsnLeuLysSerCysPhePheIleAla 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 ------LysSerLysValProPhe-----PheGlyGluIlePheGlyAlaLeu 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 TIGCIGGICAACCIGCIAACCITIGGCCIGGAGGIGIGITIIGGCCGCAGGCAICACCIAI 397
                                                                                                                                                                                                                                     GIGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGC 457
                                                                                                                                                                                                                                                                          458 ATTGGTCCAGTGCTGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGG 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 887 CTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG--- 943
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331 ValArgAlaGlyAlaMetGlyLeuLeuGlnSerValValLeuGlyPheMetSerLeu 350
                                                                    ...----Lysile 33
                                                                                                                                                                                                                                                                                                                                                                                          34 IlevalValAlaSerIleAlaAlaGlyValGlnPheGlyTrpAlaLeuGlnLeuSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             578 AGCCTCTTTCTCATCCCAAGGCCGGCTGGCTAGCAGGGCTG-----
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                                                       24 ProLeuAlaProSerLysLeuTrp------
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Db 53 SerLeuLeuThrPrOTyrValGlnLeuLeuGlyllePrOHisLysTrpAlaAlaTyrlle 72 0., 452 cmgggrgamggggggggggggggggggggggggggggggg	73 TrpLeuCysGlybroileSerGlyMetLeuValGlnbroileValGlyTyrTyrSerAsp	Qy 512 CACTGGCGTGGACGCTATGGCCGCGCGCGCCCTTCATCTGGGCATGTCCTTGGGCATC 571 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1	Qy 572 CTGCTGAGCCTCTTTCTCATCCCAAGGGCCGCCTGGCTAGGAGGCTGCTG 622 ::	Qy 623 TGCCCGGATCCCAGGCCCCTGGAGCTGCCATGCTGGGC 667	Oy 668 GTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTT 727 11 11 11 11 11 11 11 11 11 11 11 11 11	OY 728 GACCTCTTCGGGGACCCGGACCACTGTCGCCGGCCTACTCTATGTGTGT 784	Oy 785 ATCAGTCTTGGGGGTGCCTGGGCTACCTCCTG 817 :::::::	Qy 818 CCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGC 877	Qy 878CTCTTTGGCCTGCTCACCTCACCTGCGTAGCAGCCACACTGCTGGTG 934 ::: ::::: :: Db 228 PhelleleSerlleValLeuLeullePhelleThrValLeuAlaLeuThrVal 245	Qy 935 GCTGAGGAGCAGCGCTGGGCCCCACCAGCAGCAGAAGGGCTGTGGGCCCCCTTG 994	Qy 995 TGGCCCACTGCTGTCCATGCCGGCCCGCTTGGCTTTCCGGAACCTGGGCCCCTGCTT 1054	QY 1055 CCCCGGCTGCAGCTGCTGCCGCATGCCGGCCGGCCGGCTCTTGGTGGCT 1114	Qy 1115 GAGCTGTGCAGCTGGATGGCACTCATGACGTTTTACACGGATTTCGTGGGC 1174	Qy 1175 GAGGGCTGTACCAGGGCTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAACACTAT 1234	Qy 1235 GATGAAGGCGTTCGGATGGCCAGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTC 1294	OY 1295 TTCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCC 1354	1355	
1241	0y 314 GCAGGGGGCTGCCCCAGACCCTGGGCCCCAGACATAGGGCCCCAGACATAGGGCCAGACATAGGGCCCAGAGGGCCCAGAGGGCCCCAGAGGGCCCCAGAGGGCCCCAGAGGGCCCCAGAGGGCCCCAGAGGGCCCCAGAGGGGCCCAGAGGGGCCCAGAGGGGCCCAGAGGGGGCCCAGGGGGG	Qy 274GGCGGGTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCT 225	1300	Qy 206 rgcggccrcrccrccrrgcrgccgc	Qy 161 AGGCGCCCATTTCTGCCAGCCTTTGGTGCCGGTCCAGCTTCTCAGCC 114	OY 113 CATGCTCAACACCTGCTGCTGGGGCACCTCAGGGGACACGTCTCATCACTCAGATC 54	CTGGCC : roGlyG	RESULT 30 Q92TB9 ID Q92TB9 PRELIMINARY; PRT; 512 AA.	AC Q92TB9; DT 01-MAY-1999 (TrEMBLrel. 10, Created) DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) DT 01-UN-2002 (TrEMBLrel. 21, Last annotation update)			RP SEQUENCE FROM N.A. RC TISSUE-LEAF; RA Noizerud N., Delrot S., Lemoine R.; RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.	CC -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY). DR EMBL; AF063400; AAC99332.1; DR InterPro: IPR003662; sub_transporter. DR Pfam: PF00083; sugar_tr; 1.	DR TIGRFAMS; TIGR01301; GPH_sucrose; 1. KW Transmembrane. SQ SEQUENCE 512 AA; 54520 MW; 4D76A7854A7DF903 CRC64;	2.17e-13 Length: 333.00 Matches: 40.54% Conservati	Mismatches: Indels: Gaps:	US-09-759-143-110 (1-3410) x Q9ZTB9 (1-512) Qy 332 CAGCTCTTGCTGGTGAACCTTTTGGCCTGGAGGTGTTTGGCCGCAGGCATC 391	Db 33 LysLeulleLeuvalalaAlarlealaAlaGlyvalGlnPheGlyTrpAlaLeuGlnLeu 52 Oy 392 ACCTATGTGCTGCTGCTGGAGGTGGGGGTAGAGGAGAGTTCATGACCATGGTG 451

Page 42

- 1	λō		qa	 939 GlyGlyAspGlyProAlaGlyPro
-	gg	657 -GlyLeuProGlyAspAspGlyGluArgGlyAspAspGlyGluValGlyProArgGlyLe 676	O	1217 CGGTGCCTCGGCTCAGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTTCTGGCCTTCTGGCTTCTGCTTCTGCTCTGCTCTTCT
-	Οy	2123 GCCCCAGCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAG 2070	ī 2	
_	QQ	676 uProGlyGluProGlyProArgGlyLeuLeuGlyProLySGlyProProGlyProProGl 696	2	
~	Οy	2069 AGAGCCACATTACTTTGGCAGCAACAGAACTGGCGGCCAGCCCGGCAGCCCCATGGGGC 2010	δλ	AAGGTCAT
_	Dp		qq	973 LysAspGlyLe
J	Qy	2009 TAACAGGAGCGGGGAGCTGGGACCCAGTGAGGCAGGCCCTCCAACAGTGTGCTGG 1953	δλ	1130 TCCAGCTGCACAGCTCAGCCACG
-	qq		qq	989 GlnGlyLysThrGlyProProGl;
~	ογ	TAGCAA	Qy	1070GCTGGTGCAGCCGGGGA
_	· 6		qa	1008 GlyGluThrGlyProMetGlyGl
	^	AGTAAATGGCGACCAGGCCCCCACGGCCCGACGGACAGGCCCAGGCCAGGCCGACGCAGGCCGACGGCACGGCACGGCACGGCACGGCACGGCACGGCACGGCACGACG	Qy	1019CCCGGCATGGACAG
-	7 6		qq	1028 GlnGlyLeuProGlyValAlaGl
	1 8		Qy	968 CTGGCTCGGTGGGGCCCAGCG
	S &	766 Hisborghy reserved to the control of the contro	QD	1044GlyProAlaGl
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-	gg	800 AspGlylleArgGlyLeuLysGlyThrLysGlyGluLysGlyGluAspGlyPheProGly 819	à)
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_	QQ	820 PheLysGlyAspMetGlyIleLysGlyAspArgGlyGluIleGlyProProGlyProArg 839	g i	1092 GIYGIUAFGGIYPFOAIA
•	Qy	1715 TGGGCTCACCCACCACACGTACGGAGACATCACAGGCAGAGGCCCCGCAGAGCGCGG 1656	δ	TCATGAAGGCATAGACA
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•	٥y	1655 GTGGAGGTGGGAGCAGGCCACTGCCTCCAGCACGTGTCCATTAGGGAAGGGAG 1599	0y .	725 AGAGCAGGGCCTCCAGTGGAGTG
ı	ф		අ <u>ග</u>	
J	Qy	1598 CTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAG 1545	Qy	665 CCAGGATGAGCAGTGCCAGCTCC
ı	qq	 871 alProGlyLeuProGlyTyrProGlyArgGln	qa	1133 aGlyArgAspGlyLeuG
J	Οy	1544 CACCICCAGIGICCCCICGGIAITIGGGCAGGAACACCIGCITCICCCGGIGGT 1491	Qy	605 AGCCGCCCTTGGGATGAG
1	QQ		qa	1150 ovalGlyProproGlyGluAspG
J	Qy		Οy	569 TGCCCAAGGACAGTGCCCAGATG
ш	qq		q _Q	1170 ySerLysGlyAspLysGlyGluG
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Ц	Dβ		qa	1189 rolleGlyGlnProGlyProSer(
J	^o	GGAAAGCIGCCACAAATAGAATAGATGCTGAGTGAAATGCTGAAAGCIGCAAAAGAAAAAAAAAA	Qý	452 GCACCATGGTCATGAACTTCTCC
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ر	à	TTO THE TAIL TO SEE THE COURT OF THE TENT	Qy	392 TGATGCCTGCGGCCAAACACACC
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J	οy	CCCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCT	Qy	335 GCTGGGCTTTCCGGT
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	1217	GCTCAGCTCTGGGCACGCCTGGTACAGCCCCTCGCCCACGAAATCC	1158
	953		972
	1157	AAAACAGCGTGAAGGTCATGACTGCCA	1131
_	. 973	LysAspGlyLeuProGlyHisProGlyGlnArgGlyGluThrGlyPhe	988
. •	3	CAGCTG	101
	98	lnGlyLysThrGlyProProGlyProProGlyValValGlyProGlnGly	1007
	1008	GUIGGINGCAGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1020
	1019	CCGGCATGGACAGTGGGGCGACAAGGAGGGGGCCGACAGCCCTTCTG	696
	1028	rLy	1043
	896	99	918
	1044	SAS	1055
	917	CTACGCAGGTGAGGAAGATGAGGGTGAGGCCAAAGAGGCCACT	873
	1056	GlyLeuArgGlyPheProGlyAspArgGlyLeuProGlyProvalGly	101
	872	AGGGGCCA	846
	1072	aGly	1091
	4	SCACTG	786
	on .	GlyGluArgGlyProAlaGlyAlaAlaGlyProIleGlyIlePro	1106
	785	TCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAG	726
	1107	GlyArgProGlyProGlnGlyPro	1114
		AGAGCAGGGCCTCCAGTGGAGTGAAGCACACTGGCCACAGAAGTCCAGGAGCCCCACGC	999
	1115	ProGlyProAlaGlyGluLySGlyValProGlyGluLySGlyProGlnGlyPro-Al	1133
	. 665 . 1133	CCAGGATGAGCAGCTCCAGGGCCCTGGGATCCGGGCAGCAGCAGCTGCTAGCC	606 1150
	605	AGCCGCCCTTGGGATGAGAAAGAGGCTCAGCAGGA	570
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	569	TGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGT	510
	1170	ySerLysGlyAspLysGlyGluGlnGlyProProGly-ProThrGlyProGlnGlyP	1189
	509	CACTGCTGAGCCTAGGAGCGGGACACAGACCAGCCCAGC	453
	452	CATGAACTT	393
	1207	iii lnGlnGlyLeuPheGlyGlnLysGlyAspGluGlySerArgGly	1221
	392	TGATGCCTGCGGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGA	336
	1222	ProProGlyProValGlyLe	1240
	335	GCTGGGCTTTCCGGTGCCGCA	315

Tue Jun 10 11:28:25 2003

Query Match: 5.37% Indels: 464 DB: 11 Gaps: 68	US-09-759-143-110 (1-3410) x Q60467 (1-1840)	Qy 3068 GGTCCTGCAGTAGCTCCAAACAGGGTTGTGGAGCTGGTGGGGAAAGTTGGGGGTAGGGGA 3009	Oy 3008 AAGTIGGGGGTAGGGAAATTTTGGGCAGTGCCTTCATCAGCCAGTCCTAGAGAGA 2952 11	Oy 2951 GTAGAGGGGAGT 2940 :::	Qy 2939 GGAAGTGGGGGAACCAGGCTGGGCCAAGAGAAGAGGGGTGGTTAGGAAGCCGTTGAGA 2880	Qy 2879 CCTGAAGCCCCACCCTCTACCTTCAACACCCTAACCTTGGG 2835	Qy 2834 TAACAGCATTTGGAATTATCATTTGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGGCA 2775	OY 2774 TTTGGGGGCCAGACCCCAGGAGAAGAAGATTCTGGCAATGATC 2730	Qy 2729 AGCCCAATGACCAGCTATCTCAGGGA	Qy 2699 GATTGTTGGGGATCCCCACCCTACCCAAATATTAGACACCAACACAAAAAGCTAGCAA 2640 11	2639 TGGATTCCCTTCTACTTTGTTAAATAAATAAGTTAAATATTTAAATGCCTGTGTCTCTGT	Db 592 OGINGLYPFOARG	2519 GCAAAAAGACAGTGCTGTGGGCTGAGGGGACCTGGTTCTTGTGTGTTGCCCCTCAGGACT	Db 617 617 Oy 2459 CTTCCCCTACAAATAAGTCATATGTTCAAATCCATGGAGGAGGAGTGTTTCATCCTAGAAAC 2400	Db 617 617	Qy 2399 TCCCATGCAAGAGCTACATTAAACGAAGGTGCAGGTTAAGGGGCTTAGAGATGGGAAACC 2340		Qy 2339 AGGTGACTGAGTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCTCAACTAGGAGG 2280	2279 CTAGCTGTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCCAGTGCATG	Qy 2219 GAGCCTTCTGGCTCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTC 2160
338AGAGCTGGGCTTTCCGGTGCCGCAGCGGCGCTCACCCACACACA	1134 GlyArgAspólyLeuGlnGlyProValGlyLeuProGlyProAlaGlyPro-Va 1151	281 TGGGCCAGGGGGGGGGGGCGGTTCAGGCACTCCAGAACTGCTTCG 228	227 TCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAGGAA 168 1171 rLysGlyaspLysGlyGluGlnGlyProProGlyProThrGlyProThrGl 1191	167 TCAGCCAGGCGCCATTTCTGCC	144AGCCCTTGGTGCCGGTCCAGC 123 1	122 TTCTCAGCCCATGCTCAACACCTGCTGCTGGGGGCACCTCAGTGGGGACACGTCTCATC 63 11	62 ACTCAGATCCTGGCCGAGGCGCGGGGGGGTGTCACCCGGAGCC 22	RESULT 29 060467 ID Q60467 PRELIMINARY; PRT; 1840 AA.		type V colla longicaudatus Metazoa; Chos utheria; Rode	<pre>Cricetulus. NCBI_TaxID=10030; [1]</pre>	SEQUENCE FROM N.A. MEDLINE-92105142; Greenspan D.S., Cheng W., Hoffman G.G.; "The pro-alpha-1(V) collagen chalm: Complete primary structure, distribution of expression, and comparison with the pro-alpha-1(XI)		Interpro; IPR000087; Collagen. Interpro; IPR0000885; Fib_collagen_C. Interpro; IPR001791; Laminin, G.		Pfam; PF01410; COLFI; 1. Pfam; PF01391; Collagen; 18. Pfam: PF02210: TSPN: 1.	m; PD00000	SMART; SM0038; COLFI; 1. SMART; SM00282; LamG; 1. SMART; SM00210; TSPN; 1.	PROSITE; PSU0294; PRENTLATION; UNKNONN_1. Collagen Collage 3200ENCE 1840 AA; 184174 MW; 32CS6821EF64CE75 CRC64;	Alignment Scores: 2.15e-13 Length: 1840

Db 870	943 1055 943 956 935 935 935	 Qy 668
	676 uProGlyGlubroGlyProArgGlyLeuLeuGlyProLysGlyProProGlyProProGl 696 2069 AGAGCCACATTACTTTGGCAGCAGCAGCGGGGCCAGCCGGCGCGCGC	1605AAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCA 1566
	8 8 8 8 8 8 8	

870	GlyValProGlyLeuProGlyTyrProGly 879
1286	AGATGGCGCACTGCAGGAACAGCCCCAGGCTGCCCATCCGAACGCCTTCATCAT 1233
1232	AGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCCCCT 1176
1175	CGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCC
1115	CAGCCACGAAGAGCCGGCGCAGGGGGGCATGCGGCAGCACCAGCTGGTGC :::
1055	GAAGCAGGCCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGCATGGACAGCAGTGGGGCC 996
995	ACAAGGAGGGGCCGACACCCTTCTGCTGGCTCGGTGGGGCCCAGCGCTCCTCAG 936 :::
935	CCACCAGCAGTGTGGCTGCTACGCAGGTGGAGGAGGTGAGGGTGAGCCAGCC
985	ACTAGG 852
851	GGGCCAGGGCACTGGTGTCCCAGTCAATGG 822 GlyProThrGlyGluThrGlyProMetGlyGluArgGlyHis1018
821 1019	
761	CCTGGCGACAGTGGT
725 1051	AGAGCAGGCCTCCAGTGGAGTGAAGCACCTGGCCACAGAAGTCCAGCAGCCCCA 669 :::
668	GlyalaLeuGlyLeuLysGlySerGluGlyProProGlyProProGlyPro 1087
. 638	GCCTGGGATCCGGCCACAGCAGCCCTGCTAGCCGGCCCTTGGGATGAGAAGAGGC 579
578 1096	TCAGCAGGAGGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCAC 519 ProAlaGly1098
518	GCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAA 459 ::: ::
458	TGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAGGGGGCA 399
398	CATAGGTGATGCCTGCGGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 339

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1208 euPheGlyGlnLysGlyAspGluGlySerArgGlyPheProG 1222	383 CGGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAGAGGCTGGGCTT 327	326 TCCGGTGCCGCAGCGGGC 306 :::	TCACCCACACCTCTGGACCATAGTGGCCA	laVa 1	274 -GGCGGGTAGGGCTCAGGGCACTCCAGAACTGCTTCGTCTCGGC 221	220	1301 oLeuGlyProLysGlyGluArgGlyGluLysGlyGluAlaGlyProSerGlyAlaAlaGl 1321	197 TCCTCCTTGCTGCCGCCAACTGCCTAGGAATCAGCCGCGGGCCCCA 153	152 TTTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCAA 1	1340G1 1354	104 CACCIGCIGCIGGGGCACCICAGIGGGACACGICTCAICATCACICAGAICCTGGCCGAG 45	44 GCGCGCGCTGTCACCCGGA 25	1374 hrGlySerProGly 1378	901.7 28 90103 PRELIMINARY; PRT; 1840 AA. 90103 09103 01-CCT-2000 (TrEMBLrel. 15, Created) 01-CCT-2000 (TrEMBLrel. 15, Last sequence update) 01-CCT-2000 (TrEMBLrel. 15, Last sequence update) 01-CCT-2000 (TrEMBLrel. 15, Last sequence update) 01-GCT-2000 (TrEMBLrel. 12), Last annotation update) 02-GCT-2000 (TrEMBLREL. 12), Last annotation update) 03-GCT-2000 (TrEMBLREL. 12), Last annotation update)
Dp	oy GD	yo q	Qy	Ор	Qy Db	Οy	QΩ	Qy Db	٥y	qq	oy Db	δy	qq	RESULT OF STANDARD

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2699 GATTGTTGGGGATCCCCCACCCTACCCAAATATTAGACACCCAACAGAAAAGCTAGCAA 2640
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                                                                                                                                                                                                                                                                                3008 AAGTTGGGG---GTAGGGGAAATTTTGGGCAGTGCCTTCATCAGCCCAGTCCTAGAGAGA 2952
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                                                                                                                                                                                                                                                433 GlyProGlyMetProAlaAsnGlnAspThrIleTyrGluGlyIleGlyGlyProArgGly 452
                                                                                                                                                                                                                                                                                             453 GluLysGlyGlnLysGlyGlu------ProAlaIleIleGluProGlyMet---Leu 468
                                                                                                                                                                                                                                                                                                                                                                       469 IleGluGlyProProGlyProGluGlyProAlaGlyLeuProGlyProProGlyThrThr 488
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                              Collagen.
SEQUENCE 1840 AA; 183986 MW; AD38F5FF886B923C CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
PROSITE; PS00761; SPASE_I_3; UNKNOWN_1.
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Query Match:
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δλ	2279 CTAGCTGTTAACCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCCAGTGCATG 2220	qa —	:::
οy	GTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTC	٥y	
qq	648 oGlyProSerGlyProPro	qq	
yo 4	3GAGAGAGGAGAGGGAC	Qy Dp	1274 GCAGGAACAGCCC
3 8	-ciyiterrociyaspaspoliyotuargoliyaspaspoliyotuValulyarokrgGlyLe	Qy	1217 CGGTGCCCGGCTC
5 A		qa	 951 AsnGlyProGlnG
Qy	2069 AGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGC 2010	δλ	
qa	694 yProProGly-ValThrGlyMetAspGlyGlnProGlyProLysGlyA 710	අි ි	
٥y	2009 TAACAGGAGCGGGGAGCTGGGACCCAGTGAGGCCCTCCACCCCAATGTGCTGG 1953	Å å	1097 GCAGGGTGCGGGC
ΟQ	710 snValGlyProGlnGlyGluProGlyProProGlyGlnGlyAsnProGly 727	3 8	1043 COAGGTTCGGAR
oy t	AAGTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACGTGTGTAGCAA	දු සි	
3 2		δō	983 CCGACAGCCCTTC
5 A	744 LysGlyProLeuGlyLysProGlyLeuProGlyMetProGlyAlaAspGlyProProGlyLeuProGlyMetProGlyAlaAspGlyProproGly	qq	1010 Pro
οy	TGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGAAGG	ογ	923 TGGCTGCTACGCA
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qa ·	818 PheLysGlyAspMetGlyIleLysGlyAspArgGlyGluIleGlyProProGlyProArg 837	g (
οy	1715 IGGCTCACCACCACCACGACGAGACATCACAGGCAGAGGCCCCGCAGAGCGCGG 1656	oy.	
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2	CACCACA AGRICACO CONTAINS AND ACTOR AGRICACO ACTOR ACT	Qy	596 TTGGGATGAG
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δλ		Qy	560 ACAGIGCCCAGAI
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Qy	1430 CGGCTGAAGCTGTCACCACGGCCACACTGTGGGACAGGCATGTGGCCACCGGCAGCCACAG 1371	δλ.	
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δō,	1370 GGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCAGCCGGT 1311	<i>~</i>	::

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1310	CCATGACCAGAGAGAAGACCAGGGAGATGGCGCACT :	1275 936
1274 937	GCAGGAACAGCCCCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCT :	1218 950
1217	CGGTGCCCGGCTCAGGCCACGCCCTGGTACAGCCCCTCGCCCACGAAATCCGTGT :	1158 970
1157		1098 978
1097	GCAGGGTGCGGGCATGCGGCACACACTGGTGCAGCCGGGAAGCAGGCGCC :	1044 995
1043	CCAGGTTCCGGAAAGCCAAGCGGCATGGACAGCAGTGGGGGGGG	984 1009
983	CCGACAGCCCTTCTGCTGCTGGTGGGGCCCAGCGCTGCCTCCTCAGCCACAGCAGTG (111 1111	924 1024
923	TGGCTGCTACGCAGGTGAGGAGAGAGGTGAGCAGCCAAAGAGGCACT	873 1040
872	ProGlyProAlaGlyLeuProGlyLysAspGlyProProGlyLeuArgGlyPheProGly	846 1060
1061	GGGCACTGGTGTCCCAGTCAATGGCAGCAGGAGGTAGCCCA (804 1080
803 1081	GGCAGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGCGACAGTGGTCCG :	744
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656	GCAGTGCCAGGCTCCAGGGCCTGGGATCCGGGCACCGCACCCTGCTAGCCAGCC	597 1151
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443	GCAGAGGCGCCACATAGGTGATGCCTG	384

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laGlyA 920 278 slyGlu 939	CCGTTCAGGC 245 ::: yGlnLysGly 959 -TCTGCTCCA 212 		1 4 9 7	ACCCGG 26 ProGl 1074	mi; Mus. H.; gene.";
oGlyAspLeuA	CAGGGGCCGT ::: luAspGlyGlnTCT	ySerProGlyAlaProGly -AATCAGCCAGGGGCCCAT rGlyGlnProGly-ProVa	19AlaProGlyProCACCTCAGTGGGGACACTC	-CGAGGGGGGGGTGTCACCGG	uteleostc Murinae; Yoshioka collagen
almetValGlyProProGlyAlaLysGlyGluLysGlyAlaProGlyAspLeuAlaGlyAGGCTCACCCACACACTGGACCATAGTGGG	LysglygluAlaGlyArgAlaGlyGluProGlyAspProGlyGluAspGlyGluAlaGlyGluBroGlyAspProGlyGluAspGlyGluAspGlyGluAspGlyGluAspGlyGluAspGlyGluAspGlyGluAspGlyGluAspGlyGluAspGlyGluAspGlyGluCsGlyCCCAACCCAGAACTGCTCGGCTCTGCTCCAAll	spValGL	G1	lyPr	pdate) update) tebrata; Muridae; nomiya Y.
GlyProProGlyAlaLysGlyGluLysGlyAl GGCTCACCCACACACATAGTGGG-	GlyGluProGl GlyGluProGl GGC GlyEuLysGl	GAAGCTGCGCCTCCTCGTTGCTGCCCGC ProGlyProThrGlyProProGlyMetLysGlyA	TTCTGCCAGCCCTTTGGTG	rGlybeuProG	PRELIMINARY; PRT; 1838 AA 7-1998 (TrEMBLrel. 08, Created) 1-2002 (TrEMBLrel. 21, Last sequence up. 2002 (TrEMBLrel. 21, Last annotation len al(V). 1-2002 (TrEMBLrel. 21, Last annotation len al(V). 2-2002 (TrEMBLrel. 21, Last annotation len al(V). 2-2002 (TrEMBLrel. 21, Last annotation len al(V). 2-2002 (Trel. 2011) 2-2002 (T
ProProGlyA TCACCCACAG	LysGlyGluAlaGlyArgAlaGlyG ACTCCAGAACTGCTTCGTCTCGGC-	CCTCTCCTCTCT hrGlyProPro	CTTTGGTG SlyLeuAlaGl GCTCAACACC - -	3ATCCTGGC spproglyth	ULT 27 008207 008207 018207 018207 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 21, Last sequence) 01-JUN-2002 (TrEMBLrel. 21, Last sequence) 02.541 03.04 03.04 04.05 05.04 05.04 05.05 06.05
almetValGly	LysGlyGluAl ACTCCAGAACT AlaProGly	GAAGCTGCGGC ProGlyProTP	TTCTGCCAGCCCTTGGTG- 11 161yGluargGlyLeualaG TCTCAGCCCATGCTCAACAC 1	TCATCACTCAGATCCTGGC- 	PRELIMINARY 1998 (TrEMBLrel. 1998 (TrEMBLrel. 2002 (TrEMBLrel. 2002 (TrEMBLrel. 2003 (TrEMBLrel. 2004). 2014; Metazoa; Cho 2014; Metazoa; Cho 2015; Metazoa; Cho 2016; Metazoa;
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90 O	oy oy ob	oy oy	Qy Dp Qy	oy oy	RESULTA OBBSO7 OBBSO7 OBBSO7 OD DT OO OD DT OO OD DT OO

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2699 GATTGTTGGGGATCCCCCACCTACCCAAATATTAGACACCAACACAGAAAAGCTAGCAA 2640
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                                               Length:
Matches:
Conservative:
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            1838 AA; 183691 MW;
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Page 36

ζ	GTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAGCAGAGC	q <u>a</u>	
oy Oy	209 IYVALARGGIYPTOALA	Qy	1234 ATAGTGTCTCGGGCCTCGGTGCCCGGCTCL ::
d y	roGlyGluAspGlyArgAsnGly GGAGCGGGAGCTGGGACCCAGT 	λ, dg	
da y	yGluProGlyProProGlyProProGlyArgLeuValGlyAlaGlyI AGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATG	Qy Dp	
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G & E	GIYPTOATGGIYPTOLYSGLYASPPTOGIYPTOFIOLIYALASGGCTGCGGCAACACCATATAGGCAGTGACAGACTGGCTGGCTTGCGCAGCACCACCATATAGGCAGTGACAGACTGGCTGGCTTGCGAGACAACAGAGAGAGAGAGAGAGAGAGAGAGA	δγ.	994 CAAGGAGGGCCGACAGCCCTTCTGCTGG
oy da		Qy Db	934 CACCAGCAGTGTC
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Qy	CTCACCCACCACACACAACAACAACAAGGCCAGAGGCGCGGTGG CTCACCCACCACACACAACAACAAAGGCCAGAGGCGCGGTGG :-::::	QV Dp	865 GGTGCCCAGGTAGGGGGCCAGGGCACTGGTU
\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	AGGTGGGAGCAGGCCACTGCCTCCAGCACCACGTGTANAPDITAGG	Qy Dp	805 CAGGCAGCCCCAAGACTGATCATGAAGGC
g v	GAAGGGAGCTCCAGGCTTAGGG	ζς	746
Oy Dp		Oy Op	700 GCACACCTGGCCACAGAAGTCCAGCAGCCCC
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QY	TGTAGGGCAGGATCTGCAGGCCTGAGAAGGTGAACCCGGTGAG -ValGlyProProGlyGlnGlyPheProGlyAlproGlyAsn	QV Dp	635TGGGATCCGGGCACAGCACCCTGCTAGC
ογ		QV Dp	577 CAGCAGGATGCCCAAGGACAGTG
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Qy	1319CCAGCGGTCCATGACCAGAGAGAGACCAGGGAGATGGCGCACTGCAG 1271 	Oy Dp	418 TICCAGCAGCAGAGGCGCACATAGGTGATC
oy ·	1270 GAACA	oy —	358 GGTTAGCAGGTTGACCAGCAAGAGCTGGGC:::

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Query Match: 5.39% Indels: 444 DB: 11 Gaps: 73	US-09-759-143-110 (1-3410) x Q60444 (1-1549) QY 3039 GGAGCTGGTGGGGAAAGTTGGGGGAAAGTTGGGGGAAATTTTGGGCAG 2980		Oy 2979 TGCCTTCAT 2965 Db 11111		Db 76 ArgGlyThrProGlyIleThrGlyProLysGlyAspArgGlyGlnThrGlyThr 93 Oy 2925 CCAGGCTGGGCCAAGAGAAGAGGGGTTAGAGAAAGCCGTTGAGAAGCCCTAGAAGCCCAAC 2866		2865 CICTACCTTCCATCAACCCTAGGGTAACAGCATTTGGAATTATCATTTGGGGT	ValAlaGly		Oy 2745 GATTCTGGCAATGATCAGCCCAATGACCAGCTATCTCAGGGGACCTGATTGTTGGGGATC 2686	Db 136 rgGlyGluLysGlyGluProGlyArgProGlyAspP 148	Qy 2685 CCCCACCCTACCCAAATATTAGACACCAACACACAGAAAAGCTAGCAATGGATTCCCTT 2629	Db 148 roAlaValGlyProGlyGlyAlaGlyAlaLysGlyGluGlySGlyAspAlaGlyLeuPro- 167	QY 2628 CTACTTTGTTAAATAAAAATTTAAATTTTAAATGCCTGTGTCTCTGTGATGCCAACAG 2569	Db 167 167	QY 2568 AAGGACCAACAGCCACATCTGATAAAAGGTAAGAGGGGGGTGGATCAGCAAAAAGACA 2509	OY 2508 GIGCIGIGGGCIGAGGGAACCIGGTICTIGIGTGTGCCCCTCAGGACTCTICCCCTACA 2449	Db 181 184	QY 2448 AATAAGTCATATGTTCAAATCCCATGGAGGGGGTGTTTCATCCTAGAAACTCCCATGCAAG 2389	185AlaLeuProGlyAspProGlyProLys	OY 2388 AGCTACATTAAACGAAGCTGCAGGTTAAGGGGCTTAGAGAACCAGGTGAGTGA	2328 TTTATTCAGCTCCCAAAAACCCTTCTTCTAGGTGTGTCTCAACTAGGAGGCTAGCTGTAAA	::: ::: :::::	Qy 2268 CCCTGAGCCTGGGTAATCCACTGCAGGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTG 2209	Db 210 roThrGlyAspSerGlyProProGlyGluLysGlyAspProGlyArgProGlyProProG 230	Qy 2208 GCCTCCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCC 2167	230 1YFIOVALGIYSCIALGGAYALGASPGIYGIUYALGIYGIUUSSGIYYALGIUGIYA 2166 TCAGAGGAGCAGCCCTAGAGAGAGAGAGAGAGAGAGAGAGAG	
Db 364 ValLysArgLeuTrpClyIleValAsnPheLeuLeuAlaIleCysLeuGly 380	Oy 1400 CACAGTGTGGCCGTGGTG	1418ACAGCTTCAGCGCCCTCACCGGGTTC	DD 401 AlaLeuGlyAspProLeuProProSerGluGlyIleLysAlaGlyAlaLeuThrLeuPhe 420 Qy 1445 ACCTTCTCAGCCCTGCAGATC	Db 421 SerValLeuGlyValProLeuAlaileThrTyrSerIleProPheAlaLeuAlaSerIle 440	Qy 1490 TACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGC 1549 ::		449 GlnGlyLeuSerLeuGlyValLeuAsnLeuAlaIleValIleProGlnMetPheValSer	OY 1574 TICCTGCAGGCCTAAGCCTGGAGCTCCCTTCCTAAT 1612 Db 469 ValLeuSerClyPtoTrpAspAlaLeuPheGlyGlyGlyAsnLeuProAlaPheValVal 488		Db 489 GlyAlaValAlaAlaLeuAlaSerGlyIleLeuSerIleIleLeuLeuProSerProPro 508	RESULT 26 GROAD	5	01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel.		. 21	OC Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Cricetinae; OC Cricetulus. OX NCBI_TaxID=10029;			RT "The carboxyl-terminal half of type VII collagen, including the non- RT collagenous NC-2 domain and intron/exon organization of the			DR InterPro; IPR002223; Kunitz_BPTI. DR Pfam; PF01391; Collagen; 22.	DR Pfam; PF00014; Kunitz_BPT1; 1. DR PRINTS; PR00759; BASICPTASE. DR DATACH. PROGRAM: 0		DR PROSITE; PS50279; BPTI_KUNITZ_2; 1. KW Collagen; Serine protease inhibitor.		ent Scores: 1.8e-13 Length:	: ative: 6 hes: 4

Db 36 LysiiometValValAlaSeriieAlaAlalyValiciii Qy 392 ACCTATGTGCGCCCTCTGCTGCTGGAAGTGGGGGTAG :: :: :: :: :: :: :: :: :: :: ::	Oy 452 CTGGGCATTGGTCCAGTGCTGGCCTGGTCTGTGTCC	Qy 512 CACTGGCGTGGACGCTATGGCCGCCGCCGCCCTTCA 111:::	Qy 572 CTGCTGACCTCTTCTCATCCCAAGGGCCGGCTGCC :::::::::	Qy 620CTGTGCCCGGATCCCAGGCCCTGGAGC 111 1 1 1 1 1 1 1 1	Qy 671 GGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTC ::: Db 153 TrplleLeuAspValAlaAsnAsnMetLeuGlnGlyP	QY 731 CTCTTCGGGACCCGGACCACTGTCGCCAGGCCT	Qy 788 AGTCTTGGGGCCTGCCTGGCTACCTCCTGCCTGCCACCACACACA	Qy 830TGGGACACCAGTGCCCTGGCCCCTACCTGG	QY 884 GGCTGCTCACCTCATCTTCCTCACCTGCGTAGCAG	Qy 941 GAGGCAGCGCTGGGCCCCACCGAGCCAGCA	989	Oy 1043 GGGGCCCTGCTTCCCCGGGTGCACCAGCTGTGCTGCC Db 286	Qy 1103 CTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCA 	Oy 1163 GATTCGTGGCGAGGGCTGTACCAGGCGTGCCCA	325 325	Qy 1280 GCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGC ::: 11 ::: 1 Db 345 ValValLeuGlvalathrSerleuGlvalasolleu	7 6
384	1601 CCCTTCCCTAATGGACACGTGGAGGCAGTGGCCTGCTCCCACCTCCACCGGG 1660	1661 CTCTGCGGGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAG 1720	aLeuAlaSerIleTvrSerSerGlvSerGlvAlaGl				004077 PRELIMINARY: DPT: 623 AA	4, Created) 4, Last sequence	Sucrose transport protein. SUT. Vicia faba (Broad bean). Filkarota: Vifidialantae. Strontonhuts: Embruoshut.	SpermatOphyta: Magnoliophyta: eudicotyledoms; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.	SEQUENCE FROM N.A. TISSUE-COTYLEDON; Weber H., Borisjuk L., Heim U., Sauer N., Wobus U.; A role for sugar transporters during seed development; Molecular	icrose carrier in ra	F. SUBCELLOLAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY). EMBL, 293774; Z93774: CABO7811.1; - InterPro; IPR003662; sub_transporter. Fram: Prof0083; sugar_tr; 1. TIGRPMs: TIGRN1301: GPH sucrese.	Transmembrane. SEQUENCE 523 AA; 55229 MW; F8EBF170212D191A CRC64;	Alignment Scores: Pred. No.: Score: 337.50 Matches: Percent Similarity: 40.38* Conservative: 76 Macches: Abset Local Similarity: 25.77* Macmatches: 10.56	Indels: Gaps:	US-09-759-143-110 (1-3410) x 004077 (1-523)

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CGCATGCCCCGGACCCTGCGCCGG 1102
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ThrSerAlaLeuIleTyrValLys 250
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ThrGluAspGlyGlySerSerGly 270
                                                                                                                                CCCGCTCCTAGGCTCAGCCAGTGAC 511
                                                                                                                                                                                                    CATCTGGGCACTGTCCTTGGGCATC 571
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elleAlaAlaGlySerIleAlaVal 115
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rAlaAlaAspLeuGlyHisSerPhe 132
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| IleGlyIlePheValValGlyPhe 152
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-----LysArgProMetTrpIle 291
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|LeuAlaArgGlyValGly---Gly 363
SGAGGTGTGTTTGGCCGCAGGCATC 391
                                                                AGAGGAGAAGTTCATGACCATGGTG 451
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                                                                                                                                                                                                                                                                                                                                                                                                                rccacregaegcccrecrcreac 730
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sAlaAsnLeuLysSerCysPhePhe 232
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------GlyGlyThrValGly 324
                     ::::
|GlnPheGlyTrpAlaLeuGlnLeu 55
                                                                                                   SHISHISThrTrpAlaAlaTyrIle 75
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1181 CTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAA 1240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1121 TGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGG 1180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 LysGlnTrpSerProAspGluAlaAspGluGluProProSerSerGlyLysIlePro--- 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 LeuasnTrpIlealaTrpPheProPheIleLeuPheAspThrAspTrpMetGlyArgGlu 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 IleTyrGlyGlyThr-----AlaGlyGlnGly------LysLeuTyrAspGln 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 SerLysValAla----- 383
                                                                                                                                                                                                                                                                                                                                                      173 GlyAspThrArgArgMetArgSerAlaAsnAlaPheTyrSerPhePheMetAlaValGly 192
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                                                                                                                                  ArgCysGlnSerSerPheGlyArgArgArgArgProPheIleAlaSerGlyAlaGlyCysVal 112
                                                                                                                                                                                                                       113 AlaIleSerValIleLeuIleGlyPheAlaAlaAspIleGlyTyrLysAlaGlyAspAsp 132
                                                                                                                                                                                                                                                            620 CTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTG 679
                                                                                                                                                                                                                                                                                                                                   680 GACTICTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGG 739
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53 SerLeuLeuThrProTyrValGlnLeuLeuGlyIleProHisLysTrpAlaAlaTyrIle 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCCAGGAGGAGTGC---CTCTTT
                                      452 CTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGAC
                                                                                                             512 CACTGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATC
                                                                                                                                                                                      572 CTGCTGAGCCTCTTTCTCATCCCAAGGGCC------GGCTGGCTAGCAGGG---CTG
                                                                                                                                                                                                                                                                                                133 MetThrLysThrLeuLysProArgAlaValThrGlyPheVallleGlyPheTrpIleLeu
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       1550 AGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCT 1609
                                                                            1610 AATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGGCGTCTGCGGG 1669
                                                                                                                                                      1670 GCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGGTGAGCCC------ACCGAG 1720
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                                                                                                                 -----AlaLeuIleVal 404
                                                                                                                                                                                        405 PheSerileLeuGlyIleProLeuAlaileThrTyrSerValProTyrAlaLeuIleSer 424
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                                                                                                                                                                                                                                                                                                                                                                                                            465 GlyGlyAsnSerProSerLeuAlaValAlaAlaValAlaAlaPheAlaSerGlyLeuVal 484
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                                          445 IleValIleProGlnValIleValSerLeuGlySerGlyProTrpAspGlnLeuPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Apium.
NCBI_TaxID=4045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512 AA; 54426 MW; 2637535216FF1ED2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJN-2002 (TrEMBLrel. 21, Last annotation update)
Sucrose transporter SUT2B.
SUT2B OR SUT2A.
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Mismatches:
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Best Local Similarity:
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ATTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGCTGCT ::	TGGGGCACCTCAGTGGGACACGTCTCATCACTCAGATCCTGGCCGA 	-GGCGCGGGCTGTCACCCGGAGCC 22 :: aGlyGluLysGlySerProGlyAla 936	501 AA.	.ed) sequence update) annotation update)	ohyta; Embryophyta; Tracheophyta .cotyledons; core eudicots; Vita	'E BERRY; Delrot S., Romleu C.; oression in yeast of a grape berry	(2000). . MEMBRANE PROTEIN (BY SIMILARITY		4FD19DFAFE539077 CRC64;	Length: 501 Matches: 163 Conservative: 84 Mismatches: 207 Indels: 25	501)	aggaggagaggccgcagcttctggagcagagccgagacgaagcagttctggagtgcctga ::: argglnargglyarg	ACGCCCCCTGAGCCCTACCGCCTGCCCACTATGGTCCAGAGGCTGTGGGTGAGCCGC	CTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTAACCTTTGGCCTGGAG 	GTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAG [1] ::::::::::::::::::::::::::::::::::::	GAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCG	:::::::::::::::::::::::::::::::	CTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCCGC	ysAsnSerArgPheGlyArgArgArgPr
	י פ	ProProGlyProProGlyProAl	PRELIMINARY; PRT;	(TrEMBLrel. 13, Creat (TrEMBLrel. 13, Last (TrEMBLrel. 21, Last	vactose transporter. Vitis vinifera (Grape). Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eu Vitis.	11) SEQUENCE FROM N.A. STRAIN-CV. UGNI BLANC; TISSUE-GRAPE BERRY; Ageorges A., Issaly N., Picaud S., Delrot "Identification and functional expression	OSE CALTIET."; it Physiol. Biochem. 38:177-185(2000). SUBCELLUER LOCATION: INTEGRAL MEMBRANE PROTEIN APP 20146. ADDRESSED.	Friedry; AADD3289.1, Tro; IPR003665; sub_transporter PF00083; sugar_tr; 1. WMs; TIGR01301; GPH_sucrose; 1.	501 AA; 54075 MW;	Scores: 9.57e-14 338.50 milarity: 40.29% .Similarity: 26.59% ih: 10	-143-110 (1-3410) x 09SP63 (1-501)								
Qy 153 Db 888	Qy 93 Db 902	Oy 45 Db 921	RESULT 23 Q9SP63 ID Q9SP63	AC 095P63; DT 01-MAY-2000 DT 01-JUN-2002 DT 01-JUN-2002	OS Vitis vi OS Eukaryot OC Spermato OC Vitis. OX NCBI_Tax	RP SEQUENCE RC STRAIN=C RA Ageorges RT "Identif	Plan Plan -1- FMRT	Inte Pfam TIGR	SEOUE	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Ouery Match:	US-09-759-143	Oy 191 Db 8	Oy 251 Db 13	Oy 311 Db 30	Oy 371	Qy 431	Db 62	4.	Dib 82

Vo 45	551	GCATCCTGCTGGCTGCTTTCTCATCCCAAGGCCGGCTGGCT
0y		CAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCAGCTGCTATGGTG 66
qq	122	
oy d	9	3GGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTC 72
Q C	4	yPheTrpLeuLeuAspValAlaAsnAsnValThrGlnGlyProCysArgAlaLeuLe
Οy	(3)	CGGGACCCGGACCACTGTCGCCAGGCCTACTGTC
qq		aAspLeuThrGluLysAspHisArgArgThrArgValAlaAsnAlaTyrPheSe
Qy	779	TICATGATCAGTCTTGGGGGCTGCCTGCCTGCCTGCCTGCCT
Dp	181	lyTr
Οy	824	TTGACTGGGACACCAG
QQ	201	rgilePheTrpPheThrSerThrSerSerCysAsnAlaAspCys
Qy	881	TTTGGCCTGCTCACCCTCATCCTCCTCCTGCGTAGCAGCCACACTG 928
qq	217	AsnLeuLysSerAlaPheLeuLeuAspIleIlePheIleAlaIleThrThr 233
οy	929	Ö,
qq	234	
ОУ.	80	TCCTTGTCGCCCCATGCTGTCCATGCCGGGCCCGCTTGCTTTC 1033
qq	249	erArgSerThrHisIleSerGluGluMetAlaGluSerThrHisAlaGlnGluAlaPh
οy	1034	GGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGCCTGC
QQ	269	LeuTr
οy	1094	TITLE TO THE TRANSPORT OF THE TRANSPORT
qq	276	JyrLeuSerGlySerIleTrpIleIleLeuPheValThrAlaLeu-
Qy	1130	TGGCACTCATGACCTTCACGCTGTTTTA
op '	295	YTrpPheProPheLeuLeuPheAspThrAspTrpMetGlyArgGluIleT
QY	1190	GCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCG
qq	315	γĽγ
Qy	1250	TGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCAT
Db	329	tGlyAlaLeu
οy	1310	ACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTT
Db	349	GluLysLeuCysArgLysTrpGlyAlaGlyPheValTrp361
Qy	1370	STGGCTGCCGGTGCCATGCCTGTCCCACAGTGTGGCCCGTGGTGACAGCTTCAGCC 14
Db	362	 11 GlyLeuSerAsn 365
Οy	1430	SCCTGCAGATCCTGCCCTACACACTGGCCTCCTC 14
Db	366	.:. euMetLeuIleLeuSerAlaVa
Qy	1490	CGGGAGAAGC
QQ	383	LysHisMetAsp 386

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y	1730	383 GlyAsnProGlyAlaAspGlyGlnProGlyAlaLys-GlyAlaAsnGlyAlaPro 400 1548 CTAGCACCTCCAGTCTCCCCTCGGTATTTGGCAGGCAACCTCCTCTCCCCGGTGGTAG 1489 401GlyIleAlaGlyAlaProGlyPheProGlyAlaAr 412 1488 AGGGGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAGCTGAACCGGTGGGGGC 1429 1188 AGGGGGCCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAGCTGAACCCGGTGGGGCG 1429 111	1428 GCTGAAGCTGTCACCACGCCACACTCTGGGACAGGCATGTGGCACCGGCAGCCAGC	1257 CTGCCCATCCGAACGC	1104 AGCCGCCAGGCAGCGCATCCCGCACCACCAGCTGCTGCAGCCGGGAAGCAGGCGC 1045 521
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947	CTGCCTCCTCAGCCAC	930 580
929		883 594
α σ	AAGGGCACTCCTCCTGGGTGCCCAGGT	855 614
854	yAlaGlnGlyProProGlyProAl	817 634
816 634	A B	781 654
780	AAGGCATAGACAGAGTAGGCCTGG	730 674
729	TCAGAGGCAGGGCCTCCAGTGGA	670 693
699		640 713
639	S = 42	580 731
579	5 – %	520
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479	CCAGGCCCAGCACTGGACCAATGCCCA	453 784
452	GCACCATGGTCATGAACTTCTCCTCTAACCTCATGAACTTCTCCTCTAACCTCTAACCTTCTTCTTAACCTTCTAACCTTCTT	424 804
423	υ — ο	364
363	3 CCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGC	316 835
315	S AGCAGGCGGCTCACCACAGCCTCTGGACCATAGTGGGCCA	268 853
267	7 AGGGCTCAGGGGCCGTTCAGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTC	214 868
213		154

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Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T., Jaenisch R., Prockop D.J.;
Structure of a full-length cDNA clone for the prepro alpha 1(I) chain of human type I procollagen.";
Biochem. J. 253:919-922(1988).
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MEDLINE-88329734; PubMed-2843432;
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                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91138770; PubMed-1995349;
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COLIA1 gene bind cell-specific nuclear proteins.";
FEBS Lett. 279:9-13(1991).
                                                                                                                                                                                                                                                                                                        Chu M.L., de Wet W., Bernard M., Ramirez F.;
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Promoter structure, AluI repeats, and polymorphic transcripts.";
J. Biol. Chem. 260:2315-2320(1985)
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF017178; AAB94054.2; -.
InterPro; IPR000087; Collagen.
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
                                                                                                                     Last sequence update)
Last annotation update)
                                                                     PRT; 1461 AA
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MEDLINE=85130970; PubMed=2857713;
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MEDLINE-89025644; PubMed=3178743;
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                                                                                                   01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1999 (TrEMBLrel. 12,
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Pfam; PF01391; Collagen; 18.
                                                                    PRELIMINARY;
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3571 nProGly 3573
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                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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               Probom; PD000007; Collagen; 2.
Probom; PD002078; Fib_collagen_C;
SMART; SM0038; COLFI; 1.
SMART; SM00214; VWC; 1.
                                                                                                                           1461 AA; 138630 MW;
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342.50
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Pfam; PF00093; vwc; 1.
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10.04 TTCCCTANTGGACACGTGGGGCACTGGCGGCCTGCTCCCCCCCCCC	CGCTC 1663 Db	1723		1782 3083	-GGGC 1816 QY		3123	1885	sGluA 3143	1942 3162	1964	3182	ACTEGG 1987	3202	2047	3209	2083	2143 3236	2203	3245	226	3255	2303		3279	3AAACA 2416	3299
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2933 CACTICCACICCCCTCIACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTT 2992
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3299 rSerAlaCysGly--
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RC TISSUE-SUBCOMMISSURAL ORGAN; RA Meiniel A.; RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. RUS LISSUE-SUBCOMMISSURAL ORGAN; RY TISSUE-SUBCOMMISSURAL ORGAN; RX MEDLINE-20465125; PubMed=11008217; RY "Subcommissural organ/Reissner's fiber complex: characterization of SCO-spondin, a glycoprotein with potent activity on neurite RT SCO-spondin, a glycoprotein with potent activity on neurite RT Glia 33:177-191(2000); RK Glia 33:177-191(2000); RK Glia 34:464545; ARS ARS SAST6 MW: 724C5FRR777F13DA CPC64.	5.76e-14 Length: 5146 344.50 Matches: 308 24.12% Conservative: 79 City: 23.18% Mismatches: 564 6 Gaps: 87	US-09-759-143-110 (1-3410) x Q8SPM4 (1-5146) QY	180 TGGCGGCAGCAAGGAGGGCGCAGCTTCTGGAGCAGAGCGACGA 230	DD 2559 ArgSerCysMetAspProProProLysAsnGlyAlaProCysProGlyPro 2576 Qy 279 CCACTATGGTCCAGAGGCTGTGGGTGAGCCGCGCTTGCGGCACC 323		429 AGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCC 1	Oy 489 CGCTCCTAGGCTCAGTGACCACTGGCGTGACGCTATGGCCGCGCCCCTTCA 548 1	Oy 609 TAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCTGGAGCTGGCACTGC 656 Db 2677 ysValCysGluLysGlyAlaLeuLeuCysGlu-ProGlyGlyCysProValProCys 2695 Oy 657 TCATCCTGGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTTCACTCCACTGGAGG 716 Db 2696GlyTrpSerAlaTrpSerSer

2723	ATGCCTTCATGATCAGTCTTGGGGGCTGCTGG
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17	TGGTGCAGCGATTCGGCACTCGAGCAGTCT aGlyCysAlaCysProThrGlyLeuPheLeuHisAsnSerSerCy
56	GTGTGGCAGCTTTCCCTGT
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94	CTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGGTGACAGCTTCAGCCGGTGACAGACA
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544	GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCTTAAGCCTGGAGCTCCC 16
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Οy	2163 TGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCAT 2222		01-JUN-2002 (TrEMBLr 01-JUN-2002 (TrEMBLr
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G qa	GlyLeuSerGlyGlnLysGlyAspGlyGlySerProGlyLeuProGlyAsn		Eukaryota; Metazoa; Mammalia; Eutheria;
Qy	CTAGTTGAGACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGT	OC OC	Bovidae; Bovinae; Bo NCBI_TaxID=9913;
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CACTGCCCAAAATTTCCCCTACCCCCAACTTTCCC------ 3012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC---CCAACTTTCCCCACCAGCTCCACAACCCTGTTTGGA----- 3054
                                                                                                                                                                                  GIGIIGGIGICIAATAITIGGGIAGGGIGGGGGGAICCCCAACAAICAGG 2702
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                                             AAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTT 2402
                                                                                      eProGlyMet-Pro----- 1234
                                                                                                                                                                                                                                ACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGA 2522
                                                                                                                                                                                                                                                             roLysGlyAsnProGlyProGlnGlyProPro----- 1260
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-------ProGlyLeuProGlySerLys-----GlyGluProGly 1226
                                                                                                                                       ACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGAGT 2462
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	489 SerGlyValLeuAlaileValLeuLeuProLysProSerLysAspAlaAlaSerLysLeu 508 1682 GATGTCTCC 1690	Qy	447 TGCTGC 634 sGlyIleGlnGlyValAla
509	::: SerLeuSer	Qy	495 TAGGCTCAGCCAGTGACC
20		qa —	
S02 S02;	ELIMINAF	δλ	CACTGTC
MAR- MAR- JUN-	01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	d y	653GlyAspPro
e IV 4A5.	en alpha 5 cha	qq	: :: 664 sProGlyLeuProGlySe
mus aryo	Mus musculus (Mouse). Eukaryota, Eukaroa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla: Entharia: Endantia: Enturomathi: Muridae: Murinae: Mis	Qy	667CGTGGGGCTGCTGG
I_Ta	MCBI_TaxID=10090; MCGiffer (MCBI_TaxID=10090); MCBI_TaxID=10090; MCBI_TaxID=100900; MCBI_TaxID=10090; MCBI_TaxID=10090; MCBI_TaxID=10090; MCBI_TaxID=10090; MCBI_TaxID=10090; MCBI_TaxID=10090; MCBI_TaxID=100900; MCBI_TaxID=10090; MCBI_TaxID=100900; MCBI_TaxID=10090; MCBI_TaxID=10090; MCBI_TaxID=10090; MCBI_TaxID=10090; MCBI_TaxID=10090; MCBI_TaxID=10090; MCBI_TaxID=10090	qa	684 yLeuProGlyGlnProGl
UENC	E FROM N.A. =20536494; PubMed=10965041;	Qy	723 TCTCTGACCTCTTCCGGG
to F	Saito K., Naito I., Seki T., Oohashi T., Kimura E., Momota R., Kishito Y., Sado Y., Yoshioka H., Ninomiya Y., Prifformatial Burnowich of Novel Section 2012	qa .io	702 yilebroGlyIleGlyBr
the		5 6	
ĭ.	U. B.	3 A	831 GGGACACCAGTGCCCTGG
erP	InterPro; IPR000087; Collagen. InterPro; IPR001442; ProcollagnC4.	qa	: 733 tGlyProAspGlyProPr
	Pfam; PP01413; C4; 2. Pfam; PP01391; Collagen; 24. Pronoum: DD000007: Collagen; 3	Qy	871 -GGAGTGCCTCTTTGGCC
	FICECOM, PD003923; ProcollagnC4; 1. SAMPT. SMOOTH: C4. 2	qa	753 eGlyLeuProGlyProPr
Collagen SEQUENCE	nn. :E 1691 AA; 161823 MW; 81340DF1792208FA CRC64;	o d	930 TGGTGGCTGAGGAGGCAG
Alignment Sc Pred. No.:	Length:	3 8	
Simi	Score: 345.50 Matches: 274 Percent Similarity: 28.91% Conservative: 55	qa	 786 oGlyArgThrGlyLeuAs
Best Local S Query Match:	ity: 24.08% Mismatches: 5.38% Indels:	Qy	1050 recrecedecrecace
	II Gaps:	qa	806 nProGlyProValGlyPr
ر 1 - ا		QY	1098 GCCGGCTCTTCGTGGCTG
1	CCGCCACCAAAGGCTGCCAGAAATGGCGCCTGGCTGATTCCTAGGCAGTTGGCGGCAG	- QC -	 826 oProGlyThrProGlyPr
Ω ,	ProglyFroProglyAlaProglyPheProglySerLySGlyASP	Oy	1156
-l r.	189 CAAGGAGGAGAGGCCGCAGCTTCTGGAGCCAAAGCCAAAGCAAGTTCTGGAGTGCCT 248	qa	842 oGlyGluLysGlyAspPr
י ר		δλ	1170 TGGGCGAGGGGCTGTACC
9 10	onecode control of the control of th	qa	862 gGlySerProGlyLeuPr
0 0	-CCAGAGGTTGTGGGGTGGGGGGGGGGGGGGGGGGGGGGG	Qy	1230 ACTATGATGAAGGCGTTC
286		qq	878Glyse
327	できた。 できない かいかい かいかい かいかい かいかい かいかい かいかい かいかい か	Qy	1275 AGTGCGCCATCTCCCTGG
909	navconcorrections and the second seco	qq	yvalLysGlyGluMe
387	GCAT	Qy	1321GC
622		qq	913 oGlyArgSerGlyAlaPr
		ا وي	1365 CTTTCCCTGTGGCTGCCG

Qy Db	447	 GlnGlvV	494
àò	6	AGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGCCCTTCATCTGG	2
, do	S		652
Οy		ACTGTCCTTGGGCATCCTGCTGAGCCTGCTTTCTCAACCAAGGGCCGGCTGGCT	.
qq	653	-GlyAspProGlyGlnThrIleThrGlnPro	664
Qy	615	TGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGG	999
qq	664	ProGlyLeuProGlySerProGlyArg	
Qy	299	CAGG	N
QQ	684	yLeuProGlyGlnProGlyLeuProGlylleLeuGlySerLysGlyGluProGl	
Qy	723	TCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTG	770
QQ	702	ylleProGlyIleGlyProProGlyProProGlyProLysGlyPheProGlyllePro	721
Oy	771	TCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGCCTACCTGCCTG	
Db	722	GlyProProGlyAlaProGlyAlaProGlyArgMe	733
ΟÝ	831	GGGACACCAGTGCCCTGGCCCCCTACTGGGCACCCAGGA	870
Dp	733	tGlyProAspGlyProProGlyProProGlyPheProGlyProLysGlyGluProGlyPh	753
Qy	871	-GGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGC	929
qa	753		773
٥y	930	TGGTGGCTGAGGAGGCAGGGCTGGGCCCACCGAGCCAGCAGAAGGGCTGTCGCCCCCT	686
Db	773	oLysGlyaspargGlyPheProGlyProSer	786
QY	066	CCTTGTCGCCCCATGCTGTCCATGCCGGGCCCCCTTGGCTTTCCGGAACCTGGGCGCCCC	1049
QQ	786	oGlyArgThrGlyLeuAspGlyLeuProGlyProLySGlyAspValGlyProAsnGlyGl	908
Qy	1050	SCACCAGCTGTGCTGCCG	1097
qq	806	nProGlyProValGlyProProGlyLeuProGlyIleGlyLeuGlnGlyProProGlyPr	826
δy	6	CTCTTCGTGGCTGAGCTGTGCAGCTGCACTCATGACCTTCACGCTGTT-	1155
QQ	826	ProGlyThrProGlyProIleGlyGlnProGlyLeuHisGlyIl	
Qy	1156		11
qq	842	spProGlyProProGlyPheAspValProGlyLeuProGlyGl	98
δλ	1170	GCTGTACCAGGCGTGCCCAGAGCTGAGCCGGCACCGAGGCCCGGAG	1229
qq	862	GlySerProGlyLeuProGlyAlaProGlyLeuIleGlyPr	877
δy	1230	TCGGATGGCAGCCTGGGCTGTTCCTG	1274
Dp QQ	878	GlySerProGlyValProGlyLysAlaGlyValProGlyPheP	893
Qy	1275	GGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGT	
ΩĐ	893	alLysGlyGluMetGlyMetMetGlyProProGlyProProGlyProLeuGl	
Qy	1321	GCAGGGATTCGGCACTCGAGCAGTCTATTTGGC&AGTGTGGCA	1364
Db	913	/LeuLysGlyAspAspGlyMetGlnGlyGlnProGly	932
ΛO	1365	CTTTCCCTGTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGG	1415

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1634 AGTGGCCTGCTCCCA------
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                                           808 rSerArgThrGlyGlnArgThrArgClnArgProGlyHisProProProGluArgGlySe 828
 ---HisProProProGluArgGlySerGlyProArgGlyThrArgProPro-AlaProSe 808
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                     100 TGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACTCAGATCCTGGCCGAGGCGC 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 ACCTATGTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAGGAAGTTCATGACCATGGTG
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Daucus carota (Carrot).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
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                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003663; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
TIGRFAMs; TIGR01301; GPH_sucrose; 1.
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346.50
42.35%
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943
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                                                                                                          ---GACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  884 GGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG
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q	150Gly-ThrArgProProAlaProSerSerArgThrGlyGlnArg-ThrA 165	1 8	
Qy	GACA	ΛĀ	
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δδ	1804 GGATGGGGCCACCTGGGACA	. Оу	928 CAG
අු	rgProProAlaProSerSerArgThrGlvGlnArgThrA	qq	498 rSer
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 S 1		Db	518 r-G
8		λŌ	853 GGG
οy	1726 CCTGGCCT	7 6	
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QQ	295 oProProGluArgGlySerGlyProArgGlyThrArg307	i i	
δy	1549 GCTAGCACTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTA 1490	Š i	
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අු	ThrGlyGlnArgThrArgGlnArgProGlyHisProProGluA	Qy	
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ф	423 rgGlySerGlyProArgGlyThrArgProProAlaProSerSerArgThrGlyGlnArgT 443	2 6	
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ò	1048 GCCGCCCAGGTTCCGGAAAGCCAAGCCGGCCCGGCATGGACAGCAGTGGGGCCACAAGGA 989	Oy	157 GCC

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1529 GGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCT 1588
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                     487 AlaIleSerGlyValLeuAlaIleValLeuLeuProLysProSerLysAspAlaAlaSer 506
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                                                                  --GCTCCCTTCCCTAATGGACACGTGGGTGCT
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Rivailler P., Quink C., Wang F.;
Sirrong selective pressure for evolution of an Epstein-Barr virus
LMP2B homologue in the Thesus lymphocryptovirus.";
J. Virol. 73:8867-8872(1999).
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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MEDLINE=20440633; PubMed=10970361;
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MEDLINE-20304984; PubMed-10846073;
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                    Moghaddam A., Koch J., Annis B., Wang F.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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425 ThrArgIleGluSerLeuGlyLeuGlyGlnGlyLeuSerMetGlyValLeuAsnLeuAla 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Physiol. 118:1473-1480(1998).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
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MEDLINE-99063785; Pubmed-9847123;
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94 HisCysGlnSerSerPheGlyArgArgArgProPheIleAlaSerGlyAlaGlyCysVal 113
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                                                                                                                                                                                                                                                                                                                                                                                                             GGGCTGCTGGACTTCTGTGGCCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTCTGAC
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                                                                                CTGCTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTG-
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1190 GGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGG 1249
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 GGCGTGGGGCTGCTGCACTTCTGTGCCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTC 724
                               142 GlyPheTrpLeuLeuAspValAlaAsnAsnValThrGlnGlyProCysArgAlaLeuLeu 161
                                                                                         162 AlaAspLeu---ThrGluLysAspHisArgArgThrArgValAlaAsnAlaTyrPheSer 180
                                                                                                                                               |||:::::::|||
|181 LeuPheIleAlaValGlyAsnValLeuGlyPheAlaThrGlySerTyrSerGlyTrpPhe 200
                                                                                                                                                                                            ---ATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTC 880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGACCTCTTCCGGGACCCGGACCAC----TGTCGCCAGGCCTACTCTGTCTATGCC
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                                                                                                                              383 LysHisMetAsp-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .02 ValAlaGlyAlaThrSerIleValValAlaValLeuIleIleGlyPheSerAlaAspIle 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vitis Vinifera (Grape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
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LeuValGlyHisLeuSerAspArgCysAsnSerArgPheGlyArgArgArgProPheIle
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-SHIRAZ; TISSUE-FRUIT;
Davies C., Wolf T., Robinson S.P.;
"Three putative sucrose transporters are differentially expressed in
                                                                                                                                                                                                                                                                                                                                    grapevine tissues.";
Plant Sci. 147:93-100(1999).
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AF021808; ARF08329.1;
InterPro; IPR003662; Sub_transporter.
Pfam; PF00083; Sugar_tr; 1.
TIGRFAMS; TIGR01301; GPH_SUCIOSE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane.
SEOUENCE 501 AA; 53938 WW; 4D0D4DE2EF2F4BA8 CRC64;
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164
85
205
159
25
                                                                         0950K6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Matches:
Conservative:
Mismatches:
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40.628
26.758
5.438
                                                             PRELIMINARY;
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NCBI_TaxID=29760;
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Best Local Similari
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CTGCGGCAGACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAA 1809 :::		CACCCACGTGTCCATTAGGGAGGGAGCTCCAGGCTTAGGGCCTGGCA 1578	### AGACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GCTGGTGCAGCGGGAAGCAGGCGCCCAGGTTCCGGAAAGCCAAGGGGG 1020 [1]
1868 CTGCGCACACACATATAGGCAGTGAN :::	1730CCACCCTGGCCTC 240 LeuProGlyThr-AlaGlyLeu 1690GGAGACATCACA 259 pGlyAlaLySGlyAspThrGly 1647 279 luAsnGlyAlaProGlyGlnVa	1625 CACCCACGTGTCCATTAGGG		70 28 19 48 59

qq	461	:::
Οy	899	AGGCCAAAGAGGCACTCCTCCTGGGTGCCCAGG
qq	469	
Qy Db	854 486	AGGGGCCAGGGCACTGGTGTCCCAGTCAATGGCAGGCAGGT 810
δy	809	36CAGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGT 75
- qa	504	
Qy	749	3T
QQ	518	LeuProGlyAlaLysGlyLeuThrGlySerProGlySerProGlyPro
Oy	731	GAGTGAAGCACACTGGCCACAGAAGTCC
qa	538	laGlyAlaProGlyGlnAspGlyArgProGlyF
0 <i>y</i>	_	ACGCCCAGGATGAGCAGTCCAGGGCC 63
QQ.		aArgsıysınsersiyvalmetsiyrneProsiyProLyssiyAlaAla 5
Oy Db	635	TGGGATCCGGGCACAGCAGCCCTGCTAGCCACCGGCCCTTGGGATGAGAAGAGGCTCA 576 ::
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۸٥	455	ATGGTCATGAACTTCTCCTCTACCCCCCACTTCCAGCAGGGGGGGCACA
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٥y	395	TGATGCCTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 33
qa	616	
Qy	338	AGCTGGGCTTTCCGGTGCCGCAGCAGGCGGCTCACCCACAGCCTCTGGACCATA
Dp	636	::: sProGlyGluGlnGlyAlaPro
Qy	281	GGGCCAGGCGGGTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTC
QQ	655	rGlyProAlaGlySerArgGlyGluArgGlyPheProGlyGluArgGlyAla11 673
Qy	224	AGCTGCGGCCTCTCCTCCTTGCTGCCGCCAACTGCCTAGGAA
qq	673	
Qy	164	CCAGGGGCCCATTTCTGCCAGCCTTTGGTGCC
qa	691	GluAlaGlyAlaProGlyAlaProGlyGlyGlnG
Qy	128	TCCAGCTTCTCAGCCCATGCTCAACACCTGCTGTGGGGCACCTCAGTGGGGACA 72
qq	707	roSerGlyLeuGlnGlyMet-ProGlyGluArgGlyAlaGlyGlyLeuProGl
Qy	7.1	CGTCTCATCACTCAGATCCTGGCCGAGCGCGCGCGCTGTCACCCGGAGCCAGCGCGT 15
qα	727	roLysGlyAlaAspGlyAlaPro
Qy	14	GCAGG 10

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504 GCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCATG 445
                                                                                                                                                                                                                                                                                                                                                             670 eProGlyGluArgGlyValGlnGlyProProGlyProAlaGlyProArgGlyAsnAsnGl 690
                                                                                                                                                    708 ySerGlnGlyAlaProGlyLeuGlnGlyMetProGlyGluArgGlyAlaAlaGlyLeuPr 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                      772 uAlaGlyProSerGlyProAlaGlyProThrGlyAlaArgGlyAlaProGlyAspArgGl 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 CCCATTTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGCT 97
                                                                                                                                                                                     564 AAGGACAGTGCCCAGATGAAGGGCCGCCGGCGGCCATAGCGTCCACGCCAGTGGTCACTG
                                                                                                                                                                                                                                                                                                                                       GTCATGAACTTCTCCTCTA----CCCCCACTTCCAGCAGCAGAGGCGGCACATAGGTGATG
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                                       ---GCTCCAGGGCCTGGGATCCGGG
                                                                         590 yAlaProGlyAsnAspGlyAlaLysGlyAspThrGlyAlaProGlyAla-----ProGl
                                                                                                              624 CACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCC
                                                                                                                                                                                                                           oGly-----ProLysGlyAspArgGlyAspAlaGlyProLysGlyAlaAspGly----
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Alpha 1 type I collagen.
Rana catesbelana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranaa.
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2528 GGTGGATCAGCAAAAAGACAGTGCTGTGGGCTGAGGGGACCTGGTTCTTGTGTGTTGCCC 2469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1988 ACCCAGTGAGGCAGGCCCTCCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTGG 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 ----GlnProGlyllePro-------GlyProProGlyProProGl 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GlyProArgGlyGluArgGlyProPr 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 oGlyAlaProGlyArgAspGlyIleProGly----- 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 y------ProalaGlyLeuGlyGlyAsn------PheAlaPr 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 oGlnMetSerTyrGlyTyrAspGluLysSerAlaGlyIleSerMetProGlyProMetGl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ProGly--ProGln---Gly 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||::: |||||||
33 CysValValAspGly------ArgThrTyrAsnAspLys------43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 --- AspValTrpLysProGluAlaCysGlnIle-------CysVal-CysAs 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 pGluGlyThrIleLeuCysAspGluValIleCysGluAsp---ileGlyAspCysProAs 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 nTyrGlnThrGlySer---ValValGluGlyProLySGlyGluThr----
                                                                                                                                                                                                                                                        F59BB550C9873F04 CRC64;
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Indels:
                                                                                                                                                                                                                                                                                                              Length:
Matches:
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Matrix Biol. 18:89-103(1999).

EMBL; AB015440; BAA29028.1; -
InterPro; IPR000087; Collagen.
InterPro; IPR001007; VWF_C.
Pfam; PF01410; CoLFT; 1.
Pfam; PF01410; CoLFT; 1.
ProDom; PD000007; Collagen; 3.
ProDom; PD000078; Fib_collagen; 3.
ProDom; PD00078; Fib_collagen; 3.
SMART; SM00314; VWC; 1.
                                                                                                                                                                                                                                     Collagen.
SEQUENCE 1445 AA; 137252 MW;
                                                                                                                                                                                                                                                                                                                            354.50
31.75%
26.47%
5.69%
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Best Local Similarity:
Query Match:
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Tue Jun 10 11:28:25 2003

CysProG	PheCysProGluGluTyrValSerProAspAlaGluValIleGlyValGluGlyPro 103
тстстс	TCTTGTGTGTTGCCCCTCAGGACTCTTCCCCTACAAATAAGTCATATGTTCAAATCCCAT 2424
GGAGTG GlyPro	GGAGGAGTGTTTCATCCTAGAAACTCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGT 2364
GGGGCTT	
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-TCTCTA(yProPro	TCTCTAGGTGTGTCTCAACTACGAGGCTAGCTGTTAACC
pGluLys	
A166A6CU	igenigabeletitiseeliteelitahanaileaaakeleaaakeeletitasaakeelitasaa 1700
GTCAGGC	CCAGTCAGGCAGCCCTAGAGACTGGGGAGGAGGAGGGACGCCCCAGCCCCAGCTGT 2106
Gly	GlyProPro
GCTACGC	GCAGCTACGCACCTCAGCACACACAGCGTGGCAGAGAGACCACATTACTTTGGCAGCAA 2046
AAACTGC yProMet	CAGAAACTGGCGGCCAGCCCGCAGCCCCATGGGGCTAACAGGAGCGGGGAGCTGGGA 1988
1	
аСІУГУ	sProGlyArgProGlyGLuArgGlyProProGlyProGlnGlyAlaArgGl 243
-CCCCAA uProGly	CCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAA 1911
CTACCTC : eSerGl}	ATACTACCTGTGTAGCAAAGTAAAYGGCGACCAGACCTGGGGCAGACATAT 1851 ::: yPheSerGlyLeuAspGlyAlaLysGlyAspThrGlyProAlaGlyProLysGlyGluPr 278
CAGTGA: ySerPro	AGGCAGTGACAGACTGGCTGAGGTGGACAATGGAGCCCATAAACAGGGATG 1800
	GGGCCACCTCKKGACAGCAGGAAGGCACTATCCAGGATGGCAGG 1756
uArgGly	ArgProGlyProProGlyThrAlaGlyAlaArgGly-AsnAspGlyAlaV 317
AGGCAGA yalaal	TCCAGGCAGATGCCCCGGCCCGGAACCACCCTGGCCTCGGTGGCCTCACCACCACCACA 1696
ACGGAG	CGTACGGAGACATCACAGGCAGAGGCCCCGCAGAGCGCGGGTGGAGGT 1648
AlaAla	GlyalaLysGlyGluAlaGlyProGlnGlyAlaArgGlySerGluGlyPro 355
GGGAGC Glyval	GGGAGCAGGCCACTGCCTCCAGCACCACGTGTCCATTAGGGAAGGGA 1600
CCAGGCT	GCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTA 1546

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1485 GAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGGGGCGCT 1426
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                                                                                                                                                                                                                                                                                       1425 GAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGGCACCGGCAGCCACAGGGAAA 1366
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                                                                           1545 GCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGG 1486
                                                                                                                                                                                                                                                                                                                                                                                              1365 GCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCAGCCGGT---- 1311
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506 aGlyProLysGlySerPro----- 512
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                                                                                                                                                                                                                                                                                                                     466 oSerGlyLeuProGlyProProGlyGluArgGlyGlyProGlySerArgGlyPheProGl 486
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2594 TGCCTGTGT-------CTCTGTGATGGC-----AACAGAAGGACCAAC 2559
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                                                                                                                      258 GGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCT 199
                                              602 lyGlyThrGlyGlyThrGlyProArgSerGluGlyAlaGlyCySProAlaArgGlyAlaG 622
                                                                                            198 CICCTCCTCGTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCT 139
                                                                                                                                                                                     ------GGTCCAGCTTCTCAGCCCATGCTCAACA 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MOV-1996 (TrEMBLrel. 01, Created)
01-MOV-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Collagen alphal (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wurtz T.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; 278279; CAB01633.1;
InterPro; IPR000087; Collagen.
R InterPro; IPR000085; Fib_collagen_C.
R InterPro; IPR001007; WWE_C.
R Fam; PF01410; COLLagen; 18.
R ProDom; PD002079; Fib_collagen; 2.
R ProDom; PD002079; Fib_collagen, 2.
R SMART; SM00214; VWC; 1.
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| 640 spGlyAlaProGluArgGlySerGlyLeuProGlyProGly----
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283
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362
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59
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY; TISSUE=TOOTH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER 1 1
SEQUENCE 1453 AA; 137887 MW;
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357.00
31.84%
27.06%
5.73%
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Db 30 ProProArgArgAspGlyGlyAsnArgGlyAspGlyAlaProGluArgGlySerGly-Le 49 Qy 2121 CCCAGCCCCAGCTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAGAAGAGCCAC 2062 Dh 49 iProGlyCycglyCarproGlyCa	2061 ATTACTTIGGCAGCAACAGAAACTGGCGGCCGGCCGCGCAGCCCCATGG	Db 72 yGlyArgGlyAraGlyAlaArgGluArgAlaAlaArgProGlyValArgValProArgPr 92 Qy 1971 CTCCACCCCAATGTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGTTGTCA 1912 Db 92 oGlyGluProVal	1856		Oy 1659 GC	Qy 1557 TCCTCACTGCTAGCACCTCCAGTGTACTTGGGCAGGAACACCTGCTTCTCC 1498	Oy 1440 CCGGTGAGGGCGCCTGAAGCTGTCACCACGCCACACTGGGACAGGCATGTGGGA 1384	Qy 1323 TGCACCAGCCGGTCCATGACCAGAGAAGACCAGGAGATGGCGCACTGCAGGAAC 1267 Db 265ProAlaGlyTrpGlyGluProGlyGlyAr 274 Qy 1266 AGCCCCAGGCTGCCATCCGAACGCTTCATCATAGTGTCTCCGGGCCTGGTGCCGGG 1207 Illili Illili Db 274 gGlyProGlyla ArgGluArgAla
Db 446 ThrGlyGlyHisProAlaAlaProGlyAlaProGlyProArgSerProArg 462 Oy 410 GCAGAGGCGCACATAGGTGATGCCTGGGCCAAACACCTCCAGGCCAAAGG 357 Db 463 ThrGluArgArgArgArgArgArgAlaGlaArgGlyHisProProGlyAlaGlyGlaArg 482	356TTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAG 11	DD 502 OARGThrCluArgArgGLySerAlaGlnArgGLyHisProProGlyAlaGlyGl 522 Qy 281 TGGGCCAGGGGTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTG233 [1] [1] ::: Db 522 nArgProSerGlyProThrGlyGlyHisProAlaAlaProGlyAlaProGlyProAr 541 Qy 232		RESULT 12 041973 ID 041973 AC 041973 PRELIMINARY; PRT; 727 AA. AC 041973; PRELIMINARY; PRT; 727 AA. DT 01-JAN-1998 (TrEMBLrel. 05, Carated) DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)	DE Hypothectical 69.4 kDa protein. GN GAMMAHV.MIOC. OS murid herpesvirus 4. OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae; OC Gammahorpesvirinae. OX NCBI_TaxID=33708; RN [1] RP SSQUENCE FROM N.A.		an	Pred. No.: Score: Score: Score: Best Local Similarity: 31.50% Conservative: Best Local Similarity: 28.06% Mismatches: 229 Mismatches: 289 Ouery Match: 12 Gaps: 49 US-09-759-143-110 (1-3410) x 041973 (1-727) Qy 2181 CCCCTTGGAAGGCCTCCAGTCAGGCAGCAGGAGGAGGAGGAGGACGC 2122

ογ	166 CAGCCAGGCGCCCATTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTC 107	. qa	143GlnArgGlyHisProProPro
qa	961 SerProGlyAlaValG	οy	1382 CGGCACCACAGGGAAAGCTGCCACACTGGCCAAAT
οy	106 AACACCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACTCAGATCCTGGC 49	QQ	153 GlnArgProSerGlyProThrGlyGlyHisPro
qa	972 Gly-	Qy	1322 GCACCAGCCGGTCCATGACCAGAGAAGAAGACCAGGG
ÃО.	48	QQ	
qa	991 oGlnGlySerArgGlyGluLysGlyAspThrGlyAlaSerGlyAlaAsnGlySerPro 1010	Ωy	1262 CCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTC
RE O9	RESULT 11	qq	184 -GlnArgGlyHisProPro
IL A	1	Qy	1202 CTCTGGGCACGCCCTGGTACAC
I C	01-MAY-2000 (TrEMBLrel. 13, Creat 01-MAY-2000 (TrEMBLrel, 13, Last	qq	197 rGlyProThrGlyGlyHisProAlaAlaProGlyAla
DI	01-MAY-2000 (TrEMBLrel. 13,	Qy	1157 AAAACAGGGGAAAGGTCATGAGTGCCATCCAGCTGC
88	Herpesvirus papio. Viruses; dsDNA viruses, no RNA st	QQ	217 rGluArgArgGlySerAle
88	Gammaherpesvirinae; Lymphocryptovirus NCBI TaxID=10394;	Qy	1097 GCAGGGT
RN		qq	232 yAlaGlyGlnArgProSerGlyProThrGlyGlyHis
R RA RA		Qy	1058 GGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCC
R	Hayward (5.5.) Submitted (DEC-1999) to the EMRI/GenBank/DDEI databases	QΩ	248 oGlyAlaProGly-ProArgSerProArgThrGluA
D S	ENBL; AF200364; AAF22950.1; SEOURNCE 608 AA: 60458 MW. 48F82ACROAD9627 CPC64.	Qy	998 GCGACAAGGAGGGGCCGACAGCCCTTCTGCTGC
S 8	5	QQ	268 lyHisProProProGlyAlaGlyGlnArgProSerG
Pr	3.51e-15 Length:	Qy	941 CCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAC
Pe	t Similarity: 35.05% Conservative:	qa	288 laProGlyAlaProGlyProArgSerProArgThrG
38	. 5.80% 1.2	Qy	881 AGAGGCACTCCTGGGTGCCCAGGTAGGGGGCCA
SO .	US-09-759-143-110 (1-3410) x Q9Q5K9 (1-608)	QQ	нів
Qy	1805	Qy	836 TGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGC
qa		QD	AlaPro
Qy	1760 CGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCCTGGCCTCGGTGGGCTCACCCCACCA	Qy	776 CATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTC
qa	31 TrpGlyProCysProAlaProSerProProProAlaPheGlnValHisGlyPro 48	qq	ArgArgA
δō	1700 CCACACGTACGGAGACATCACAG	Qy	
qa	 49 ArgSerProArgThrGluArgAi	qq	GlyProThrGlyGlyHisProAlaAlaProGl
Qy	1652 GAGGTGGGAGCCACTGCCTCCAGCACCCACGTGTCCATTAGGGAAG	δλ	
qa		qq	
δλ	1592 GCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCAC 1551	Qy	623 ACAGCAGCCTGCTAGCCAGCCGGCCCTTGGGATGAC
qa		qa	398GlyGlnArgProSerGlyPro
QY	1550 IGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGT 1491	Οy	566
qa	 108 ProGlyAlaGlyGlnArgProSe	<u>අ</u>	
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qa	128 ProGlyProArgSerProArgThrGluArgArgArgGlySerAla 142	අධ ,	431 ArgGlyHisProProProGly
٥٧	1442 ACCCGGTGAGGCGGCTGAAGCTGTCACCACGCCCACACTGTGGGACAGGCATGTGGCAC 1383	ογ	470 GCACTGGACCAATGCCCAGCACCATGGTCATGAACT

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ATGCGGCAGCAGCTGGTGCAGC 1059
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                                       TAGACTGCTCGAGTGCCGAATCGCT 1323
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GluArgArgArgGlySer-AlaGln 307
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ArgArgArgGlySerAlaGlnArgG 268
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656 hrGlyAlaG 1067GGTG 676 roProGlyG	1033	979	919 TGCTACGCA 720	872 735	Qy 838 GGTGTCCCAGTCAATGGCAGGCAGGA	Oy 778 GGCATAGACAGAGTAGGCCTGGCGAC Db 764ProGlyAsp	Oy 724 GAGCAGGCCTCCAGTGGAGTGAGC	Qy 665CA Db 798 lyAlaArgGlyGluThrGlyGlyFro	628	Qy 568 GCCCAAGGACAGTGCCCAGATGAAGG	Oy 508 ACTGGCTGAGCCTAGGAGCGGGACAC	Qy 448 CATGGTCATGAACTTCTCCTCTACCC ::	Oy 388 GCCTGCGGCCAACACACCT Db 868SerProGlyGlnProGlyAla	343	Qy 304 CACCCACAGCCTCTGGACCATAGTGG :: Db 904 snAspGlyGlnSerGlyPro-ProGl	Qy 247 GGCACTCCAGAACTGCTTCGTCTC 	Qy 193
	1923 TCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCCTGCG 1864	1863 GCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGAGCGCATAAA 1808 	1807 CAGGGATGGGCCACCTGGGACAGGA		1747 GATGCCCGGGCCCGGAACCACCCTGGCCTCGGTGGGCTCACCCACC	1687 GACATCACAGGCCCCGCAGAGCGCGGGGGGGGGGGGGGG	CCAGCACCAGTGCCATTAGGGAAGGGAGCAAGGACCAGTGTCCATTAGGGAAGGGAGCAAGGGAGCAGTGTCATTAGGGAAGGGAGCAGGTGTCATTAGGGAAGGGAGCAGTGTCATTAGGGAAGGGAGGAGTGTGAAAAAAAAAA			1519 GGGCAGGAACACCTGCTTCTCCCGGTGTAGAGGCCAGTGTGTAGGGCAGGATCTG 1460		GGCACCGGCAG-+-CCACAGGAAAGCTGCCACACTGGCCAAATAGAC rdGlyAarGlnG PFIGING PFIGI		GGCGCACTGCAGGAACAGCCCCAGGCTGCCCATCCGAACGCCTTCATCATAGTG	1228 TCTCGGGGCTCGGTGCCCGGCTCAGCTCTGGGCACGCCCTGGTACA	GCCCCTCGCCCACGAAATCCGTGTAAACAGCGTGAAGGTCATGAGTGCCATCCAGCT	GCGCAGGGTGCGGGCATGCGGCAGCACACACA
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Db	656	hrGlyalaGlnGlyargArgGlyIleGlyGlyArgAlaGlyAsnTyrGlyAlaThrGlyP 676
Qy	1067	3TGCAGCCGGGAAGCAGGCGCCCAGGTTCC
Db	919	roProGlyGlnLysGlyGluMetGlyProProGlyAsnValGlyLeuGlnGlyProProG 696
Qy	1033	GAAAGCCAAGCGGGCCCGGCATGGACAGCAGTGGGGGGCGACAAGGAGGGGGCCGA 980
QQ	969	
Qy	979	BGCTC
Db	710	ro71yProSerGlySerProGlyProAsp719
Oy	919	CTACG
Db	720	GlyproAlaGlyAlaGluGlyAspArgGlyProValGlyProMetG 735
Qy	872	CCTCCTGGGTGCCCAGGTAGGGGGCCAGGGCACT 839
Db	735	lyProSerGlyProSerGlyMetProGlyGluArgGlyAspAsnGlyGluProGly 753
Qy	838	GGTGTCCCAGTCAATGGCAGGAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATGAA 779
QQ	754	
Qy	778	GGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGA 725
Db	764	
Qy	724	GAGCAGGGCTCCAGTGGAGTGAAGCACACCTGGCCACAGAAGTCCAGCAGCCCCAGG- 666
Db	778	heAlaGlyProProGlyArgSerGlyAsnProGlyProGlnGlyGluLeuGlyProThrG 798
Qy	665	
Db	798	lyAlaArgGlyGluThrGlyGlyProGlyProSerGlyProThrGlyAspP 815
Qy	628	CGGCACAGCACCCTGCTAGCCGCCCCTTGGGATGAGAAAGAGCTCAGCAGGAT 569
qq	815	roglyproglnglyproLeuglyalaproglyglnglnglygluargglygluThrGly- 834
Qy	568	CCAAG
Db	835	836
Qy	508	ACTGGCTGAGCCTAGGAGCGGGACACAGACCAGCCCAGC
Db	837	
Qy	448	CATGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAGAGGCGCCACATAGGTGAT 389
Db	851	rediyalaginglyproproglyproThrglyproserGlyasnAlagly 867
Oy	388	GCCTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGAC 344
Db.	898	SerProGlyGlnProGlyAlaArgGlyGluProGlyGlnSerGlySerP 884
Qy	343	CAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCA
Db	884	roglyglnProglyLeualadlyArgThrGlyProSerGlyGluArgGlyAspLysGlyA 904
Oy	304	CACCCACAGCCTCTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGGGGGCCGTTCA 248
QQ	904	snAspGlyGlnSerGlyPro-ProGlyProProGlyProAlaGlyProAlaGlyGlnSer 923
Qy	247	GGCACTCCAGAACTGCTTCGTCTCGGCTCTGCAGAAGCTGCGGCCTCTCT 194
Db	924	aG1
Qy	193	
qa	941	AlaGlyL

2897 TTAGGGAAGCCGTTGAGACCTGAAGCCCTCTACCT	2699 GATTGTTGGGGATCCCCCACCCTACCCAAATATTAGACACCAAAAAGCTAGCAA 2640 153GlyProProGlyProProGlySerArgGlyProGlnGlyLeuThrGlyPr 169 2639 TGGATTCCCTTCTACTTTGTTAAATAAATAAATTAAATT	GCAAAAAGACAGTGCTGTGGGCTGAGGGACCTGGTTCTTGTGTGTTGCCCCT		2190 AGACTGAAACCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGG 2132 330
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Db 644	698 y 698 601 10 6034 PRELIMINARY; PRT; 1414 026634; 01-NOV-1996 (TERMELEI. 01, Created) 01-NOV-1996 (TERMELEI. 01, Last sequence 01-JUN-2002 (TERMELEI. 01, Last annotatian Alpha-1 collagen.	OS Strongylocentrotus purpuratus (Purple sea urchin). Strongylocentrotus purpuratus (Purple sea urchin). C Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; OC Echinoldea; Euchinodea; Echinoda; Strongylocentrotidae; OX Strongylocentrotus. OX NCBI_TAXID=7668; RN [1] RP SEQUENCE FROM N.A. RX EXPOSITO J. Y., D'Alessio M., Solursh M., Ramirez F.; RA Exposito J. Y., D'Alessio M., Solursh M., Ramirez F.; RT alpha-2(T) collagen J. Biol. Chem. 26:15559-15562(1992). DR EMBL; M92040; AAA30035, I DR InterPro; IPR000087; Collagen DR InterPro; IPR0000885; Fib_collagen	Fram: FF01410; CoLF1; 1. Pfam: FF01410; CoLF1; 1. Probom: PF01391; Collagen; 2. Probom: PD002078; Fib_collagen_C; 1. SMART; SM00038; CoLF1; 1. Collagen. SEQUENCE 1414 AA; 133025 MW; 94D9CDA71A9FD73F Ignment Scores: 2.58e-15 Length: ore: 364.00 Matches: forcett Similarity: 30.88% Conservative:	Match: 3029 GGGAAGTTV 111 43 GIYASPLYS6 2969 AGCCAGTCC 2969 AGCCAGTCC 62 ProProG1y 2930 GGGAACCAG 111 11 11 11 11 11 11 11 11 11 11 11 11

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δ	2120CCAGCCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGAGAA 2067	δλ	1154 ACAGCGTGAAGGT
qQ		qq	
Qy	2066 GCCACATTACTTTGCCAGCAACAGAAACTGGCGGCCAGCCCGGCATGG 2013	Qy P	1109 CGAAGAGCCGGCG
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ò	2012	Z a	ProProAraAr
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oy ·	TGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCCCAGGCCTGCGGCAGACA	qq	470 GluProGlyGlyA
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Š 5	1832 TGAGCTIGGACAATGGAGCCCATAAACAGGGATGGGGCCCACTIGGGACAGCAAGGCAC 1773	qa	500 GlyMetGlyGlyT
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3 5		qa	. 537 AsnArgGlyAspC
ìò	AGAGGGC	δλ	755 GACAGIGGICCGC
3 8	valadagiliardalaalaargProGlyValatg-ValProArgProGlyGluProValP	qa	549 LeuProGlyProC
3 .		QY	704 TGAAGCACACCTC
Š	CCACGIGICCAITAGGGGAAGGGGGCTTCAGGGCTTAGGGCCTGGCAGGGAAGCTGGTCATCA +	qa	568 TrpGlyGluProC
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δo, i	TeAACCCGGTGAGGGCGGCTGAAGCTGTCACCGCCACACTGTGGGACACATGTTTTTTTT	qa	611
QQ		QY	479 CCAGGCCCAGCAC
oy.	TGGCACCGGCAGCCACAGGGAAAGCTGCCACATGGCCAAATAGACTGCTCGAGTGCCGA	qa	616
QQ	GlySerArgSerPro	QY	419 CTTCCAGCAGCA
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Qy	974	CTTCTGCTGGCTCGGTCGGCCCCACCGTG 945
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qa	490	ProArgProGlyGluProValProProGly
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Db	200	 GlyMetGlyGlyThrGlyGlyThrGlyProArgSerGluGlyAlaGlyCysProAlaArg 519
Qy	851	GGGCCAGGGCACTGGTCCCAGTCAATGGCAGGCAGGA
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qa	537	
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ογ	656	GCAGTGCCAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCCGG 600
QQ	588	ProArgProGlyGluProValProProGly
Qy	599	TTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGT
qq	009	ilyGlyThrGlyGl
Qy	539	GTGGTCACTGGCTGAGCCTAGGAGCGGGACACA
QQ	611	SerGluGlyAlaG
ΟY	479	CCAGCACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCC
QQ	616	
Qy	419	CTTCCAGCAGCAGAGGGGGCACATAGGTGATGCCTGCGGGCCAAACACACCTCCAGGCCAA 360
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Qy	359	TAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGCGGCTC
Dp	627	ProArgargaspGlyGlyasnargGlyaspGlyAlaP
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	Db 278 euTyrPheAlaGluGluValProLeuMetAlaTyrGlnProHisHisLeuSerAspSer- 297	· 8	"Complete seau
		RT	
	298	RN	J. Virol. /I:58 [2] SEQUENCE FROM
0	Qy 1033CCGGAA- 1038	R'S	STRAIN=WUMS; Latreille P.,
1	 311 snSerLysSerLysLeuAspMetSerAlaValAspAsnAlaThrGlyAsnAsnProGluS 331	DR	Submitted (APR EMBL; U97553;
0	Оу 1038 1038	S S	Hypothetical poses
_	Db 331 erSerTyrGluIleAsnLysAsnAlaLysHisLeuThrProIleValGlnGluGlnAsnG 351	Alic	Alignment Scores:
Ü	Qy 1039	Pred. Score:	e:
1	Db 351 luSerPheSerAspGlyPro-GlyAlaValLeuValAsnLeuThrSerLeuArgHis 370	Perc	Percent Similarity: Best Local Similari
J	Qy 1082 ATGCCCCGCACCCTGCGCCCGGCTCTTCGTGGCTGAGCTGTGGAGCTGGATGGCACTCATG 1141	Que: DB:	Query Match: DB:
_	Db 371 LeuProProAlaMetHisSerValLeuLeuValMetAlaLeuSerTrpLeuSerTrpPhe 390)-sn	US-09-759-143-110
0	OY 1142 ACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTGTACCAGGCGTGCCAGA 1201	Qy	2939 GGAAG
ı	Db 391 ProPhePheLeuPheAspThrAspTrpMetGlyArgGluValTyrHisGlyAspProLys 410	QQ	III:: 3 GlyTh
J	OY 1202 GCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTG 1261	QY	2879 CCTGA
1	Db 411 GlyAspGluSerAlaValLysAlaTyrAspAlaGlyValArgGluGlyAlaPhe 428	qq	20 GlyAl
J	QY 1262 GGGCTGTTCCTGCAGTGCGCCAFCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGTG 1321	QY	2819 TTATC
	Db 429 GlyLeuLeuAsnSerValAspLeuGlyIleSerSerPheLeuIleGluProMetCys 448	qa	26
J	QY 1322 CAGGGATTGGGCACTGGAGGGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCT 1378	Qy	2759 CCCCA
	Db 449 GlnArgMetGlyAlaArgLeuValTrpAlaMetSerAsnPheIleValPheAlaCysMet 468	qq	30 ProPr
J	Qy 1379 GCCGGTGCCACATGCCTGTCC1399	Qy	2699 GATTG
1	Db 469 AlaGlyThrAlaIleIleSerLeuValSerValAsnGluTyrIleThrGluGlyIleGln 488	Dp	33
J	Qy 1400 CACAGIGIGGCCGIGGIGGACAGCTICAGCCGCCCTCACC 1438	Qy	2639 TGGAT
ч	leGlyGluAsnArgAlaIleLysIleAlaSerLeuValValP	qa	33
0	QY 1439 GGGTTCACCTTCTCAGCCTGCAGAICCTGCCCTACACAGTGGCCTCCCTCTACCACGG 1498	٥y	2579 GATGG
_	Db 509 GlyPheProLeuSerIleThrTyrSerValProPheSerIleThrAla 524	qa	34 AspG1
,	QY 1499 GAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGT 1543	Qy	2519 GCAAA
u	Db 525GluLeuThralaAspThrGlyGly 532	QQ	42 AlaPro
ш С	RESULT 9	Qy	2465 AGGAC
, 4	ID 041972 PRELIMINARY; PRT; 706 AA.	qq	62 ArgSe
. ப ப	DT 01-JAN-1998 (TrEMBLrel. 05, Created) DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)	QY	2405 AGAAA(
	DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) DE Hypothetical 66.4 kDa protein.	qq	74 ArgGl
ψ O	SN GAWMAHV.MIOB. OS murid herpesvirus 4.	Qy	2345 GAAAC
	OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; OC Gammaherpesvirinae.	qa	90 oArgP
υĸ		Qy	2285 AGGAG
14. IE		qq	104 rGlyG
re're		٥٧	2225 TGCAT
щ	Dal Canto A.J., Speck S.H.;	qa	112 uGly-

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AAGCCCCACCCTCTACCTTCCATCAACACCCTAACCTTGGGTAACAGCATTTGGAA 2820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STIGGGGAICCCCCACCCTACCCAAATATTAGACACCAACACAGAAAAGCTAGCAA 2640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATTIGGGAIGAGIAGAATTICCAAGGICCIGGGIIAGGCAITIIGGGGGGCCCAGA 2760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCCTTCTACTTTGTTAAATAAATAAGTTAAATATTTAAATGCCTGTGTCTCTGT 2580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCTCAACT 2286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAGAAGAAGATTCTGGCAATGATCAGCCCAATGACCAGCTATCTCAGGGGACCT 2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CICTICCCCIACAATAAGICATAIGITCAAAICCCAIGGAGGAGIGITICAICCI 2406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGTTAAGGGGGCTTAGAGATGG 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3GCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCCAG 2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProGlyGluProVal------ProProGlyGlyMetGlyGlyTh 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31y-----ThrGlyProArgSerGl 112
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| IyProGlyAlaArg------GluArgAlaAlaArg-ProGlyYvalArgValPr 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erProProAlaGly------TrpGlyGluProGlyGly------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roArgArg-----
uence and genomic analysis of murine gammaherpesvirus
                                                                                                                                  Wamsley P., Waterston R.H.;
RR-1997) to the EMBL/GenBank/DDBJ databases.
AAB66421.1; -.
Protein. 6413 MW; 9AD7A4AFDEB8748B CRC64;
                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                           5894-5904(1997).
                                                                                                                                                                                                                                                                                              1.84e-15
365.50
29.39%
25.54%
5.87%
                                                                                           N.A.
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Oy 510 ACCACTGGCGG Db 124 spLysCysSer Qy 570 TCCTGCTGAGG Qy 621 TGTGCCCGGAI Db 144 leServalAla Qy 621 TGTGCCCGGAI Db 164 hrAsnmetAs Qy 663 TGGCGTGGGC Qy 723 TCTCTGACTC Qy 723 TCTCTGACCTC Qy 783 TGATCAGTCT Db 204 eualaAspLe Qy 783 TGATCAGTCT Db 223 rpMetAlaVal Qy 831 GGGACACCAGG Db 243 rp Qy 878 Qy 927 TGCTGGTGGC Qy 927 TGCTGGTGGC Qy 927 TGCTGGTGGC Qy 927 TGCTGTGGCC Qy 927 TGCTGTGGCC	0y 197 TCCTCTTGCTGCCGCAACTGCCTAGGAATCAGCAGGCGCCCATTTCTGCCAGCCCTT 138 712 9ProGlyValArgValProArg	A d y d d y d d See P d d y d d y d d See P d d d See P d d d d d d d d d d d d d d d d d d
723	SOLT 8 SOR5 QSOX5 PRELIMINARY; PRT; 612 AA.	RE 109
663	71 CGTCTCATCACTCAGATCCTGGCCGAGGCGGGGGT 35 ::: :: ::111	Qy Dp
621	04 CACCTGCTGCCATGGGGCACCTCAGTGGGGA	QQ QD
570	37 TGGTGCCGGTCCAGCTTCTCAGCCATCTAAA 11	Qy Db
510	97 TCCTCCTTGCTGCCGCCAACTGCCTAGGAATCAGCCAGGGGCGCCCATTTCTGCCAGCCCTT	da da
Qy 450 TGCTGGGCATT :: Db 104 leTrpLeuCys	257 GGGCGGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTC 198 1	Qy Qo
Qy 390 TCACCTATGTC ::::::: :::: Db 84 euSerLeuLeu	308 GGCTCACCCACACCTCTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGG 258	oy Oy
Qy 330 CCCAGCTCTTC	359 AGGTTAGCAGGTTGACCAGCAAGAGCTGGGGTTTCCGGTGCCGCAGCAGGGC 309	Qy Dp
Qy 270 CCGCCTGGCCC Db 48 rSer	419 CITCCAGCAGCAGCACACATACGTGATGCCTGCGGCCAAACACACCTCCAGGCCAA 360 	Qy Db
Qy 219 GAGCCGAGACC 	479 CCAGGCCCAGCACTGGACCAATGCCCACCATGGTCATGAACTTCTCCTCTACCCCCA 420	Qy Dp
Query Marcn: DB: US-09-759-143-110 (1-3410	539 GCCGCCCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACACAGA 480 [1]	Q
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	616 ArgvalproArgProGlyGluProValProProGly	do Qo
	596 TrpGlyGluProGlyGlyProGlyProGlyAlaArgGluArgAlaAlaArgProGlyVal 615 656 GCAGTGCCAGCTGCCAGGGGCCTGGGATCCGGGCACAGCCAGCCTGCTAGCCAGCCGG 600	Oy Oy
RT "Three putative sucr RT grapevine tissues."; RL Plant Sci. 147:93-10 CC -!- SUBCELLOLAR LOCA	CysGlySerProGlyLeuGlySerArgSer CACAGAAGTCCAGCA	oy Oy

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CTGAGGAGGAGCGCTGGG-------CCCCACCGAGCCAGCAGGG 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pMetLeuAspLeuAlaAsnAsnThrValGlnGlyProAlaArgAlaLeuL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTGTCTATGCCTTCA 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eu---SerGlyProAspGlnArgAsnSerAlaAsnAlaIlePheCysSerT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITGGGGGCTGCCTGGCTACCTCCTGCCTGCCATTGAC-----T 830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aValThrileIleGlyPheSerAlaAspIleGlyTyrLeuLeuGlyAspT 164
                                                                                                                                                                                                                                                                                                                                                                  eLeuSerCysMet11eAlaAlaGlyValGlnPheGlyTrpAlaLeuGlnL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGC--------
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crose transporters are differentially expressed in
                                                CATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                             65711 MW; 8FC3FBD6AB439078 CRC64;
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142
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193
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Matches:
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366.50
40.60%
26.44%
5.71%
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	QQ	61	gr i	
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	QQ	62 AspGlyGlyAsnArg	2 6	
	δý	2519 GCAAAAAGACAGTGCTGTGGGGTGAGGGGACCTGGTTCTTGTGTGTTGCCCCTC 2466	7 A	
	Db	70 AlabroGluArgGlySerGlyLeuProSlyProGlyCysGlySerProGlyLeuGlySer 89	ì è	
	oy da	TAAGTCATA	qa	
	3 8	Y The type to the	Qy	1445 TGAACCCGGTGAGGGCGGCTGAAGCTGTCA
	ි අ <u>ය</u>		qa	378
	٥y	TTTATTCA	oy.	
	qq	::: ::: 118 OArgProGlyGluProVal	<u>a</u> :	388 GLySerArgSerPro
	Qy	TAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCCAG	Z	1922 AICECIGCACCEGICCAIGACCAGANG
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	ž 8	ZZZS TGCATGGGGCCTTCTGGCCTCCCTGTGTAAGTCCAGACTGAAACCCCTTGGAAGGCCT Z166 140 uGlvAlaGlvCsProAla-ArdGlvAlaGlvProAlaTroGlvAlaG 157	qa	401 GlyArgGlyProGlyAlaArgGluArg
1966	, vo		Qy	1211 CCGGCTCAGCTCTGGGCACGCCCTGGTACA
	qq	:::	qa .	411AlaArgProGlyVal
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	QQ	190	3 . č	
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	QQ	199 ProGlyGlyArgGlyProGlyAlaArgGluArgAlaAlaArgProGlyValArgValPro 218	3 8	
	٥y	1976 AGGCCCTCCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCT 1917	à f	1022 GelectriceAttecActes Freesche 1
	qq	219 ArgProGlyGluProVal 224	3 8	
	οy	1916 IGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCCTGCGGCAGACA 1857	\$ E	408 GlubroGlvGlvardglvbroGlvalabrd
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	ογ	1832 TGAGCTGGACAATGGAGCCCATAAACAGGATGGGGCCACCTGGGACAGGAAGGCAC 1773	₹ £	090 GGGIGAGGCCAAAGAGAGACACICCICCI 1 1 1 1 1 1 1 1 1 1
	qq	248GlyAlaGlyProProAlaTrpGlyAlaGlyProProArgArgAspGly-GlyAs 265	ò	851 GGGCCAGGCATGGTGTCCAGTCAATGG
	oy.		7, qa	548 GlyAlaGlyProProAlaTrp
	2	205 NAIGGLYASPGLYALAPYOGLUARGGLYSETGLYLEUPYOGLYPYOGLYCYSGLYSERPY 285	۸٥	812GGTAGCCCAGGCAGCCCCAAGACTGA
	٥٧ وم	1724 TGGCCTCGGTGGGCTCACCACCACCACGAGGGAGACATCACAGGCAGAGGCCCGC 1665 11	g qq	
	a a		Oy	755 GACAGTGGTCCGGGTCCCGGA

ACCACGGCCACACTGTGGGACA---GGCATG 1389 ||| || || || || |||||::: |||::: -ProGlyProGlyCysGlySerProGlyLeu 387 GTGTAGGGCAGGATCTGCAGGGCTGAGAAGG 1446 GAGAAGACCAGGGAGATGG---CGCACTGCA 1272 A---GCCCTCGCCCACGAAATCCGTGTAAA 1155 -----TCCAGCTGCACAGCTCAGCCA 1110 ----TGCGGCACCACTGGTGCAGCCGGG 1056 GGCTTAGGGCCTGGCAGAAGCTGGTCATCA 1563 CCTTCATCATAGTGTCTCCGGGCCTCGGTGC 1212 TTCCGGAAAGCCAAGC----- 1023 GGAGGTGGGAGCAGGCCACTGCCTCCAGCAC 1623 TCCCCTCGGTATTTGGCCAGGAACACCTGCT 1503 ACACTGGCCAAATAGACTGCTCGAGTGCCGA 1329 |||| gGlyAlaGlyProProAlaTrpGlyAlaGly 457 |||| || || ||||| || |||||| yProProAlaTrpGlyAlaGlyProProArg 360 gAla----- 410 yGlyMetGlyGlyThrGlyGlyThrGlyPro 437 | ||| ||| ||| yAspGlyAlaProGluArgGlySerGlyLeu 477 GACAAGGAGGGGCCGACAGCC----- 975 uGlySerArgSerProProAlaGlyTrpGly 497 -CTICIGCIGGCIGGGGCCCAGCGCIG 945 gGluArgAlaAlaArgProGlyValArgVal 517 OArgSerGluGlyAlaGlyCysProAlaArg 547 T-----GGGTGCCCAGGTAGG 852 GCAGGCAGGA------ 813 | |||||| |pGlyAlaGlyProProArgArgAspGlyGly 564 SATCATGAAGGCATAGACAGAGTAGGCCTGGC 756 PAGTGTGCTGCTACGCAGGTGAGGAGATGA 897 y----- 527 BAAGAGGTCAGAGGAGGCCTCCAGTGGAG 705

qq	219 AlaCysGlyTyrLeuValGlyAlaMetAspTrpGlyHisSerValLeuGlyArgLeuLeu 238	
δλ	GGCACCCAGGAGAGTGCCTCTTT	Db S40
g À	239 GlySerGluTyrGlnValIleTyrPhePheSerAlaLeuThrTrpGlyValPheLeulle 258 899 ATCHTCTTCACCTGGGA	Qy 1832 AGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCGCCATTTAC 1891
g qa		547 AlaG
δο do	917GCAGCCACACTGGTGGCTGAGGAA	Oy 1892 TTT 1894
oy.	CCCACCGAGCCAGCAGAAGGCTGTCGCCCCCTCCTTGTCGCCCCACTGCTGCCATGC 10	
qa		041971; PRELIMINARY; 041971;
δλ		01-JAN-1998 01-JAN-1998 01-DEC-2001
qa .	LeuGlyGluArgProArgSerPheSerAlaLeuGlyGluAlaAsnSerValThrSerSer	Hypothetical 73.2 kDa protein. GAMMAHV.M10A.
o o	1016	OS murid herpesvirus 4. OC Viruses; dSDNA firuses, no RNA stage; Herpesviridae;
δλ	CTTCCCGGGCTGCACCAGCTGTGCTGCCGCACCCGCACCCTGCGCGCTCTTCGTG 1	
DÞ	::: 355LeumetLysAlaIlePheAsnMetProAsnHisTyrArgPheLeuCysIle 371	
Qy		RX MEDLINE-97366649; PubMed-9223479; RA Virgin H.W. IV, Latreille P., Wamsley P., Hallsworth K., Weck K.E., RA Dal Canto A.J., Speck S.H.;
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o G	1172 GCCGAGGGCGTGACCAGGGGTGCCCAGAGCTGAGCCGGGCACCGGGGGCCCGGAGACAC 1231 114 1 1 1 1 1 1 1 1 1	
δy	1232 FATGATGAAGGGTTCGGATGGGCTGGGGGCTGTTCCTGCAGTGCGCCATCTCCCTG 1291	STRAIN-WUMS; Clatelile P., Mansley P., Waterston R.H.;
QQ	412 TyrGluArgGlyValGluValGlyCysTrpGLyLeuCysTleAsnAlaValSerSerAla 431	NL SUDMILLEG (APK-1194) to the EMBL/Genbank/DUBJ databases. DR EMBL; U97553; AAB66420.1; KW Hynorherical protects.
δ	GTCTTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTG	
a :		ent Scores: No.: 1.5e-16 Length:
à a	1332 GCCAGIGIGGGCAGCTITCCCTGTGGCTGCCGGTGCCGGTGCCGGTGCGGGTGTGGCC 1411 452 MetGlvTurpheValPheValPheValPheStrentleGlvThrSerLeuIleGlvLeupheProGluvalIne 471	Score: 382.50 Matches: 285 Percent Similarity: 29.90% Conservative: 43 Rest Local Similarity: 25.90% Mismatches: 29.
λō	GTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGGCCTGCAGCATCCTGCCC	6.14% Indels:
Dp		-09-759-143-110 (1-3410) x 041971 (1-774)
දු දි	1472 TACACACTGGCCTCCTCTACCACCGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGG 1531 :::	Oy 2939 GGAAGTGGGGGAACCAGGCTGGGCCAAGAGAAGAGGGGTGGTTAGGGAAGCCGTTGAGA 2880
δ	GACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAG	2879 CCTGAAGCCCACCTCTACCTTCAAGACCCTAAGGAAAACATTGGGAAAACATTGGAAA
- qa		48 GlyAlaGlyProProAla
Οy	1592 CCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGGAG	Qy 2819 TTATCATTTGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGGCATTTTGGGGGGCCAGA 2760
qq	511 520	Db 54TrpGlyAlaGly 57
δ	CCACCCGCGCCTCTGCCTGTGATGTCTCCGTACGTGGGGGGGG	27
qo ;	AspCysAlaAlaLeuThrCysMetValGlnLeu	58 ProProArgArg61
Š Š	CCCACCAGGCCAGGCTGCTTCCGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGAT	2699 GATTGTTGGGGATCCCCCACCTACCCAAATATTAGACACCAACAGAAAAGCTAGCAA
an	532AtaginilelleValGLyAtaGLy539	Db 61 61

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CCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTAC 1891
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                alValValLeuSerAlaSerSerIleSerLeulleGlyCysIle 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9223479;
P., Wamsley P., Hallsworth K., Weck K.E.,
                                                                                                                                                                                                                                                                                                                                                                                     nomic analysis of murine gammaherpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston R.H.;
he EMBL/GenBank/DDBJ databases.
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285
43
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478
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5, Last sequence update)
9, Last annotation update)
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Matches:
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---GGCCGGGGCATCTGC 1750
                                                 1751 CTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTGTT 1810
                                                                                                 811 ATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGC 1870
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                        ------GluIleValProLeuLysGlnAlaArgGlyLeuGly
                                                                     545 ThrAspValAlaileileSerSerMetValPheileAlaGlnLeulleValSerLeuSer
                                                                                                                         565 ValGlyProLeuValSerTrpMetAspThrThrCysAlaValLeuTyrAlaSerThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                   1871 CIGGGICIGGICGCCATITACITIGCIACACAGGIAGIATIT 1912
                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (MAR.2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024519; AAH24519.1; -.
Hypothetical protein.
                                                                                                                                                                    ||| ::::::
585 LeuSerPheLeuAlaAlaIleAlaAlaMetPheValLeuTyr 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 112 AA; 11393 MW; B9D9DE79FEF09FB7 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 11.4 kba protein (Fragment).
Mus musculus (Mouse).
1700 GIGGIGGGIGAGCCCACCGAGGCCAGGGIGGTICCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.93e-25
512.00
95.50%.
91.89%
                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-COLON;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 TTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 LeuTyrSerLeuValTrpLeuIleSerProIleLeuGlyPheLeuLeuGlnProIleIle 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 GGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCA 556
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                                                                                                                                                                                                                                                                    MEDLINE=21372467; PubMed=11479596;
Fukamachi S., Shimada A., Shima A.;
"Mutations in the gene encoding B, a novel transporter protein, reduce melanin content in medaka.";
Nat. Genet. 28:381-385(2001).
EMBL; AF332510; AAK77024.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 ArgArgSerArgGlyArgLeuIleLeuHisSerMetValMetPheGlyArgGluPheCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 TTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGGAAGTGGGGGGTAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   626 CCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTTGCTGGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 AlaAlaAspPheIleAspGlyProIleLysAlaTyrLeuPheAspValCysSerTyrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          740 GACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             557 CTGTCCTTGGGCATCCTG------CTGAGCCTCTTTCTC------
                                                                                                         Membrane-associated transporter protein B.
Oryzias latipes (Medaka fish).
Bukaryota: Metazoa: Chordata: Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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|154 ValSerGluLeuValSerAspArgSerSerArgSerThrTrp---
                                                                                                                                                                                                                                                                                                                                                                      576 AA; 63411 MW; 13A5C9828ABEE894 CRC64;
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144
95
198
164
                                                           (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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Matches:
Conservative:
Mismatches:
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                              PRT;
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456.00
39.77%
23.96%
7.11%
                                PRELIMINARY;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                              01-DEC-2001
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                                                                            01-DEC-2001
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QQ	δλ	qa	Qy	qa .	QY	qa	Oy	Dβ	Qy	q	Qy	qa .	δλ	qa .	ò	qα	QY	Db	ΟŊ	ΩP	Οy	QQ	QY	qq	QY	qq	ΟY	Dp	οy	qq	Qy	QD	Qy	Dp	Qy	Db
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	R Jalali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	RA Merkulov G., Milshina N.V., Mobarry G., Morris J., Moshrefi A.,	RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,	RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	RA Spier B.C., Staden Klamos 1., Simpson M., Skupski M.P., Smith T., RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun B.,	KA SVIISKAS K., Tector C., Turner K., Venter E., Wang A.H., Wang X., RA Wang ZY., Wassarman D.A., Weinstock G.M., Weissenbach J.,	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R. F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L	X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu R.A., Myers E.W., Rubin G.M., Venter J.C.,	The genome Science 287:	DK EMBL; AEU0352; AAF50110.1; DK FlyBase; FBgn0035968; CG4484, SO SEDIENE 599 AA: 66057 MW: C5381D334CFBF78R CRC64:		Length:	ilarity: 39.43% Similarity: 23.66%	Indels: Gaps:	US-09-759-143-110 (1-3410) x Q9VSV1 (1-599)	TOUR TOUR TOUR TOUR TOUR TOUR TOUR TOUR	46 ArglysThrArqPheGluMetPheArgleHSerAlaIleAlaMetAlaIleGluPheAla		Tredecococos actions to the contract of the co	**************************************		oo mismetaermetriii ilpoijuedaerriedijenijenijermenemenemenemenemenemenemenemenemeneme	OY 497 GGCTCAGCCAGTGACCTGGGGAGGCTATGGCCGCCGCCCTTCATCTGGGCA:556	**)	DA 126 TENESCRITCH CHECK TO THE HILL SHOW TO THE SECOND TO	5966AGG 59	TAE TO LEAR TO A CONTRACT OF THE PROPERTY OF T	140 Deductionalynsphiadly1911111717111000 Deductional Decided Setupolary Construction Constructi	GCCGGGLIGGCLIGGCCCGGGGGCLIGGCCCCGGGGGGGG	100 clyselvaintahedvaiselelytyselvillillitelyticselviasselsi	641 CTGGACTGCCACTGCTCATCCTGGGGGGTGCTGGACTTCTGTGGCCAG	186 TyrLysPheAlaVall1eLeuThrIleLeuGlyMetValLeuLeuAspPheAspAlaASp	Oy 695 GTGTGCTTCACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCACTGT 754	ZOG IIII CYSOLIIII FI OALGAIGIIII 171 LEGLEGASPMECCYS VALFI OGLGGIAGIII	Oy 755 CGCCAGGCCTATTGTTTGTTGTTGTGTTTGGGGGCTGCCTGGCTACTTG 814

Dp	225	ProLysAlaMetThrMetPheAlaLeuPheAlaGlyPheGlyGlyThrIleGlyTyrAla 244
Οy	815	TGCCTGCCATTGGGACACCAGTGCCCTGGCCCCCTACCTGGG
qq	245	:::
Qγ	875	CCTCTTTGGCCTGCTCATCTTCCTCACGTGCGTAGCAGCCACTC
qa .	265	::: rvalpheThrLeuvalThrIleIlePheAlaValCysTyrLeuIleThrValThrT
Oy	929	GGCTGAGGAGG
qq	285	eArgGluIleProLeuProLeuIleGluGlnAspGluLeuLeuArgProLeuSer
Qy	958	
Db	305	nAlaIleLysLysGluLeuLysLysLysAsnAsnThrIl
Qy	959	ACCGAGCCAGCAGAAGG
qq	325	 heuGluLeuGlnMetAlaSerAspAspProLysArgLeuGluAlaL
Qy	977	CCCTCCTTGI
qq	345	erTyrGlnAsnGlyTyrSerProAlaValGluLysGlnGly
δy	1001	TCCATGCCGGCCCGCTTGGCTTT
Db	365	yrAspAlaProValSerLeuLysAlaTyrLeuLysSerIl
٥٧	1049	TGCTTCCCCGGCTGCACCAGCTGTGCTGCC
Dβ	385	
ογ	1109	GAGCTGTGCAGCTGGATGGCACT
Db	394	ThrasnLeuPheCysTrpMetGlyHisValThrTyrCysLeuTyrPheThrAspPhe 41
οy	1169	SCHETACCAGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGA 12
Dp	414	lGlyGluAlaValPheHisGlyAspProThrAlaAlaProAsnSerGluAla
٥y	1229	CACTATGAAGGCGTTCGATGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCC 1288
Dβ	434	snTyrGlualaGlyValArgPheGlyCysTrpGlyMetAl
Qy	œ	TGGTCTTCTCTCTGGTCAFGGACGGCTGGTGCAGCATTCGGCACTCGAGCAGTCTAT
Dp	454	IleTyrSerLeuSerValThrLysLeuMetLysTrpPheGlyThrLysAlaVa
Qy	1349	GTGGCTGCCGGTGCCACA
qq	474	eserGlyMetileTyrTyrGlyileGlyMetLeuValLeud
QY	1400	CTCAC
Db	494	rpGlyValLeuValPheSerThrSerAlaGlyIleLeuTyrGlyThrIle 51
δŷ	1460	SATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGAGAA
Dp	511	nrValProPheIleLeuValAlaArgTyrHisAlaLysAsnCysPhe
Qy	1520	accgaggggacactggaggtgctagcagtgaggacagcctgatgaccagcttcc
qq	530	
Qy	1580	CAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTG
QQ	531	AsnGly
Qy	1640	CIGCICCCACCICCACCGCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTG 1699
qa	532	532

Db 301 AlaValTyrLeuAl	341	Qy 1520 AATACCGAGGGA 	Qy 1580 CCAGGCCCTAAGCC 	1640	Qy 1700 GTGGTGGGTGAGCC	1760	Qy 1820 ATTGTCCAGGTCAG 	(n >	DT 01-MAY-2000 (TrEMBLrel. DT 01-MAY-2000 (TrEMBLrel. DT 01-JUN-2000 (TrEMBLrel. DE CG4484 protein.				RA George R.A., Lewis S.E. RA Sutton G.G., Wortman J. RA Brandon R.C., Rogers Y. RA Wan K.H., Doyle C., Bax		Burtis Cherry de Pab Dodsor	RA Durbin K.J., Evangelist RA Fosler C., Gabrielian A RA Glodek A., Gong F., Gor
Alignment Scores: Pred. No.: 2531.00 Bercent Similarity: 98.208 Best Local Similarity: 97.808 Mismatches: 0uery Match: 6 Gaps:	CS (1-	Oy 440 ATGACCATGGTGCTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGC 499	Qy 500 TCAGCCAGTGACCACTGGACGTGACGCTATGGCCGCCCCTTCATCTGGGCACTG 559 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 560 TCCTTGGGCATCCTGAGCCTCTTTCTCAAGGGCGGGCTGGCT	QY 620 CTGTGCCCGGATCCCAGGCCCTGGAGCTGGACTGCTCATCCTGGGCTGGGGCTGCTG 679 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 680 GACTTCTGTGGCCAGGTGCTTCACTCCACTGGAGGCCCTGCTTCTGACCTCTTCCGG 739	Qy 740 GACCCGGACCACTGTCGTACTCTATGCCTTCATGATCAGTCTTGGGGGC 799	QY 860 GGCACCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACGTGGTAGCA 919	Oy 920 GCCACACTGCTGGTGGCTGAGGAGGCAGCGCGCCCCCCCC	Oy 980 TCGGCCCCTCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCGCTTCGGGAAC 1039	Qy 1040 CIGGGCGCCTGCTTCCCCGGCTGCACCAGCTGCCGCATGCCCCGCACCCTGCGC 1099	Qy 1100 CGGCTCTTCGTGGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTAC 1159 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 1160 ACGGATTTCGTGGGCGAGGGCTGTACCAGGCGTGCCCAGAGCTGAGCCGGCACCGAG 1219	Qy 1220 GCCCGGAGACACTATGATGAGCGTTCGGATGGCGCGCCTGGGGCTGTTCCTGCAGTGC 1279	Oy 1280 GCCATCTCCTGGTCTTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGA 1339	Oy 1340 GCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGCCTGCC
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AGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCTGTTATGGGCTCC 1819
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er S.E., Holt R.A., Evans C.A., Gocayne J.D.,
cherer S.E., Li Pw., Hoskins R.A., Galle R.F.,
S.E., Richards S., Ashburner M., Henderson S.N.,
an J.R., Yandell M.D., Zhang Q., Chen L.X.,
rs Y.-H.C., Blazel R.G., Champe M., Prediffer B.D.,
rs Y.-H.C., Blazel R.G., Nanson C.R., Miklos G.L.G.,
ni A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
P.V., Berman B.P., Bhandari D., Bolshakov S.,
n M.R., Bouck J., Brokstein P., Brottier P.,
n M.R., Bouck J., Brokstein P., Brottier P.,
D.A., Butler H., Cadieu E., Center A., Chandra I.,
y S., Dahlke C., Davenport L.B., Davies P.,
her A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
elista C.C., Ferriera S., Fleischmann W.,
ian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                    NaservalAlaAlaPheProvalAlaAlaGlyAlaThrCysLeuSer 320
                                                                                                                                                                                                                                                                                                                                                                                                    er (Fruit fly).
rthropoda: Tracheata; Hexapoda; Insecta;
Endopterygota; Diptera; Brachycera; Muscomorpha;
lidae; Drosophila.
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0y 1244 GTTCGGATGGCCTGGGCTGTTCCTGCACTGCCCATCTCCTGTGTTTCTCTGT 1303 11	QY 1424 TCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483	Qy 1544 GCTAGCAGTGAGGACCTGATGACCAGCTTCTGCCAGGCCCTAAGCTTGGAGCTCCC 1603 Db 421 ThrSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440 Qy 1604 TTCCCTAATGGACACGTGGGTGCTGGAGCCAGTGCTCCCACCTCACCTCA	0y 1664 TGCGGGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAGGCC 1723	Oy 1784 CTGTCCCAGGTGGCCCCATCCTTTATGGGCTCCATTGCCAGCTCAGCTGTC 1843	SUI SK	DT 01-DEC-2001 (TERBELEAL. 19, Created) DT 01-DEC-2001 (TERBELEAL. 19, Last sequence update) DT 01-DEC-2001 (TERBELEAL. 19, Last sequence update) DT 01-DEC-2001 (TERBELEAL. 19, Last annotation update) DE Hypothetical 33.4 kDa protein. OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). OC Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; OC Cercopithecinae; Macaca.	
Some teach	1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuL	Ob 41 ProLeuLeuGluValGluValGluGluLysPheMetThrMetValLeuGlyIleGly 60	584 TITCTCATCCCAAGGGCGGGCTAGCAAGGGCTGCTGTGCCGGATCCCAGGCCCTG	704 ACTCCACTGGAGGCCCTGCTCTGACCTTCCGGGACCCGGACCACTGTCGCCAGGCC 101 Th!	824 ATTGACTGGGACACCAGTGCCCTACCTGGGCACCCAGGAGAGTGCTTTTTTTT	944 GCAGCGCTGGGCCCACCGAGCCAGCAGAAGGCTGTCGGCCCCTTGTCGCCCCAC	0y 1064 CACCAGGTGGCTGCCCCCCCCCCCCCCCCCCCCCCCCTTCCTGGCTGGCTGCT

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		rGCTG 343 euLeu 20	rGCCG 403 alpro 40	FGGT 4 eGly 6	3TGGA 523 rgGly 80	3CCTC 583 erLeu 100	CCTG 643 coLeu 120	TGCTTC 703 Cysphe 140	19600 763 ala 160	CCTGCC 823 ProAla 180	CTTT 883 buPhe 200	GAGGAG 943 GluGlu 220	CCAC 1003 OHis 240	GCTG 1063 gLeu 260	GTGC 1123 nCys 280	GCTG 1183 yLeu 300	AGGC 1243 uGly 320
553 553 0 0 0		CGGAAAGCCCAGCTCT 	GCAGGCATCACCTATGTC	ACCATGGTGCTGGGCA	GCCAGTGACCACTGGC 	TTGGGCATCCTGCTGA LeuGlyIleLeuLeuS	TGCCCGGATCCCAGGC 	GGCTGCTGGACTTCTGTGGCCAGGTGT 	CCGGACCACTGTCGCC/ 	CTGGGCTACCTCCTGCC 	ACCCAGGAGGAGTGCC7 	ACACTGCTGGTGGCTGI 	GCCCCTCCTTGTCGCC 	TTCCGGAACCTGGCCCCTGCTTCCCCGGCT 	CTCTTCGTGGCTGAGCT 	SATTTCGTGGGCGAGGC 	CGGAGACACTATGATGA
Length: Matches: Conservative: Mismatches: Indels: Gaps:	(1-553)	TIGITCCAGAGGCTGTIGGGTGAGCCGCCTGCTGGGGCACCGGAAAGCCCAGCTCTTGCTG 	GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGATT 	CTCTGCTGCTGGAAGTGGGGGTAGAGGAGATCATGACCATGGTGCTGGGCAT 	CCAGTGGTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGG 	CGCTATGGCCGCCGCCCGCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCT 	TTTCTCATCCCAGGGCCGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCTV 	3CGTGGGCTGCTGGAC 	CTCCACTGGAGGCCCTGCTCTGTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGC 	TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCT 	TGACTGGGACACCAGTGCCCTGGCCCCTACGGCACCCAGGAGGAGTGCCTCTT 	GGCCTGCTCACCTCATCTTCCTCACCTGGGTAGCAGCCACACTGCTGGTGGCTG 	GAGCCAGCAGAAGGCTGTCGGCCCCCTCCTTGTCGCCCA 	'GGCTTTCCGGAACCTG 	CACCAGCTGTGCTGCCGCATGCCCGCCACCTGCGCCGGCTCTTCGTGGCTGAGCTGT 	AGCTGGATGGCACCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTT 	ACCAGGGCGTGCCCAGAGCTGAGCCGGCACCGAGGCCCGGAGACACTATGATGATGAAGG
2.59e-176 2861.00 100.00% : 100.00% 44.58%	3410) x Q96JT2	AGAGGCTGTGGGTGA(TGCTAACCTTTGGCC 	TGCTGGAAGTGGGGG 	TGGGCCTGGTCTGTGT 	GCCGCCGCCGGCCCT 	TCCCAAGGGCCGGCTC 	GAGCTGGCACTGCTCATCCTGGGCGTGG 	rGGAGGCCCTGCTCTC	TCTATGCCTTCATGAT	3GGACACCAGTGCCCT 	FCACCCTCATCTTCCT	GCAGCGCTGGGCCCCACCGAGCC 	TGCTGTCCATGCCGGCCCGCTTGGCTT 	rGTGCTGCCGCATGCC 	rGGCACTCATGACCTT 	SCGTGCCCAGAGCTGA yValProArgAlaGl
. No.: e: ent Similarity: Local Similarity y Match:	9-143-1	Z84 ATGGTCC MetValG	344 GTCAACC 21 ValAsnL	404 CCTCTGC 41 ProLeuL	464 CCAGTGC 61 ProvalL	524 CGCTATG ArgTyrG	584 TTTCTCA 101 PheLeuI	644 GAGCTGG 21 GluLeuA	704 ACTCCAC' 141 ThrProL	764 TACTCTG 161 TyrSerVa	824 ATTGACT(181 IleAspT)	884 GGCCTGC 201 GlyLeuL	944 GCAGCGC7 	1004 TGCTGTCC 241 CysCysP1	1064 CACCAGC7 261 HisGlnLe	1124 AGCTGGA7 281 SerTrpMe	1184 TACCAGGC
Pred. No Score: Percent Best Loc Query Ma DB:	-09-75	÷ 8	Oy Dp	oy Db	Qy Db	Oy Dp	Oy Db	Oy Dp	oy Dp	Oy Dp	oy Db	QY	Oy Dp	Qy Db	Qy Db	Oy Dp	Qy

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364 GCTTTCCCTGTGGCTGCCGGTGCCATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT 1423
1244 GITCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTG 1303
                                                                             1304 GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA 1363
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                                                                                                   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 59.4 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini; Cercopithecidae;
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"Isolation of full-length cDNA clones from macaque brain cDNA libraries.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AB060851; BAB46871.1: -.
Hypothetical protein.
SEQUENCE 553 AA; 59392 MW; 0718F3A91FB3BF1E CRC64;
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NCBI_TaxID=9541;
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Q95KI5;
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Q959K5 Vitis Vinit
Q41972 murid herpe
Q26634 strongyloce
Q965k9 herpesvirus
Q41973 murid herpe
Q53079 rattus norv
Q93251 rana catesb
Q95076 daucus caro
Q95603 daucus caro
Q9563 vitis vinit
Q95755 apium grave
Q04077 vicia faba
Q60444 cricetulus
Q9103 mus musculu
Q9103 rattus norv
Q60467 cricetulus
Q95103 rattus norv
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O77753 canis famil
Q9sp14 alonsoa mer
Q910b9 oncorhynchu
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080605 arabidopsis
028396 equus cabal
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Q9m535 euphorbia e
Q9fv16 lycopersico
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Q15094 homo sapien
                             Q8r110 mus musculu
Q90z74 oryzias lat
Q41971 murid herpe
                                        oryzias lat
murid herpe
macaca fasc
                   Q9vsv1 drosophila
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"Identification and characterization of prostein, a novel prostate-specific protein."
Cancer Res. 61:1563-1568(2001).
EMBL, AV033593; AAK54386.1; -.
SEQUENCE 553 AA; 59322 MW; OAFA23FBC742A667 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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Q9ESQ2
Q8SPM4
O76045
Q9SP63
Q9S7Z5
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Q8207

Q9J103

Q60467

Q9ZTB9

Q43653

Q9XHL6

Q9QZS0

Q15094
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Q77753
Q9SP14
Q910B9
Q944W2
Q80605
Q28396
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Q9M535
Q9FVL6
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Q90274
Q41971
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093251
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MEDLINE=21139094; PubMed=11245466;
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                                          361
359
357
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                                                            Q96jt2 homo sapien
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11565.772 Million cell updates/sec
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                                                                       ; Search time 121.5 Seconds
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                     protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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sp_unclassified:*

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Search completed: June 9, 2003, 18:34:21 Job time: 8556 secs

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HSPE54C06 406 bp DNA linear STS 18-NOV-1998
H.sapiens flow-sorted chromosome 1 HindIII fragment, SC1pE54C06,
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2453 GGGGAAGAGTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTC 2512
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                                                                                                                                   Eukaryota. Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 406)

2 (sregory, S., Kettleborough, R., Langford, C., Ross, M.T. and Hunt, S.E. Direct Submission
Submitted (18-NOV-1998) The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
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                                                                   2513 TTTTGCTGATCCACCCCCCTCTTACAGGATGTGGCCTGTTGGTCTGT
                                                                                 1 | GGGGAAGAGTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTC
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/clone_lib="SClpE"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                        2693 AACAATCAGGTCCCCTGAGATAGCT 2717
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Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 9 10-OCT-2000;
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                                                                                                                                                                        | [Dases 1 to 272] | Balling-Medel.P.A., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H. Reagents and methods useful for detecting diseases of the prostate Patent: US 6130043-A 11 10-0CT-2000; Location/Qualifiers
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                                        PAT 16-MAY-2001
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                                                       Sequence 11 from patent US 6130043.
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Matches 265; Conservative
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AUTHORS
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PAT 16-MAY-2001
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Billing-Medel P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 8 10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2207 GCCAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAG 2266
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Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Bolling-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Boldon, J., Grandos, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 12 10-0CT-2000;
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                                                               Sequence 8 from patent US 6130043.
AR112287
AR112287.1 GI:14092187
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RESULT 40
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Dilling-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Ganados, E.M., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Groborts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H. Reagents and methods useful for detecting diseases of the prostate Patent: US 6130043-A 10 10-0CT-2000;
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                                                                                                                       3034 AGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAA 3093
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                                                                                                                                         121 GCCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCGTTGGGGAATCTCACACAGAAACT
                                                                                                                                                                                                                                                                  1 AAGGCACTGCCCAAAATNNCCCCTACCCCCAACTTTCCCCTACCCCCAACTTTCCCCACC
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Pred. No. 3.4e-39;
0; Mismatches 1; Indels
                                 Indels
 Score 291; DB 6; L
Pred. No. 7.1e-40;
); Mismatches 3;
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59087 ITGGCCAAATACTCACTGTAGAATTCTGTAAG-GCATCAAAGAAGAAGAGGATCTGCCTCCCC 59029
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                                                                                                                                                                                                                                                                                                                                                                                                                              21; Gaps
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4: contig of 2717 bp in length
4: gap of unknown length
5: contig of 4269 bp in length
7: contig of 4640 bp in length
7: contig of 3279 bp in length
7: contig of 3189 bp in length
7: contig of 381 bp in length
7: contig of 3821 bp in length
7: contig of 3820 bp in length
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0; Mismatches 122; Indels
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Best Local Similarity 77.3%;
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S Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Andio-Oduola, B., Ali-osman, F.R., Allen, C., Andio-Oduola, B., Ali-osman, F.R., Allen, C., Andio-Oduola, B., Andio-Oduola, B., Andio-Oduola, B., Banka, T., Barbaria, J., Benton, J., Bindge, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Birkett, C., Burrell, K.L., Byrd, N.C., Carch, P., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, T., Ferraguto, D., Edwards, C.C., Elhaj, F., Ferraguto, D., Flagoy, N., Garca, N., Gill, R., Gao, J., Garcia, A., Garca, P., Hawes, A., Hernandez, J., Harris, C., Harris, K., Hart, M., Haulyk, S., Hume, J., Jackson, L.E., Homsl, F., Homsl, F., Homsl, F., Homsl, F., Homsl, F., Homsl, F.,
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                                                                                                                                                                                                                                                                                                                  TCTACTCATCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAA 2858
                                              -----GATGTTCCTG 1145
                                                                                                                    AGCCTGGTTCCCCCCACTTCCACTCCCCTCTACTCTCTAGGACTGGGCTGATGAAGGC 2978
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                     AGTTTGGTTCCCTGATTGCCCACTTCTCCCTA-------TGGGAAAGG
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                                                                                           2859 GGTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCTCTTTGGCCC
                                            TCTCTTCATCCTAATTGAGAGCCATAA-----
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Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J. Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Lucier, R., Martindale, A., Martinda, E., Martindale, A., Martinda, E., Martindale, A., Martinda, E., Martindale, A., Martinda, E., Marssey, E., Marchell, T., Mohabbat, K., Morgan, M., Morris, S., Miner, C., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Mosen, M., Nickerson, E., Newtson, N., Moyyon, A., Nguyen, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Petrens, L., Pickens, K., Primus, E., Pul., L., Quilles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Shooshtari, N., Sisson, I., Soderzen, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutone, H., Sutone, H., Sutone, H., Sutone, J., Sutone, J., Taylor, P., Tamerisa, A., Tamerisa, K., Wang, C., Ward, Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Walliams, G., Walliamson, A., Waleczyk, R., Wooden, S., Worley, K., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, C., Wu, Y., Wu, Y.F., Zourilla, S., Nelson, D., Weissland, M. Unpublished
J., Unpublished
J., Unpublished
J., Unicon, J., Landry, J., Landry, S., Nelson, D., Absoc, I., Landry, J., Landry, J., Landry, S., Marchock, C., and Gibbs, R., Mand, M., Wall, S., Nelson, D., Absoc, I., Landry, J., Landry, S., Marchock, C., and Gibbs, R., Mand, M., Mand, M., Mand, M., Mand, M., Mand, M., Mand, M., M., Wall,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "vorking draft' sequence. It currently

* consists of 65 contigs. The true order of the pieces

* soot known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One and Paylor Plaza, Houston, TX 77030, USA

(bases I to 198037)

Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Contact: has-halpebom.tmc.edu
Contact: has-halpebom.tmc.edu
Center project name: GRAD.efsF14
Center clone name: GRAD.efsF14
Center clone name: CHAJO-65F14
Center clone name: Plasmid:
Sequencing vector: plasmid:
Sequencing vector: plasmid:
Sequencing vector: plasmid:
Sequencing vector: 1419884 bases at least Q40
Consensus quality: 155599 bases at least Q40
Consensus quality: 166549 bases at least Q20
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1163: gap of unknown length
2425: contig of 1162 bp in length
2425: gap of unknown length
3556: contig of 1131 bp in length
3556: gap of unknown length
4752: contig of 11096 bp in length
4852: gap of unknown length
5972: contig of 1100 bp in length
6072: gap of unknown length
7818: contig of 11746 bp in length
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Worley, K.C.
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AUTHORS
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2026 GGGCTGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTG 2085
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                           1726 GGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCT 1785
                                                                                                                                                                                                                                                                                                           AGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGG 1965
                                                                                                                                                                                                                                                                                                                               575 T------TGAAATGTGGTCTGTTCAGGTGCTGTATCAAGGCTCC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                515 GAGTCTGGCTGGCCTACTGGCAGCCTCTCGCATGGAAGTCATTCTGAAGTTCTGCAGGGA 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2266 GGGTTAACAGCCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAAT
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                                                                                                                      GTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCAC
                                                                                                                                              241 TGCCTATATGGTATCAGCTGCAGGCTTGGGTCTGGTCGCCATTTACTTTGCTACACAGGT
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: http://www-spgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Unknown (protein for IMAGE:4984191)"
/protein_id="AAH24519.1"
/protein_id="AAH24519.1"
/bc.xref="GI:19353991"
/translation="PRGHVGSGSSGILAPPPALCGASACDVSMRVVVGEPPEARVYTGRICLDLAILDSAFLLSQVAPSLFMGSIVQLSHSVTAXMVSAAGLGLVAIYFATQVVF
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                                                                                                                                         ROD 07-AUG-2002
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                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammallai; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01 MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be fo through the I.M.A.G. E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 59 Row: p Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Colon, normal. 5 month old male mouse."
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCCCAATGGACACGTGGGCTCTGGCAGCGGCATCCTGGCCCCTCCACCTGCACTCTG
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                                                                                                                                  BC024519 1593 bp mRNA linear F
Mus musculus, clone IMAGE:4984191, mRNA, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6'
<1. .340</pre>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
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musculus
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                   15
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                                                                                      RESULT 38
BC024519
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                              /organism="Homo sapiens"
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                                                               Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
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Catarrhini; Hominidae; Homo.
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CORIXA CORPORATION.(US)
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/db_xref="taxon:9606"
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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qa	15 TTGGGTAGGGTGG 1	. Qy 25	2550 AIGIGGCCIGITGGICCITCIGITGCCAICACACACACACACACACACACACACACACACACAC
RESULT 35 AX140521/c LOCUS DEFINITION			
ACCESSION VERSION KEYWORDS SOURCE	AX140521.1 GI:14280639 human	Qy 26	2670 TTTGGGTAGGGTGGG 2684
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	SULT 36	
REFERENCE AUTHORS	<pre>1 (bases 1 to 772) Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,</pre>	AX200381/c LOCUS DEFINITION	AX200381 772 bp Sequence 11 from Patent W00151633.
TITLE	Skelky, Y.A. and Wang, A. Compositions and methods for the therapy and diagnosis of prostate cancer	ACCESSION VERSION KEYWORDS	AX200381.1 GI:15390177
JOURNAL FEATURES	Patent: WO C	SOURCE	human. Homo sapiens Eukaryota, Metazoa, Chordata, Crani
SOURCE BASE COUNT	e 1//2 // // // // // // // // // // // // //	REFERENCE AUTHORS	Mammaila; Eutheria; Primates; Catari (Lases 1 to 7.2) Xu,J., Dillon,D.C., Mitcham,J.L., He Reed,S.G., Kalos,M.D., Fanger,G.R.,
ORIGIN Query Match	tch 17.7%; Score 603; DB 6; Length 772;	TITLE	Stolk,J.A., Skeiky,Y.A., Wang,A. an Compositions and methods for the th cancer

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, Day, C.H., Retter, M.W.,
and Meagher, M.J.
cherapy and diagnosis of prostate
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CORIXA CORPORATION (US)
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/db_xref="taxon:9606"
1.772
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Best Local Similarity 91.8
Matches 675; Conservative
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AX106230/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171003 AGGCCCCTGGAGTTGGCCCTGCTGATCTTGGGAGTGGGGCTGCTGCTGGACTTTTGTGGCCAG 170944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 695 GTGTGCTTCACTCCACTGGAGGCCCTGCTCTTGACCTCTTCCGGGACCCGGACCACTGT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455 GCCATTGGTCCAGTGCTGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCAC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           755 CGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTC 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGCCCTGGAGCTGGCACTGCTCATCTGGGCGTGGGGCTGCTGCTGCTGTTGTGTGGCCAG
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73651 81298: contig of 7648 bp in length 81299 81399 91288: contig of 9840 bp in length 91239 91338: gap of 100 bp 91339 91338: gap of 100 bp 127752: contig of 36414 bp in length 127753 127852: gap of 100 bp 127853 17786: contig of 49634 bp in length 177487 177586: gap of 100 bp 177587: contig of 981 bp in length 17787 177586: gap of 100 bp 177587: contig of 981 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 104; Indels
                                                                                             37 178567: contig of 981 bp in length. Location/Qualifiers
                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="Rp23-272413"
/clone=!hb="RPCI-23 Female Mouse BAC"
1. .58509
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.3%; Score 623.6; DB 2
86.8%; Pred. No. 1.7e-96;
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/note="assembly_fragment"

/note="assembly_fragment"

60724. .62950

/note="assembly_fragment"

63051. .65309

/note="assembly_fragment"

65410. .67839

/note="assembly_fragment"

6740. .69956

/note="assembly_fragment"

67940. .69956

/note="assembly_fragment"

6706. .73550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_fragment"
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73651. .81298
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58610. .59459
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Matches 686; Conservative
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170763 JGCTCTTTGGCCTCCTCACCCTCATTTCCTCATCTGCATGGCAGCCACTCTGTTTGTG 170704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1054
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 772)
Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
Compositions and methods for therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                       CTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAG
                                                                                              875 TGCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG
                                                                                                                                                                                            935 GCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTTG
                                                                                                                                                                                                                                                                                                                                                                                         1055 CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCT
                                                                                                                                                                                                                                                                                             995 TCGCCCCCACTGCTGCTGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT
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Anderson,S., Barna,N., Bastlen,V., Boquslavkiy,L., Boukhgalter,B.,
Anderson,S., Barna,N. Bastlen,V., Boquslavkiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dearrk,K., Dear,J.S., Dodge,S., Faro,S.,
Glude,S., Gordette,M., Graham,L., Crand Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Ilav,G., Macden,P., Jones,C.,
Landers,T., Lehoczky,J., Levine,R., Liu,G., MacCarthy,M.,
MacGonald,P., Major,J., Levine,R., Liu,G., MacCarthy,M.,
McMenga,V., Murphy,T., Maylor,J., Nguyen,C., Micol,R., Norbu,C.,
Norman,C.H., O'Connor,T., Obonnell,P., O'Neil,D., Olliver,J.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosett,M., Roy,A., Santos,R., Schauer,S., Schubock,R.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigillo,J., Yaszillev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Direct Submission
Al Submitted (J4-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
Strave, R., Inthon, R., Nichen, R., Nichelle, R., Stamer,R., Stander, B., Stanger, B., Stanger, B., Stanger, B., Stanger, B., Stanger, S., Stander, S
                                     162177 CCCGGGTGCACCAGCTGTGCTGCCGAATGCCTCGCACCTGCGCCCGGCTCTTTGTGGCC 162236
                                                                                                                                                                                                                                                                                                  1055 CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCT 1114
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                                                                                                                                                                                                                                                               TCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 1054
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Mus musculus clone RP23-272H13, WORKING DRAFT SEQUENCE, 13 ordered
                                                                                                                               935 GCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTG 994
875 IGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG 934
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 178567)
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Mus musculus.
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Guarate, B., Brown, A., Calmarate, J., Campopiano, A., Chang, J., Changalata, J., Candrate, J., Campopiano, A., Chang, J., Colok, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gide, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kalas, C., Lawocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEvan, P., McKernan, K., Meldrim, J., Meneus, L., Norbu, C., Normon, T., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riback, M., Stantos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Ye, Vola, Y., Young, St., Zimmer, A. and Zody, M., Subrak, L., Zimmer, A. and Zody, M., Subrak, L., Zimmer, A. and Zody, M., Ye, W. J., Young, G., Letter, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 14, 2002 this sequence version replaced gi:18308540. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIRR
Web Site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contect: project Information
Center clone name: 120597
Center clone name: 272_H_13
Center clone name: 272_H_13
Sequencing vector: Plasmid; n/a: 100% of reads
Sequencing vector: Plasmid; n/a: 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175041 bases at least Q30
Consensus quality: 177048 bases at least Q30
Consensus quality: 177028 bases at least Q30
Insert size: 182000; agarose-fp
Insert size: 17307; sum-of-contigs
Quality coverage: 7.7 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o of 100 bp
contig of 2259 bp in length
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65309: cont
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67940
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65310
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

bp in length length length bp in length of 1694 bp in length bp in length bp in length in length bp in length bp in length length bp in length bp in length length bp in length length of 1739 bp in length in length of 1693 bp in length in length in length bp in length in length bp in length bp in length unknown length of 1131 bp in length length bp in length length bp in length in length in length bp in length bp in length bp in length bp in length of 1280 bp in length in length of 1671 bp in length in length unknown length of 1240 bp in le length ength unknown leng of 1882 bp i unknown leng þ ďq ďq of 1918 bp unknown len 2108 bp unknown 1 of 2115 b unknown 1 of 2108 b unknown l of 2289 b unknown lof 1740 b unknown of 2376 h unknown] of 2061 h unknown] of 1149 lunknown unknown of 1575 l unknown of 1611 h unknown of 1162 unknown of 1348 unknown of 1576 unknown of 1635 unknown 2014 contig of 1866 unknown of 1200 of 1672 unknown unknown of 1096 unknown of 1120 unknown of 1746 unknown 1248 of 1426 unknown unknown unknown unknown unknown unknown of ō oŧ ō oţ oţ of gap of contig gap of contiq contig gap of contig contig contig gap of gap of contig contig contig of of contig ō contig contig contig contig contig contig gap of contig οŧ contig of contig of gap of contig gap of contig gap of gap of gap of gap of gap of of of gap of gap of gap gap 23512: 25087: 26859: 26959: 41676: 21641: 7868: 9662: 5601: 20392: 0816: 12609: 4320: 35660: 13658: 18100: 2425: 3556: 3656: 4752: 4852: 5972: 12014: 6072: 7818:7918: 28698: 10614 11914: 18657 30817 332510 332510 334221 34321 35561 37569 37569 37569 37569 37569 41177 41677 41677 41677 41677 41677 50490 50590 52330 54545 54645 56753 56853 58640 6073 7819 9267 9267 100315 1100715 1100715 110716 10716 10 52430 2326 4753 4853 5973 1064 11643657

length bp in length in length in length in length length in length length in length in length in length bp in length bp in length bp in length in length length in length length length length length Length length length ength ength ength ength ength ength length length length length length ength unknown length ı, ų. 디 디 J Of 20%. Jf unknown le unknown of 2419 k unknown l of 2660 k unknown of 2164 k unknown of 2045 k unknown of 3090 l unknown of 2450 h unknown of 3479 l unknown of 4640 unknown of 3279 unknown of 4159 2664 unknown of 2839 unknown of 2717 unknown unknown unknown 3531 unknown of 5455 unknown 4269 unknown of oţ jo οŧ ot contig gap of contig contig contia gap of contig gap of contig of contig gap of gap of gap of ō 60931: 61031: 63481: 123743: 123843: 120979: 63581: 1613: 35092: 04682: 108313: 113868: 117889: 68860: 94992: 108413: 13968: 100424 100524 104683 104783 61032 63482 63582 66001 66001 68761 71025 71125 73170 76209 79788 82505 82605 94993 95093 108414 113869 113969 117790 120980 121080 123744 86874 91614 91714 86974 108314

455 GGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCTAGGCTCAGCCAGTGACCAC 0; Gaps Length 198037; Indels .86 DB 2; 4e-98; Pred. No. 4e-9 0; Mismatches Score 633.2; Pred. No. 4e-18.6%; ilarity 87.6%; Conservative Best Local Similarity Matches 692; Conserv Query Match

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161637 TGGCGTGGGCGCTATGGCCGCCGGAGACCCTTTATCTGGGCTCTGTCCCTGGGTGTCCTG 161696 574 515 TGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTG g g ŏ ò

634 575 CTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCC a ò

AGGCCCCTGGAGCTGGACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAG

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161757 AGGCCCCTGGAGTTGGCCCTGCTCATCTTGGGAGTGGGGCTGCTGCTGGACTTTTGCGGCCAG 161816 695 GIGIGCIICACICCACIGGAGGCCCIGCICTCTGACCICIICCGGGACCCGGACCACIGI 754 g ò

814 755 GGCCAGGCCTACTCTGTTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGGCTACCTC g à

161877

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bp in length length

length

unknown l of 1787 b

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unknown

contig gap of

58739:

815 CTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAG 874 g à

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Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bubay, C., Burch, P., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chan, R., Chen, S., Chen, R., Chen, S., Chen, R., Chen, S., Chen, R., Chen, R., Chen, S., Chen, R., Chen, S., Chen, R., Day, Carroll, L., Dady C., Duld, R., David, R., David, R., Day, Carroll, L., Dady, C., Duld, R., Douthwalte, K.J., Draper, H., Duyan-Rocha, S., Durbin, K.J., Bandra, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Reraguto, D., Flagg, N., Pord, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, P., Hahe, S., Hamilton, K., Harris, C., Harris, K., Huber, J., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Houlins, B., Jackson, E., Jacobson, B., Jia, Y., Johnson, R., Joline, J., Jackson, L.E., Jacobson, B., Jia, Y., Lucier, J., Lul, X., Lucier, S., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegd, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Mayuen, N., Mayuen, N., Mayuen, N., Mayuen, P., Martin, R., Marti
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NOTE: This is a "working draft" sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (06-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 198037)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission Submission Submission (14-701-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: Plaand;
Sequencing vector: Plaand;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 149884 bases at least Q40
Consensus quality: 159599 bases at least Q20
Consensus quality: 165599 bases at least Q20
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Unpublished
2 (bases 1 to 198037)
Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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479 Qy 1581 CAGGCCCT		Qy 1641	1940 Db 301 TGCTCCCA	598 Qy 1701 TGGTGGT	B 361	Oy 1761	717 Qy 1821 TTGTCAG	Db 480 TIGTCCAG	777 Qy 1881 TCGCCATT	Db 540 TC-CCATT	Qy 1941 CGTAGAAA	Qy 1999 CGCTCTG Db 658 CGCTCCTG	Qy 2059 AATGTGGC	, Db 718 N	Qy 2118	RESULT 31	FOCUS	DEFINITION Sequence ACCESSION ASS67036 VERSION AX267036 KRYWORDS SOURCE himan	_	REFERENCE Xu,J., Dil AUTHORS Xu,J., Dil Ralos,M.D. 5; Vedvick,T.	and Hender 1400 TITLE Compositio	60 JOURNAL PATENT: WO	1460 FEATURES source	1520 BASE COUNT 122 ORIGIN	1580 Query Match Best Local Similarit Matches 745; Conse
Db 421 CCATCCTGGATAGTG-CTTCCTGCTGCTGCTCANGTGGCCCCATCCTGTTTATGGGCTCCA 4			OY 1881 TCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAG 1:		CGTAGAAAACTICCAGCACAITGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCC	1909 CGTHARARATICCACCARCITCGGGGTGGAAGGCCTGCCTCACTGGGT-CCAACTCCC	658 CGCTCCTGTTAACCCCATGGGGCTGCCGGCTTGGCCGCCAATTCTGTTGCTGCCAAAGT	Qy 2059 AATGTGGCTCTCTGCTGCCACCTGTGCT-GCTGAGGTGCGTAGCTGCACACTGGGGGC 2:		Oy . 2118 TGGGGCGTCCC 2128	778 TN	RESULT 30 AX200380 LOCUS AX200380 DEFINITION Sequence 10 from Patent W00151633.	ACCESSION AX200380.1 GI:15390176 KEYWORDS			AUTHORS Xu,J., Dillon,C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Red,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., SkelkyY.A., Wang,A. and Meedpler,M.J. TITLE Compositions and methods for the thereon and Alamosis of prostate	Cancer of the contract of the	JOKNAL PACENT: WO U12153-A 10 19-JUL-2001; CORIXA CORPORATION (US) FEATURES Location/Qualifiers Source 1 789"Homo sapiens"	/db_xref="taxon:9606" BASE COUNT 122 a 250 c 221 g 182 t 14 others ORIGIN	Ouery Match 19.7%; Score 673.4; DB 6; Length 789; Best Local Similarity 94.2%; Pred. No. 3.3e-105; Matches 745; Conservative 0; Mismatches 40; Indels 6; Gaps	Qy 1341 CAGICTATITGCCAGIGTGGCAGCTITCCCTGTGGCTGCCGGGCCACATGCCTGTCCC 14	1 CAGTCTATNIGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCATGCCTGTCCC	Qy 1401 ACAGTGTGGCCGTGGTGACACTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGC 1-	Qy 1461 AGATCCTGCCCTACACACTGGCCTCCTCTACCACCGGAGAAGCAGTGTTCCTGCCCA 1: Db 121 AGATCCTGCCTACACACTGGCCTCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCA 18	

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GCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTTCTGG 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTAGCCCCATGGGGCTGCCGGCTGGCCGCCAGTTTCTGTTGCTGCCAAAGT 2058
TAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCC 1640
                                                             ACCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGG 1700
                                                                                                                                                                                                                                                                                                                                       TTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAG 1940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear PAT 26-OCT-2001
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., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A., Hepler,W.T.
rson,R.A.
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                 ons and methods for the therapy and diagnosis of prostate
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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9
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10 from Patent WO0173032.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 250 c 221 g 187
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19.7%; Score 673.4; DB 6; Length 789;
Best Local Similarity 94.2%; Pred. No. 3.3e-105;
Matches 745; Conservative 0; Mismatches 40; Indels 6
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
1. 789
/note="n = A,T,C or G"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 789)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Sked,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Compositions and methods for the therapy and diagnosis of prostate
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Sequence 10 from Patent WO0134802.
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/db_xref="taxon:9606"
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Pred. No. 6.5e-126;
           methods for the therapy
                                 Patent: WO 0173032-A 851 04-OCT-2001; CORIXA CORPORATION (US)
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and Henderson, R.A. Compositions and m
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Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      CATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGG
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	3222 TAATGTCGTCTTATTTAGCGGGGGGGAATATTTATACTGTAAGTGAGCAA	Qy 3276 TCAGAGTATAATGTTTATGGTGACAAAATTAAAGGCTTTCTTATATGTTTAAAAAAAA	Oy 3336 AAAAAAAAAAAA 3348 Db 2599 AAAAAAAAAA 2611	RESULT 25 AX343860 LOCUS LOCUS DEFINITION Sequence 6 from Patent W00200892. ACCESSION AX343860.1 GI:18491927 REXWORDS SOURCE Synthetic construct. ORGANISM SATHINGTONSTRUCT. ORGANISM SATHINGTONSTRUCT.	REFERENCE 1 AUTHORS cabezon Silva,T.E. and Delisse,A.M. TITLE Triple fusion proteins comprising ubiquitin fused between thioredoxin and a polypeptide of interest thioredoxin and a polypeptide of interest 500URNAL Patent: WO 0200892-A 6 03-JAN-2002; FEATURES Location/Qualifiers 6 03-JAN-2002; FEATURES Location/Qualifiers 1.1593 //Organism="synthetic construct" //db_xref="texon:32630" //db_xref="texon:32630" //note="Chimaeric (E. coli - human)" BASE COUNT 308 a 472 c 461 g 352 t ORIGIN	Query Match 28.2%; Score 961.2; DB 6; Length 1593; Best Local Similarity 99.7%; Pred. No. 2.2e-154; Date of the state

1012 420 1072 480 1132 540	1192 600 1252 660 1312 720	1372 780 1432 840 1492	1552 960 1612 1020 1672 1080 1732 1140	1792 1200 1852 1260 1912 1320 1972 1378 2032	1422
GGCCCAACCGAGCAGCAGCGAGCCGCCCCTCCTTGTCGCCCCACTGCTGTCCAGCGCCCCACTGCTGTCCCAGCGCCCCCACTGCTGTCGCCCCCCCC	CACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGC [1]	CGGCTGGTGCAGCGATTCGGCACTCGAGCAGTTTTTTGCCCAGTGTGGCAGCTTTCCCT	CACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGT [1]	CCGGGCCGGGGCATCTGCCTGGACATCCTGGATAGTGCCTTCCTGCTGCTCCCCGGGCGGG	
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 43 Row: p Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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RMGSLGLFLQCAISLVFSLVMDRLVQKFGTRSVYLASVMTFPVAAAATCLSHSVVVVT
ASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDAGGSSGEDSQTTSFLPGPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="PRAGWLAGLLYPDTRPLELALLILGVGLLDFCGQVCFTPLEALL
SDLFRDPDHCRQAFSVYAFMISLGGCLGYLLPAIDWDTSVLAPYLGTQEECLFGLLTL
IFLICMAATLFVTEEAVLGPPEPAEGLLVSAVSRRCCPCHVGLAFRNLGTLFPRLQQL
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DSAFLLSQVAPSLFMGSIVQLSHSVTAYMVSAAGLGLVAIYFATQVVFDKNDLARYSV
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                   Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 943

Web site: http://www.shgc.stanford.edu

Contact: (Dickson, Mark) macd@paxil.Stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Mam1" /lab_nost=DH108"
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/protein_id=*M8134084.1"
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/db_xref="taxon:10090"
/map="FVB/N"
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  Email: cgapbs-r@mail.nih.gov
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Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                              1700 GTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTC
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Best Local Similarity 100.0%; Pred. No. 5.4e-247;
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	14	341 CTGGTCAACCTTGGCCTGGAGGTGTTTGGCCGCAGGATCACCTATGTG	401 CGGCTCTGGTGCTGGAGTGGGGGTAGAGGAGAGTTCATGACCATGGTGCTGGGCATT	461 GGTCCAGTGGGCCTGGTCTGTGCTCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGT 1 1 1 1 1 1 1 1 1 1	521 GGACGTATGCCGCCGCGCCCTTCATCTGGGCACTCTGGGCATCCTGGGCATCTGGGCATCTGGGCATCCTTGGGCATCCTGGGGATGGGGGGGG	581 CTCTTCCAAGGGCCGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCC 6	641 CTGGAGCTGGCACTCCTCGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGC	701 TICACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAG 7	761 GCCTACTGTGTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTTGCTGCTTGGGGCTGCCTGC	821 GCCATTGGGACACCAGTGCTGGCCCCCTAGCTGGCTGCTGGGCGGCTCTGCTTACCTTACCTTACCTTACCTTACCTTGGGACACCAGGAGGACAGCCTCTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACTAC	B81 TTTGGCCTGCTCACCTCATCTTCCTCACCTAGGTACTGGGTAGGTA	941 GAGGAGGGTGGCCCACCGACCAGCAGAGGGTTGTGGCCCCTCCTTGTGGAGGGGGGGG	1001 CACTGCTGCCATGCCGGGCCCGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGG	1061 CTGCACCAGCTGCTGCCCATGCCCGCACCCTGCGCTTTCCCCGG 122 1061 CTGCACCAGCTGCTGCCGCATGCCCCGCACCCTGCGCTCTTCGTGGCTGAGCTG 112 120 CTGCAGCAGCTGCTGCTGCCGATGCCTTGCACCCTACTGCTGAGCTTG 127	1121 TGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGG 118 1121 TGCAGCTGGATGGCACTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGG 118 1280 TGCAGCTGGATGGCACTTATACACTTGTTCTACACGGATTTCGTGGGATTTCGTGGGATTTCACAGGGG 133	1181 CTGTACCAGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACATTATGATGATGATGATAA 124 1181 LTGTACCAGGCGCTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGATGAA 124 1240 CTGTACCAGGGCGTGCCAGAGCAGCAACACAACAACAAAAAAAA	1241 GGCGTTCCGATGGCCAGCTGTTCCTGCAGTCCGAGCCCGGGGCATCTCTTTTTTTT	1301 CIGGICATGGACCGCTGGAGCGATTCGGCAGTGTGCCATTTTGCCGAGTGTGAGTGTGAGTGTGTGT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSVYAFMISLGGCLGYLLPAIDWDTSVLAPYLGTÖEECLFGLLTLIFLICMAATLFYT
BEBVIGAPPERBELLYSAVSRRCCPGHVGLAFRUGTLFREKDÖLCCFWBFTLDREY
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SLVFSLVWDRLVQKFGTRSVYLASVWTFPVAAAATCLSHSVVVVTASAALTGFTFSAL
GLIPPTLASTYHREKOVFLPKYRGDGGSGSBOSYTSFLFGPFRGAL
SGILAPTLASTYRGKOPFLPKYRGDGGGSGSBOSYTSFLFGPFRGALFBNGHVGSGS
SGILAPTLASTON
                                                                                                                                                                                                                                                                                                                                                                                                                           be found
                      Direct Submitssion
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 45 Row: 1 Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                       Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M. Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Liver, normal. 5 month old male mouse."
/clond_lbe"NCI_CGAP_Li9"
/lab.host="DH10B"
/note="vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 GCCTCGGCCAGGATCTGAGTGATGAGACGTGTCCCCACTGAG--GTGCCCCACAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 CGTGTTTAGCGTGGGACGACGAGTGGTGAATTGGCACTAAAGGGCTGGCAGAAATGGGAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 GCCGAGACGAAGCAGTTCTGGAGTGCCTGAACGGCCCCCTGAGCCCTACCCGCCTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 GGTGTTGAGCATGGGCTGAGAAGCTGGACCGGCACAAAGGGCTGGCAGAAATGGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 TGGCTGCACCCTAGGAGGTTAGTGCTAGTGAGGAGGAGAGCCAC-----GGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Prcourement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.4%; Score 1583.4; DB 10; Length 3354; 74.0%; Pred. No. 1e-260; Live 0; Mismatches 671; Indels 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"Unknown (protein for MGC:32471)"

**Protein_id="Anal31311.1"

**Ab_xref="GI:31594809"

**Ab_xref="LocusID:212980"
                                                                                                                                                                                                                                                             Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="MGC:32471 IMAGE:5050610"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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/map="FVB/N"
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Matches 2456; Conserv
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                    143390 TATTIGGGTAGGGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGG 143449
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                                                                              GGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCCTCTTAGCTTTTATCA 2547
TITGAACATATGAC--TTATTTGTAGGGGAAGAGTCCTGAGGGGCCAACACACAAGAACCA 2487
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3354)
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                                                                                                                                                                                                                                        CTTATTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGATGAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCCAACTTTC
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                                                                                                                                                                                                                                                                                                                  2668 TATTIGGTAGGGIGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATIGGG
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Homo sapiens chromosome 1 clone RP11-6B6, WORKING DRAFT SEQUENCE, 7
 Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
 Kaul, R.K., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.D. Direct Submission
 Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
Direct Submission
 Submitted (18-SEP-2001) Genome Center, University of Washington,
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Mammalia, Eutheria, Primates,
1 (bases 1 to 157988)
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 (bases 1 to 157988)
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Sequencing vector: plasmid; L08752; 100% of reads

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CONTENSOR (1031/ : 12243)
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 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
 Quality coverage: 7.3x in Q20 bases; sum-of-contigs
 265 6364: contig of 6264 bp in length 6365: 15785: contig of 9421 bp in length 15786 15885: gap of unknown length 15886: gap of unknown length 15886 27947: contig of 12062 bp in length 2784 28047; gap of unknown length 16993 52092: contig of 23945 bp in length 155 81254: gap of unknown length 158813: contig of 37559 bp in length 18913: contig of 37559 bp in length 18914 157988: contig of 37559 bp in length 167988: contig of 37559 bp in length 167988: contig of 39075 bp in length.
Chemistry: Dye-terminator ET; 57% of reads Chemistry: Dye-terminator Big Dye; 4% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 154688 bases at least Q40 Consensus quality: 156347 bases at least Q30 Consensus quality: 157058 bases at least Q20 Insert size: 157388; sum-of-contigs
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 FEATURES
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|------------------------------------------------------------------------|-------------------------------------------------------------------|-----------------------------------------------------------------------|------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------|
| 64 64 64 64 64 64 64 64 64 64 64 64 64 6                               | Q Q Q Q                                                           |                                                                       | OY OY                                                            | da oy                                                                                                                                                                                                                                                                                                                                                                             | o do do                                                                                                                                                                                                | 40 da da                                                                                                                                                                                                                                                                                                                                                                                                    | 90 A A A A A A A A A A A A A A A A A A A                                                                                     |
| 3028 CCCACCAGCTCCACAACCCTGTTTGAAGCTACTGCAGAACCAGAAGCACAAAGTGCGGTT 3087 | GAAACTCAGGAGCACCCCCTGCCTGAGCTAAGGAGGTCTTATCTCTCAGGGGGGTTTA 32 [1] | 3268 GTGAGCAATCAGAGTATAATGTTTATGGTGACAAATTAAAGGCTTTCTTATATGTTTAA 3327 | 6976 bp DNA linear<br>tent WO0173032.<br>6403                    | ENVARYOLE; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  REFERENCE 1  AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.B., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.  and Henderson,R.A.  TITLE Compositions and methods for the therapy and diagnosis of prostate | JOURNAL PATCHT: WO 0173032-A 705 04-OCT-2001;  CORIXA CORPORATION (US)  Location/Qualifiers  source  /organism="Homo sapiens"  /db_xref="taxon:9606"  ABASE COUNT 1312 a 1996 c 1961 g 1706 t 1 others | 53.2%; Score 1815.8; DB 6; Length 6976; limilarity '98.7%; Pred. No. 2e-300; l. Conservative 0; Mismatches 22; Indels 2; Gaps CCTACACACTGCCTTACCACGGGAAAGCAGGTGTTCCTGCCCAAATACCGAGGTGTTCTTGCCCAAATACCGAGGTGTTCTTGCTGCCCAAATACCGAGGTGTTCTTGCTGCCCAAATACCGAGGTGTTTCTTGCTGCCCAAATACCGAGGTGTTCTTGCTGCCCAAATACCGAGGTGTTCTTGCTGCCCAAATACCGAGGTGTTCTTGCTGCCCAAATACCGAGGTGTTCTTGCTGCCCAAATACCGAGGTGTTCTTGTGTTTTTTTT | 1530 GGGACACTGGAGCTGAGCACTCTGCCTTAGGTGTTCCTGCCCAAATACCGAG 31/1  1530 GGGACACTGGAGCTGCAGCAGCAGCAGCCTGATGACCAGCCCTA 1589  [171 |

| 2 ACTITGCTACAGGGGGGGGGGCCTGCACTTGGCCAAATACTCAGCGTAGAAAA 0 CTTCCAGCACATTGGGGGGGGGGGCCTCCCTGGTCCCGGTCCCGGTCCTGTTA 1111111111111111111111111111111111                                                                                                                                                                                                                                                                                                                                                                                                                      | TYCCCACCCTGTGCTGAGGTGCTACAGGTGGGGGGCTGGGGGCTGCCTTTCCACCCTTTCCACCTGGGGGCTGGGGGCTCCCTTTCCACCTTTCCACTTGGGGGCTGGGGGCTCCCTTTCCAGGGGCTTTCCAGTTGCGTTTCCAGTTGCTTTCCAGTTGCGGGTTTTCAGTTCTTCCCCCAGTTTTCAGTTCTTCCAGTTTTCAGTTTTCAGTTTTCAGTTTTTCAGTTTTTCAGTTTTTCAGTTTTTTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 370 AGCTTCGTTTAATGTAAGCTCTTGCATGGAAGTTTCTAGGATGAACCTCTCATGCCATGGA 242                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |             | 2668 TATTTGGGTAGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGG 2727  [111111111111111111111111111111111 | 29<br>29<br>30<br>66<br>66                                                                                                        |
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| 9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 8 3 8 3 8 3 8 3 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 6 6 6 6 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 49 69 69    | \$ da \$ da \$ da                                                                                     | , da o o o                                                                                                                        |
| QY         3215         TTTGCAATAATGTCGTCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCA         3274           Db         2337         TTGCAATAATGTCGTCTTATTTAGCGGGGTGAATATTTATACTGTAAGTGAGCA         2396           QY         3275         ATCAGAGTATAATGTTTATGGTGACAAATTAAAGGCTTTCTTATATGTTTAAAAAAA         3334           Db         2397         ATCAGAGTATAATGTTTATGGTGACAAATTAAAGGCTTTCTTATATGTTTAAAAAAA         2456           QY         3335         AAAAAAAAAAAAAAAAAAAAAAA         3355           Db         2457         AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | RESULT 19 AX200996 LOCUS DEFINITION Sequence 626 from Patent W00151633. ACCESSION AX200996.1 GI:15390823. AX200996.1 GI:15390823. KEYWORDS Human. ORGANISM Homo sapiens COURCE Nammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 6976) AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Stelky, Y.A., Stelky, Y.A., Wang, A. and Maghler, M.U., Retter, M.W., Stolky, J.A., Wang, A. and Maghler, M.W., Stolky, J.A., Wang, A. and Maghler, M.W., Stolky, J.A., Mang, A. and Maghler, M.W., Stolky, J.A., Wang, A. and Maghler, M.W., Stolky, J.A., Mang, A. and Maghler, M.W., Stolky, J.A., M. Wang, A. and Maghler, M.W., Stolky, J.A., Mang, A. and Maghler, M.W., Stolky, J.A., M. Wang, A. and Maghler, M.W., Stolky, J.A., Wang, A. and Maghler, M.W., Stolky, J.A., Wang, M.W., Mang, A. and Maghler, M.W., M. A. and Maghler, M | Cancer  Location (US)  CORIAN CORPORATION (US)  Location/Qualifiers  L. 6976  Adb_xref="taxon:9606"  UNT 1312 a 1996 c 1961 g 1706 t 1 others  Match  Cancer (And taxon)  Match  Advanta (And taxon)  Match  Advanta (And taxon)  Match  Advanta (And taxon)  Match  Advanta (And taxon)   Query Match | 1590 AGCCTGGAGCTCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCTGCTCCCC 16                                          | DD 5352 AGCCCACGAGGCTGGTTCCGGGCCGGGCATCTGCCTGGCCTCGCCATCCTGG 5411  QY 1770 ATAGTGCCTTCCTGCTGTGCTGCCCATCTTATGGGCTCCATTGTCCAGC 1829 |

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 Similarity
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BASE COUNT 505
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| Qy  | 1845   | CTGCCTATATGGTGTGTGCCGCGAGGCCTGGGTCTGGTTACTTTACTTTGCTACACAGG 1904  |                      |
| οqα | 661    | CIGCCTATATGGTGTCTGCCGCAGGCCTGGTCGCCATTTACTTTGCTACACAGG 720        |                      |
| QY  | 1905   | TAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGG 1964 |                      |
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| δ   | 1965   | GGTGGAGGCCTGCCTCACTGGGTCCCAGCTCCCGCTCCTGTTAGCCCCATGGGGCTGC 2024   | Qy 30                |
| අ   | 781    | STRAGCCCCATGG                                                     |                      |
| ٥y  | 2025   | CGGGCTGGCCGCCAGTTTCTGTTGTGCCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGT 2084 | 47                   |
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| δ   | 2085   | GCTGCTGAGGTGCGTAGCTGCACAGCTGGGGGCGTCCCTCTCTCT                     |                      |
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| οy  | 2205   | AGGCCAGAAGGCCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTC 2264 |                      |
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| οy  | 2265   | AGGGTTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAA 2324 | RESULT 18            |
| q   | 1080   |                                                                   | HSM804244<br>LOCUS   |
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| Op  | 1140   | TARACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGT 1199 | VERSION              |
| o,  | 2385   | AGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGA 2442   | SOURCE<br>ORGANISM   |
| QQ  | 1200   | AGCTCTTGCATGGGAGTTTCTAGGATGAACACTCCTCCATGGGATTTGAACATATGAAA 1259  |                      |
| Qy  | 2443   | CCCCTCAG                                                          | REFERENCE<br>AUTHORS |
| qa  | 1260   | GTATTTGTAGGGGAAGAGTCCTGAGGGGCAACACAAGAACCAGGTCCCCTCAGCCCA 1319    | TITLE<br>JOURNAL     |
| Qy  | 2503   | CAGCACTGTCTTTTGCTGATCCACCCCCCTCTTACCTTTATCAGGATGTGGCCTGTTG 2562   | COMMENT              |
| QΩ  | 1320   | CAGCACTGTGTTTTGCTGATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTG 1379   |                      |
| Ωy  | 2563   | STCCTTCTGTTGCCATCACAGAGACACAGGGCATTTAAATATTTAACTTTATTTA           |                      |
| QQ  | 1380   | GTCCTTCTGTTGCCATCACAGAGACACAGCATTTAAATATTTAACTTATTTAATATAACA 1439 |                      |
| ΟŻ  | 2623   | AAGTAGAAGGAATCCATTGCTAGCTTTTCTGTGTGTGTCTAATATTTGGGTAGGGT 2682     | Codifie              |
| QD  | 1440   | AAGTAGAAGGGAATCCATTGCTTAGTTTTCTGTTTTTGGTGTTTTTTTT                 | FEATURES<br>Source   |
| Οy  | 2683 ( | GGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGA 2742 |                      |

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500 GGGGATCCCCAACAATCAGGTCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGA 1559
 HSM8U4244 2477 bp mRNA linear PRI 10-JUL-2002
HOMO SapienS mRNA; cDNA DKFZp666D0110 (from clone DKFZp666D0110).
AL832933
 German Genome Project.
This clone (DKF2p666D0110) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
 923 TGGTTCCCCCCCACTTCCACTCCCCTTACTCTCTAGGACTGGGCTGATGAAGGCACTG 2982
 800 cccaaaartrccccraccccaacrrrccccraccccaacrrrcccacacacrccaca 1859
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 223 AATGTCGTCTTATTTTAGCGGGGGGAATATTTTATACTGTAAGTGAGCAATCAGAGT 3282
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2477)
 Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S. Direct Submission
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 2743 ATCTICITCICCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTA
 863 GAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCTTTGGCCCCAGCC
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 Homo sapiens
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|------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                                                                                                | CCAGGCTCAGGGTTAACAGCTAGCTCTAGTTGAGACACCTAGAGAGAG                                                                                                                                                                                                                                                                                                                               | 1321 TCAGCCCACAGCACTGTTTTGCTGATCCACCCCCCTGTTACCTTTATCAGGATGTG 1380 2555 GCCTGTTGGTCTTTTTGCTGATCCACCCCCCCTGTTACTTTATCAGGATGTG 1380 2555 GCCTGTTGGTCCTTCTGTTGCCATCACAGGACACAGGCATTTAAATTTTAACTATTT 2614 1381 GCCTGTTGGTCCTTCTGTTGCCATCACAGGACACAGGCATTTAAATTTTAACTATTT 1440 2615 ATTTAACAAGTAGAAGGAATCCATTGCTAGCTTTTCTGTGTTGTTGTTTTTTG 2674 1441 ATTTAACAAAGTAGAAGGAATCCATTGCTAGCTTTTCTGTGTTGTTGTTTTTG 1500 2675 GTAGGGTGGGGGATCCCCAACAATGGTCCCCTGAGATAGGTTGGGCTGATCA 2734 11501 GTAGGTGGGGGATCCCCAACAATCGGTCCCCTGAGATAGGTGGTCATTGGGTGATCA 1560 2735 TTGCCAGAATCTTCTCCTGGGGTCTGGCCCCCCAAAATGCTAACCAGGACCTTGG 2794 111111111111111111111111111111111111 | AAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGTGAA AAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGTGAA AAATTCTACTCATCCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGTGAA GGAAGGTAGGGGTGGGGCTTCAGGTCTCAACCCCCTTTCTTG |
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AGCGGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCT 1484
 1424
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 IGCAATAATGTCGTCTTATTTATTTAGCGGGGGGGAATATTTTATACTGTAAGTGAGCA 3274
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ing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
ing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
lon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
srts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
ents and methods useful for detecting diseases of the prostate
nt: US 6130043-A 15 10-OCT-2000;
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Unknown. Unclassified.

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| 3950                                                         | 2446                                                           | 2506                                                           | 2566<br>4130                                                 | 2626<br>4190                                                      | 2686<br>4250                                                     | 2746                                                         | 2806                                                        | 2866                                                  | 2926                                                           | 2986<br>4550                                                        | 3046                                                                                          | 3106                                                  | 3166                                                         | 3226                                                         | 3286                                                               | 3                                                    |
|--------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------|--------------------------------------------------------------|-------------------------------------------------------------------|------------------------------------------------------------------|--------------------------------------------------------------|-------------------------------------------------------------|-------------------------------------------------------|----------------------------------------------------------------|---------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------------|------------------------------------------------------|
| CTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCT | CTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTA<br> | TITGIAGGGAAGAGTCCIGAGGGCAACACACAAAAACCAGGTCCCCTCAGCCCACAGC<br> | ACIGICITITITGCIGAICCACCCCCTCITACCTITIAICAGGAIGIGGCCIGITGGICC | TTCTGTTGCCATCACAGAGACACAGGCATTTAAATATTTTAACTATTTAATTTAACAAAGT<br> | AGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGTGTGTCTAATATTTGGGTAGGGTGGGGGGGG | ATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCT | TCTTCTCCTGGGGTCTGGCCCCCCAAATGCCTAACCCAGGACCTTGGAAATTCTACTCA | TCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAG | GIGGGGCTICAGGICICAACGGCTICCCTAACCACCCTCTICICTIGGCCCAGCTGGT<br> | TCCCCCCACTICCACTCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCAAIIIIIIIIII | AAATTICCCCTACCCCAACTITCCCCTACCCCAACTITCCCCACCAGCTCCAACCCCCCACCACCACCACACCCCAACCCCAACCCCAACCCC | TGTTTGGAGCTACTGCAGGACCAGAAGTGCGGTTTCCCAAGCCTTTGTCCATC | TCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCC | TGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGTTTAAGTGCCGTTTGCAATAATG | TCGTCTTATTTATTTACCGGGGGGGGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAA<br> | TGTTTATGGTGACAAAATTAAAGGCTTTCTTATATGTTTAAAA 3330<br> |
| 3891                                                         | 2389<br>3951                                                   | 2447                                                           | 2507                                                         | 2567                                                              | 2627                                                             | 2687                                                         | 2747                                                        | 2807                                                  | 2867                                                           | 2927                                                                | 2987                                                                                          | 3047                                                  | 3107                                                         | 3167                                                         | 3227                                                               |                                                      |
| QQ                                                           | Qy<br>Db                                                       | Qy<br>Dp                                                       | Qy<br>Db                                                     | oy<br>Op                                                          | Oy<br>Dp                                                         | δλ<br>Dp                                                     | Qy                                                          | y d                                                   | Qy                                                             | QY<br>Db                                                            | Qy<br>Db                                                                                      | Qy<br>Db                                              | Qy<br>Db                                                     | Oy<br>QD                                                     | oy<br>O                                                            | Qy                                                   |

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 1177 GGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGA 1236
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 1356
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 1477 ACTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACAC 1536
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 1957 CACATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCGGCTCCTGTTAGCCCCAT 2016
 1717 CGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGC 1776
1 (bases 1 to 2152)
Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the prostate
Location/Qualifiers
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 1417 GACAGCTTCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCGCTACAC
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Matches 2149; Conservative
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PAT 16-MAY-2001

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Sequence 16 from patent US 6130043. ARI12295

RESULT 16
AR112295
LOCUS
DEFINITION
ACCESSION
VERSION

AR112295.1 GI:14092195

| 2329 CTCAGTCACCTGGTTTCCCATCTCTAAGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | QY                        | GATGGGCAGCCTGGGGC                                                    | oy , |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|----------------------------------------------------------------------|------|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 2810                      | 2751 TGCTCCGACCCTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGCGTTCG     | r qq |
| 2269 TTAACAGCTAGCTCCTAGTTGAGACACACCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | CICATCLICATION 2730 OY    | 2091 GICCACACACAGGGGGICICGIGCAGGAGGAGGGGGGGGG                        | g &  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 1239                      | 1240                                                                 | Qy   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | G 2690                    | 2631 AAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGGTGCTGGGGAGCAGGCT      | qq   |
| 3711 TAGGGCTGCCTGACTGGAGGCCTTCCAAGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1239 Db                   | 1240                                                                 | δλ   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | GG 2630                   | 2571 CAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGTCAGT      | QQ   |
| 3651 CTGAGGTGCGTAGCTGCACAGCTGGGGGCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                           | 1240                                                                 | Qy   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 2570                      | 2511 GCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTT    | qa   |
| 3591 CTGGCCGCCAGTTTCTGTTGCTGCCAAAGTA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1239 Db                   | 1240                                                                 | Qy   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 2510                      | 2451 ATAATCTCACCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCA    | qq   |
| 3531 GAGGGCTGCCTCACTGGGTCCCAGCTCCCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                           | 1240                                                                 | Qy   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 2450                      | 2391 ATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAA    | qa   |
| 3471 ATTTGACAAGAGCGACTTGGCCAAATACTCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1239                      | 1240                                                                 | Qy   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 3G 2390                   | 2331 TGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGCT      | qa   |
| , ר                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 1239                      | 1240                                                                 | Qy   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 2330                      | 2271 TGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTT    | Db   |
| 3351 COAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 21 239 C 1239 Dh          | 1240                                                                 | ٥y   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | CTCTGCT 2270              | 2211 AAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACAT           | QQ   |
| 3251                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1239                      | 1240                                                                 | Vo   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | GTCAGG 2210               | 2151 ACACTCGGGGCTGTGTGTGGGCTGGTGCCTCTCCATCCTGGCCCCGACTTCTCT          | qq   |
| 10004 GGCCTTTGCCTGTGATGATCTTCCGTACGTGTGTGTGTGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | O 1239                    | 1240                                                                 | Qy   |
| STAIL TARIOGRACE COCCIO TO CARCOLOGO | 3 2150                    |                                                                      | QQ   |
| 1609 TAATGGACACGTGGGTGCTGGAGGCAGTGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1239                      | GATGA                                                                |      |
| 1111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1234                      | 1175 GAGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCGGGCACCGAGGCCCGGAGACACTAT      | ð á  |
| 3051 CTACCACGGGAGAAGCAGGTGTTCCTGCCC 1549 CAGTGAGGACAGCTGATGATGAGAAGTTCCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 203                       | 1971 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC    |      |
| 1489 CTACCACCGGGAGAAGCAGGTGTTCCTGCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | CGGCTCTTCGTGGCT 19/0 . QY | 1911 CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGC                   | g i  |
| 2991 CGCCCTCACCGGTTCACCTTCTCAGCCCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 111                       | 1055 CCCGGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGCTCTTGTGTTGCTTGC |      |
| 2931 CCCTGTGGCTGCCGGTGCCAATGCCTGTCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 1910                      | 1851 TCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT    | g qa |
| Ο.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 1850                      | GCTGAGGAGGCAGCGCTG                                                   |      |
| 1309   GGACCGGCTGGTCCACCGATTCGGCTCCACTCGACTTCTTTTTTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | OY CYCGCCCCCTCTTG 994 DY  | 935 GCTGAGGAGCGCTGGGCCCCACCGAGCCAGCAGAGAGGGCTGTCGCCCCCTCTG           | ٥ÿ   |
| - 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 1790                      | 1731 TGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG     |      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | GCCACACACTGCTGGTG 934     | 875 TGCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCA                    | ^O   |

TGGGGCGTCCCTCTCTCTCCCCAGTCTC 2148 GACTCTGCAGGTGGATTACCCAGGCTCAGGG 2268 CCCTTAACCTGCAGCTTCGTTTAATGTAGCT 2388 regregregreacceccacceagecr 1728 CGCCATCCTGGATAGTGCCTTCCTGCTGTC 1788 3470 CCGCTCCTGTTAGCCCCATGGGCTGCCGGG 2028 raatgiggcictctgctgccaccctgtgctg 2088 3170 SCCTGCTCCCACCTCCACCCGCGCTCTGCGG 3230 CATTGTCCAGCTCAGCCAGTCTGTCACTGC 1848 3GGGTTTCAGTCTGGACTTATACAGGGAGGC 2208 CAAATACCGAGGGACACTGGAGGTGCTAG 1548 GGTCGCCATTTACTTTGCTACACAGGTAGT 1908 AGCGTAGAAACTTCCAGCACATTGGGGTG 1968 CCACAGTGTGGCCGTGGTGACAGCTTCAGC 1428 GCAGATCCTGCCCTACACACTGGCCTCCCT 1488 GCCAGGCCCTAAGCCTGGAGCTCCCTTCCC 1608 CCTGCTCCCACCTCCACCGGGCTCTGCGG 1668 GCCCATCTCCCTGGTCTTCTCTCTGGTCAT 2870 GGGGTTTCAGTCTGGACTTATACAGGGAGGC AGCGTAGAAAACTTCCAGCACATTGGGGTG CCACAGTGTGGCCGTGGTGACAGCTTCAGC GCCAGGCCCTAAGCCTGGAGCTCCCTTCCC AGCAGTCTATTTGGCCAGTGTGGCAGCTTT

| Db       | 3591 | CTGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTG 3650                                                                |  |
|----------|------|----------------------------------------------------------------------------------------------------------------------------------|--|
| Qy       | 2089 | CTGAGGTGCGTAGCTGCACAGCTGGGGCTGGGGCGTCCCTCTCCTCTCTCCCCAGTCTC 2148                                                                 |  |
| οy       | 14   | GGCTGCCTGCCTGGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGGGGC 220                                                                      |  |
| qq       | 3711 |                                                                                                                                  |  |
| Qy<br>Db | 3771 | CAGAAGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGG 2268                                                                 |  |
| Qy       | 2269 | CACCTAGAGAAGGGTTTTTGGGAGCTGAATAAA 232                                                                                            |  |
| qq       | 3831 | TAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGC                                                                                     |  |
| oy<br>Pr | 32   | TCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCT 238                                                                  |  |
| a :      | 389L | ICAGICACCIGGITICCCATCICTAAGCCCCTTAACCIGCAGCITCGTTTAAIGIAGCT 395                                                                  |  |
| 7 a      | 95.  | CITGCATGGGGGTTTCTAGGATGAACACTCCTCCATGGGATTTGAACATATG-ACTTA 2446 CITGCATGGGAGTTTCTAGGATGAAACACTCCACCATGGGATTTGAACATATGAAGTTA 4010 |  |
| Qy       | 2447 | TITGTAGGGGAAGAGICCIGAGGGGGAACACACACAGAACCAGGICCCCICAGCCCACAGC 2506                                                               |  |
| Dp       | 4011 | TTGTAGGGGAAGAGTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCAAAG                                                                       |  |
| oy<br>1  | 50   | 256                                                                                                                              |  |
| ga       | 0    | LTTTTTGCTGATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGT                                                                             |  |
| oy<br>Ob | 4131 | TTCTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAATTAA                                                                           |  |
| Οy       | 27   | SAATCCATTGCTAGGTTTTCTGTGTTTGGTGTTTTGGGTAGGGTGGGGG 268                                                                            |  |
| QQ       | 4191 | 25                                                                                                                               |  |
| λο d     | 687  | T 274                                                                                                                            |  |
| a<br>C   | 251  | CCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATC                                                                        |  |
| oy<br>Op | 2747 | TCTTCTCCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCA 2806<br>                                                            |  |
| QY       | 2807 | CCCAAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAG                                                                            |  |
| qq       | 4371 | 43                                                                                                                               |  |
| À á      | 867  | TGGT 292                                                                                                                         |  |
| a .      | 7 1  | 3666UTTCAGGTCTCAACGCTTCCCTAACCACCCCTCTTCTCTT                                                                                     |  |
| oy<br>Dp | 2927 | TICCCCCACTTCCACTCCCCTCTACTCTCTGAGACTGGGCTGATGAAGGCACTGCCCA 2986<br>                                                              |  |
| òò.      | 2987 | **************************************                                                                                           |  |
| q q      | 51   | 61                                                                                                                               |  |
| Qy<br>Db | 3047 | TGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATC 3106<br>                                                            |  |
| ογ       | 07   | CAGCCCCCAGAGTATATCTGTTGGGGAATCTCACACAGAAACTCAGGGGCCCCC 316                                                                       |  |
| qq       | 4671 | 73                                                                                                                               |  |

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PAT 26-OCT-2001
 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A., Hepler,W.T.
and Henderson,R.A.
 1311 GGCATTGGTCCAGTGCTGGCCTGGTCTGTGTCCCTAGGCTCAGCCAGTGACCAC 1370
 1371 TGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTG 1430
 1431 CTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGTGCTGTGCCCGGATCCC 1490
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 Compositions and methods for the therapy and diagnosis of prostate
 514
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 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 others
 linear
 DNA
 Patent: WO 0173032-A 702 04-OCT-2001;
CORIXA CORPORATION (US)
 1163 t
 Ouery Match
62.8%; Score 2142.8;
Best Local Similarity 80.1%; Pred. No. 0;
Matches 2872; Conservative 1; Mismatches
 AX267728 4894 bp 1
Sequence 702 from Patent W00173032.
AX267728
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 Location/Qualifiers
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|-------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------------------------------------------------|----------------------------------------------------------------|-------|----------------------------------------------------------------|--------------------------------------------------------|------------------------------------------------------------------------------------------------------|------------------------------------------------------------------|-----------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------|-------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|------------------------------------------------------------------------|------------------------------------------------------------------------------------|------------------------------------------------------------------------|-------------|
| 575 CTGAGCCTCTTTCTCATCCCAAGGCCGGCTGCTAGCAGGCTGCTGTGCCCGGATCCC 634 | 635 AGGCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAG 694 | 695 GTGTGCTTCACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGT 754  151 | 755 CGCCAGGCCTACTCTGTCTATGATCAGTCTTGGGGGCTGCCTGGGCTACCTC 814   |       | TGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG 93 | GCTGAGGGCGCTGGCTCACCTCACTCTCACTCACGGCGCCCTCCTCCTCGCTCG | 95 TCGCCCCACTGCCTCCCTCCGGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTCCTT 105 T11111111111111111111111111111111 | 55 CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCTGCGCCGGCTGTTCGTGGCT 1 | GAGCTGTGCAGCTGGATGCCTCCATGACCTTCACCCTGTTTTACACGCATTTCGTGGCC 117 | GAGGGCTGTACCAGGTGGCCCCAGAGCTCACCCTCACGCTGTTTTACACGGATTTCGTGGGCC 209  GAGGGGCTGTACCAGGGCGTGCCCCAGAGCTGAGCCGGGCCACCGAGGCCCGGAGACACTAT 123 | GAGGGGGTGTATACCAGGGCGTGTCCCCAGAGCTGAGCCCGGGCCACCGAGGCCCGGGAGACTAT 20  GATGA | 2091 GATGAAGGTAAGGCCTTGGCAGCAGCAGAGGCTGGTGTGGGAGCCGCCCACCAGAGACG 150                                                                                                                                  | 2151 ACACTCGGGGCTGTGTGTGGGCTGTGCCTCTCCATCCTGGCCCCGACTTCTCTGTCAGG 2210 | 2211 AAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCT 2270<br>1240 1239 | 2271 TGCGGTTTCAGGAAGGCCTCTGGCTGTTAGGAGTCTGATCAGAGTCGTTGCCCCAGTT 2330                                                           | 1240 1239<br>2331 TCAPTAGAAGGAAAAGGGGAAGTTTAAAGTGTAAGAGGGAGG | 240                                                                    | 2391 ATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCAACGACTTTCCAA 2450<br>1240 1239 | 2451 ATAATCTCACCAGGGCCTTCCAGGTCAGGGGTCCTAGAAGCGTCTTGAAGCCTATGGCCA 2510 | , 1240 1239 |
| Qy<br>Dp                                                          | Qy<br>Dp                                                            | č d                                                                     | çy<br>D                                                        | 6 6 G | à à                                                            | 8 8 8                                                  | 8 8 8                                                                                                | , oy                                                             | 0 y                                                             | gg Ko                                                                                                                                   | δδ                                                                          | g Å                                                                                                                                                                                                   | Db<br>Qy                                                              | a ò                                                                                 | g qa                                                                                                                           | VO 45                                                        | G · O                                                                  | do yo                                                                              | qa                                                                     | Qy          |

| qa    | QV    | Qy                                                      | qq    | Qy                                                  | 03                                                     | qa<br>qa                                                        | رم<br>م | a o | g a                                                           | ογ                                                                | qa                                                                  | Qy                                                              | අ                                                                      | RESULT<br>AX20099 | LOCUS                                                      | ACCESSI<br>VERSION<br>KEYWORD                                             | SOURCE                                                               |                                                                      | REFEREN<br>AUTHO: | TITLE                                  | JOURN                           | FEATURE |                                                                    | BASE COU | Query   | Best I<br>Matche                                                     | Qy      | qq                                                                   | Qy      | qa                                                                     |
|-------|-------|---------------------------------------------------------|-------|-----------------------------------------------------|--------------------------------------------------------|-----------------------------------------------------------------|---------|-----|---------------------------------------------------------------|-------------------------------------------------------------------|---------------------------------------------------------------------|-----------------------------------------------------------------|------------------------------------------------------------------------|-------------------|------------------------------------------------------------|---------------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|-------------------|----------------------------------------|---------------------------------|---------|--------------------------------------------------------------------|----------|---------|----------------------------------------------------------------------|---------|----------------------------------------------------------------------|---------|------------------------------------------------------------------------|
|       | 3 186 | 69 GCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG | 50    | CCAAATACTCAGGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT | I CCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT | 989 UCCAGGITUCUGITIAGUCCCATGGGGTGCCGGGCTGGCCGCCAGTTTCTGTTG 2048 | on.     | _   | 109 GCTGGGGGCTGGGCGTCTCTCTCTCCCCAGTCTTAGGCTGCCTGACTGGAGG 2168 | CCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCCAGAAGGGCTCCATGCACTG 222 | 1741 CCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGGGGCCAGAAGGGCTCCATGCACG 1800 | 229 GAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTTAACAGCTAGCCTCCTAGT 2288 | 1801 GAATGCGGGGACTCTGCAGGTGGATTACCCAGGGTCAGGGTTAACAGCTAGCCTCCTAGT 1860 | 34                | ACTION CARGO CANDON AND AND AND AND AND AND AND AND AND AN | 349 TCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG 2408<br> | 2409 AIGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGAGTCCTG 2466 | 981 ATGAAACACTCCTCCATGGGATTTGAACATATGAAGTTATTTGTAGGGGAAGAGTCCTG 2040 | 4 - 25            | CCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | OU CCCCCTCTTACCAGATION CONTROLL | 26      | 61 CACAGGCATITAAATATTTAAACTTAATTTAACAAAGTAGAAGGGAATCCATTGCTAG 2220 |          | CTTT    | 07 CTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGGCC 2766 |         | 67 CCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAA 2826 | - 0     | 27 TGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGTGGGGTTCAGGTCTCAAC 2886<br> |
| Db 13 | Qy 18 | 0y 18                                                   | Db 14 |                                                     |                                                        | Uy 198                                                          | 74      | -   | Oy 210<br>Db 168                                              | Qy 216                                                            | Db 17                                                               | Qy 22                                                           | Db 18                                                                  | Oy 22             |                                                            | Qy 23.<br>Db 19.                                                          | Qy 24                                                                | Db 19                                                                | Oy 24(            |                                        | 1 (7                            | Qy 256  | Db 2161                                                            | Qy 2647  | Db 2221 | Qy 2707                                                              | Db 2281 | Qy 276                                                               | Db 2341 | Qy 2827                                                                |
|       |       |                                                         |       |                                                     |                                                        |                                                                 |         |     |                                                               |                                                                   |                                                                     |                                                                 |                                                                        |                   |                                                            |                                                                           |                                                                      |                                                                      |                   |                                        |                                 |         |                                                                    |          |         |                                                                      |         |                                                                      |         |                                                                        |

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3126
 3186
 2760
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 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4894)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
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/db_xref="taxon:9606"
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 3307 AAGGCTTTCTTATATGTTTAAAAA 3330
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| 1010 | Db 241 CCATGCCGGGCCCGCTTG | Qy 1070 CTGTGCTGCCGCATGCCC                                       | 1130                                                                      | 361                                                               | Qy 1190 GGCGTGCCCAGAGCTGAG                                           | 421                                                              | Db 481 CTGGCTGCTCTAGGAGTC | оу 1241                                                         | · Db 541 GCTTATTCAAAGTCTAGA                                               | Qy 1241 | Db 601 CCAGCCGCAGTGTGCCCT | Оу 1241                                      | Db 661 CCAGCTCAGGCGTCCTAG             | Oy 1241 | Db 721 TCACCCGCCTGTCCTCAC | Oy 1241                                                                                                                         | Db 781 TTCAGCAAGGGGCGTTGC                                           | Qy 1269 TCTGCAGTGCGCCATCT                                                                                                                 | Db 841 TCCTGCAGTGCCCATCT                                                                     | Qy 1329 TCGGCACTCGAGCAGTCT                    | Db 901 resecacresacagre      | Qy 1389 CATGCCTGTCCCACAGTC | Db 961 CATGCCTGTCCCACAGT           | QY 1449 TCTCAGCCCTGCAGATC | 1021                                                                      | Qy 1509 TGTTCCTGCCCAAATAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 1081                                                              |                                                            | -                                                                     | QY 1629 GAGGCAGTGCCTGCTC                    | 1201                                             | Db 1261 CCGTACGTGGGTGGTG                                         |                                                                     |
|------|---------------------------|------------------------------------------------------------------|---------------------------------------------------------------------------|-------------------------------------------------------------------|----------------------------------------------------------------------|------------------------------------------------------------------|---------------------------|-----------------------------------------------------------------|---------------------------------------------------------------------------|---------|---------------------------|----------------------------------------------|---------------------------------------|---------|---------------------------|---------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------|-----------------------------------------------|------------------------------|----------------------------|------------------------------------|---------------------------|---------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|------------------------------------------------------------|-----------------------------------------------------------------------|---------------------------------------------|--------------------------------------------------|------------------------------------------------------------------|---------------------------------------------------------------------|
|      | m (                       | AGGACAAAGTIGCGGTTTCCCAAGCCTTTTGCCATCTCAGCCCCAGAGCTGTAGTGTTTTTTTT | Db 2641 CCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCT 2700 | 3127 GTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCGTGCCTGAGCTAAGGGAGGTC | 2701 GIGCTIGGGGAATCICACACAGAAACTCAGGAGCACCCCTGCCTGAGCTAAGGGAGGTC 276 | Oy 3187 TTATCTCTCAGGGGGGGGGTTTAAGTGCCGTTTGCAAATGTCGTCTTATTTTTTTT |                           | ZOZI GGIGMAINIIIANAGINAGINAGINAGINAGINAGINAGINIANAGINIANAGINAGI | Oy 330/ AAGGCTTCTTATATGTTTAAAA 3330  NA 2881 AACGCTTTCTTATATTATATATA 3330 |         | RESULT 13                 | LAXA0/129 2904 bp DNA linear PAT 26-OCT-2001 | JON Sequence /US Ifom Faceil WOOI/303 | N SO    |                           | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. | AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., | Kalos, M.D., Fanger, G.K., Ketter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li,S.X., Wang, A., Skeiky, Y.A., Hepler, W.T. | and Henderson, R.A. TITLE Compositions and methods for the therapy and diagnosis of prostate | JOURNAL Patent: WO 0173032-A 703 04-OCT-2001; | FEATURES Location/Qualifiers | source I2904  //           | BASE COUNT 542 a 875 c 773 g 714 t | · 45+                     | Similarity 88.2%; Pred. No. 0;<br>0; Conservative 0; Mismatches 1; Indels | 770 CTTTTATION TO A TO A TOTAL TO A CTT CAGA THE CTT CAGA THE CTT CAGA THE CTT CAGA THE A CTT CA | 1 GTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTTGCCATGAC 60 | 830 TGGGACCACCAGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTG | Db 61 TGGGACACCAGTGCCCTGGGCCCCTACCTGGGCACCAGGAGGAGTGCCTCTTTGGCCTG 120 | りのも、これは、これは、これには、これには、これには、これには、これには、これには、こ | CTCACCCTCATCTTCCTCACCTGCGTAGCACCCCCACACTGCTGGCTG | Qy 950 CTGGGCCCCACCGAGCAGAGGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGT 1009 | Db 181 CTGGGCCCCACCGAGCCAGCAGAAGGCTGTCGGCCCCCTTGTCGCCCCACTGCTGT 240 |

| ,             | <del>-</del> | 90                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 69  |
|---------------|--------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| 0             | 4            | ATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCCCCCTGCTTCCCCGGCTGCACCAG 300                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |
| <b>&gt;</b> 0 | 301          | CTGTGCTGCCGCATGCCCGCACCCTGCGCGGGTCTTCGTGGGTGAGCTGTGCAGCTGGGTGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 6 0 |
| . >-          | m            | GGCACTCATGACCTTCACGCTGTTTTACACGGATTCGTGGGCCGAGGGGCTGTACCAG 118                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 68  |
| ۵             | 361          | ATGCCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTGTACAGG 420                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |
| >-            | 1190         | 0 GGCGTGCCCAGAGCTGAGCCGGCACCGAGGCCCGGAGACACTATGATGAA 124                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 40  |
| ۵             | 421          | GGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGAAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     |
| >1            | 1241         | 124                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |     |
| ۵             | 481          | 54                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 0   |
| λ             | 1241         | 124                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 40  |
| Д             | 541          | 9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 0   |
| ٨             | 1241         | 124                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |     |
| а             | 601          | 99                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 0   |
| ٨             | 1241         | 12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 40  |
| q             | 661          | 72                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 0   |
| ۶۰            | 1241         | 12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 40  |
| ą             | 721          | 78                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 0   |
| ž             | 1241         | 12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 89  |
| ā             | 781          | 84                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 0   |
| Ā             | 1269         | 13                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 28  |
| ą             | 841          | ccrecaerececcarcrecerestrererestres are accesered en 90                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 0   |
| χ, q          | 1329         | SGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCA 13                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 888 |
| 3 2           | , α          | SCORETICE SET STREET STREET SANGETT CAGCCCC TO SCORE SANGET SANGETT SANGET SANGETT SANGETT SAN |     |
| ≿ a           | 96           | . 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ~   |
| Κį            | 1449         | CAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGAGAAGCAGG 15                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 909 |
| ą             | 1021         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 980 |
| λγ            | 1509         | GTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGA 15                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 999 |
| ą             | 1081         | PACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGA 11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 140 |
| λλ            | 1569         | SCTCCCTTCCCTAATGGACACGTGGGTGCTG 16                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Ö   |
| qc            | 1141         | CAGETICCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTG 12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Ō   |
| λλ            | 1629         | GAGGCAGTGGCCTGCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGTCT 16                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 8   |
| qc            | 1201         | AGGCAGTGGCCTGCTCCACCTCCACCGCGCTCTGCGGGGCCTCTGCCTGTGTGTT 12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ق   |
| λζ            | 68           | CCGTACGTGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGCATCT 17.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 320 |
| q ;           | 1261         | CCGTACGTGGTGGGTGGGTGAGCCCACCGAGGCCCAGGGTGGTTCCGGGCCCGGGGGTGTTCT 13                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 808 |